GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2003, 11:13:02 ; Search time 17522 Seconds
(without alignments)
11673.789 Million cell updates/sec

Title: US-10-023-649-1_COPY_1_5000
Perfect score: 5000
Sequence: 1 accctacaaactaatcgatc.....ataattctagaaacgccacc 5000

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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9: gb_pr:*
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11: gb_sts:*
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16: em_fun:*
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32: em_htg_other:*
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37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5000	100.0	11484	14	AF214040	AF214040 Western e
2	3536	70.7	4471	14	WEU01065	U01065 Western equ
3	3536	70.7	4498	14	WEEVNS	X74892 Western equ
4	2766	55.3	11678	14	U01034	U01034 Eastern equ
5	2745.2	54.9	11675	14	EEEVIRNA	X63135 Eastern Equ
6	2133.4	42.7	11441	14	VEU55362	U55362 Venezuelan
7	2128.6	42.6	11420	14	AF004472	AF004472 Venezuela
8	2123.8	42.5	11420	14	AF004458	AF004458 Venezuela
9	2122.2	42.4	11444	14	EEVCOMGEN	L04653 Venezuelan
10	2120.6	42.4	11423	14	VEU55347	U55347 Venezuelan
11	2119.6	42.4	11447	14	EEVNSPEPA	L01442 Venezuelan
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13	2119	42.4	11420	14	VEU55360	U55360 Venezuelan
14	2119	42.4	11423	14	AF375051	AF375051 Venezuela
15	2119	42.4	11423	14	VEU55342	U55342 Venezuelan
16	2118	42.4	11444	14	EEVNSPENV	J04332 Venezuelan
17	2118	42.4	11445	14	AF069903	AF069903 Venezuela
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42	1584.8	31.7	7422	14	SFO251359	AJ251359 Semliki F
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ALIGNMENTS

RESULT 1
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LOCUS AF214040 11484 bp RNA linear VRL 27-JAN-2000
DEFINITION Western equine encephalomyelitis virus strain 71V-1658 nonstructural polyprotein and structural polyprotein genes, complete cds.
ACCESSION AF214040 AF143811
VERSION AF214040.1 GI:6760410
KEYWORDS .
SOURCE Western equine encephalomyelitis virus
ORGANISM Western equine encephalomyelitis virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae; Alphavirus; WEEV complex.
REFERENCE 1 (bases 1 to 11484)
AUTHORS Netolitzky,D.J., Schmaltz,F.L., Parker,M.D., Rayner,G.A.,

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          Fisher,G.R., Trent,D.W., Bader,D.E. and Nagata,L.P.
  TITLE   Complete genomic RNA sequence of western equine encephalitis virus
          and expression of the structural genes
  JOURNAL J. Gen. Virol. 81 (Pt 1), 151-159 (2000)
  MEDLINE 20109043
   PUBMED 10640553
REFERENCE 2  (bases 1 to 11484)
  AUTHORS Netolitzky,D.J., Schmaltz,F.L., Parker,M.D., Rayner,G.A.,
          Fisher,G.R., Trent,D.W., Bader,D.E. and Nagata,L.P.
  TITLE   Direct Submission
  JOURNAL Submitted (08-DEC-1999) Medical Countermeasures Section, Defence
          Research Establishment Suffield, P.O. Box 4000, Stn Main, Medicine
          Hat, Alberta T1A 8K6, Canada
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Db      2341 AATGGGGTTAAGCACCCCGTTAACACTCTGTACATTGATGAGGCATTTGCCTGCCATGCA 2400

Qy      2401 GGGACGCTGCTGGCACTGATTGCCATCGTCAAACCTAAGAAAGTGGTATTGTGCGGGGAC 2460
Db      2401 GGGACGCTGCTGGCACTGATTGCCATCGTCAAACCTAAGAAAGTGGTATTGTGCGGGGAC 2460

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Qy      2521 TGCACTGAAGTGTACCATAAAAGCATCTCTAGGAGGTGCACACAGACTGTAACCGCCATC 2580
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Qy      2581 GTCTCCACGCTCTTCTACGACAAGCGAATGAAGACGGTTAACCCATGTGCTGATAAAATC 2640
Db      2581 GTCTCCACGCTCTTCTACGACAAGCGAATGAAGACGGTTAACCCATGTGCTGATAAAATC 2640

Qy      2641 ATCATAGATACCACAGGGACCACAAAGCCGCACAAAGATGATCTGATTCTAACCTGTTTC 2700
Db      2641 ATCATAGATACCACAGGGACCACAAAGCCGCACAAAGATGATCTGATTCTAACCTGTTTC 2700

Qy      2701 AGAGGATGGGTGAAACAGCTACAGATTGACTACAAAAATCACGAAATCATGACTGCGGCT 2760
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Db      2701 AGAGGATGGGTGAAACAGCTACAGATTGACTACAAAAATCACGAAATCATGACTGCGGCT 2760
Qy      2761 GCATCGCAAGGACTTACGCGGAAAGGCGTTTATGCTGTCAGGTACAAAGTCAACGAGAAT 2820
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Db      2821 CCACTCTACTCGCAGACTTCTGAGCACGTGAACGTGTTACTTACACGCACAGAAAAACGC 2880
Qy      2881 ATTGTCTGGAAGACGCTAGCTGGTGATCCCTGGATAAAGACACTTACAGCTAAATATCCC 2940
Db      2881 ATTGTCTGGAAGACGCTAGCTGGTGATCCCTGGATAAAGACACTTACAGCTAAATATCCC 2940
Qy      2941 GGGGATTTCACGGCTTCATTGGACGACTGGCAGCGCGAACACGACGCCATTATGGCACGC 3000
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Qy      3121 ACGTTGCACCCATTCAAGCATGACAGAGCGTACTCACCTGAAATGGCACTGAACTTCTTT 3180
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Qy      3181 TGCACCAGGTTCTTTGGAGTAGACCTGGACAGTGGGTTATTTTCCGCTCCTACCGTCGCA 3240
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Qy      3301 AGAGAGGTAGCAAAGGAGTTGTCACGGCGATATCCGTGCATCACAAAAGCGGTTGACACA 3360
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Qy      3361 GGCAGGGTAGCTGATATAAGGAATAATACCATCAAGGACTACTCTCCAACAATTAATGTG 3420
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Qy      3721 CACAGCATGCTAACGTGTAAGGCTGTCCACCACCTGAACACTGGCGGAACATGTGTGGCT 3780
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Qy      3781 ATAGGGTATGGGCTTGCTGATCGCGCAACCGAGAATATCATCACTGCGGTGGCACGCTCA 3840
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Qy      4141 GATAGACAGCCAATAGCTGTCGGGACGGCTAGACTTGTGAAGCACGAACCGCTCATCATA 4200
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Db      4381 CACCTGTTCACTGCTTTCGACACTACGGATGCCGATGTCACCATATATTGCTTGGATAAA 4440
Qy      4441 CAATGGGAGACCAGGATAATCGAGGCCATTCACCGCAAAGAAAGCGTCGAAATTCTGGAT 4500
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Qy       4921 AAACCAGTCCTGTTTTCAGGCGTCGTACCACCGGCTGTACACCCCAGGAAGTACGCGGAA 4980
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Qy       4981 ATAATTCTAGAAACGCCACC 5000
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Db       4981 ATAATTCTAGAAACGCCACC 5000


RESULT 2
WEU01065
LOCUS       WEU01065                4471 bp    RNA     linear   VRL 01-JUN-1995
DEFINITION  Western equine encephalomyelitis virus nonstructural polyprotein
            gene, partial cds.
ACCESSION   U01065
VERSION     U01065.1  GI:393033
KEYWORDS    nsP1; nsP2; nsP3; nsP4.
SOURCE      Western equine encephalomyelitis virus
  ORGANISM  Western equine encephalomyelitis virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
            Alphavirus; WEEV complex.
REFERENCE   1  (bases 1 to 4471)
  AUTHORS   Weaver,S.C., Hagenbaugh,A., Bellew,L., Netesov,S.V., Volchkov,V.E.,
            Chang,G.J., Clarke,D.K., Gousset,L., Scott,T.W., Trent,D.W. and
            Holland,J.J.
  TITLE     A comparison of the nucleotide sequences of eastern and western
            equine encephalomyelitis viruses with those of other alphaviruses
            and related RNA viruses
  JOURNAL   Virology 197 (1), 375-390 (1993)
  MEDLINE   94025587
   PUBMED   8105605
REFERENCE   2  (bases 1 to 4471)
  AUTHORS   Weaver,S.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-AUG-1993) Scott C. Weaver, Biology, University of
            California, San Diego, La Jolla, CA 92037-0116 USA
FEATURES             Location/Qualifiers
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BASE COUNT     1272 a   1110 c   1116 g    973 t
ORIGIN

  Query Match           70.7%;  Score 3536;  DB 14;  Length 4471;
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  Matches 3594;  Conservative    0;  Mismatches   75;  Indels    3;  Gaps    1;

Qy       1332 AACAATTAAGAAAGTACCTGCCGTCTTTGACTCATTTGTGATTCCACGCCTTACCAGCCA 1391
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             |||||  ||||| ||  | |  ||||||  || ||||||||||||||||||||||||||||
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Qy       1512 AGAAGTGGCTGCAGCGGAAGAGATCAGAGAAGCCCTGCCACCCTTGCTCCCTGAAATAGA 1571
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Qy       1572 AAAAGAGACCGTAGAGGCAGAAGTAGACCTCATTATGCAAGAGGCAGGAGCAGGTAGCGT 1631
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Qy       1632 GGAGACACCACGAGGACACATCAGGGTGACAAGTTACCCAGGCGAAGAGAAGATTGGGTC 1691
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Qy       1692 TTACGCTATACTTTCACCCCAGGCGGTATTGAATAGTGAAAAACTGGCGTGTATCCACCC 1751
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Qy       1752 ATTGGCGGAACAAGTACTGGTAATGACTCACAAAGGTAGGGCAGGGAGATACAAAGTCGA 1811
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Qy       1812 GCCATACCACGGTAAGGTCATTGTACCAGAAGGGACGGCGGTCCCTGTTCAAGACTTCCA 1871
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Qy       1872 GGCATTGAGTGAGAGCGCTACGATCGTTTTCAACGAGAGGGAGTTCGTAAACAGATACCT 1931
             |||| ||||||||||||| ||||||||||||||||||||||||||||||||||||||||  |
Db         541 GGCACTGAGTGAGAGCGCCACGATCGTTTTCAACGAGAGGGAGTTCGTAAACAGATATTT 600

Qy       1932 GCACCACATCGCAATCAACGGAGGAGCGCTAAACACTGACGAAGAGTACTATAAGACTGT 1991
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Qy       1992 AAAGACTCAGGACACAGACTCAGAATACGTCTTCGATATTGACGCACGAAAGTGTGTTAA 2051
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Qy       2052 GCGAGAAGACGCAGGTCCCTTGTGCCTAACCGGTGATCTGGTAGATCCACCATTTCACGA 2111
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Qy       2112 GTTTGCGTACGAGAGTCTCAAGACACGACCAGCAGCACCTCACAAAGTCCCAACCATCGG 2171
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Db        781 GTTTGCGTACGAGAGTCTCAAGACACGACCAGCAGCACCTCACAAAGTCCCAACCATCGG 840
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Db        841 AGTCTATGGAGTGCCAGGTTCAGGTAAATCTGGAATCATCAAAAGCGCTGTGACTAAGAA 900
Qy       2232 AGATCTGGTTGTGAGTGCGAAGAAGGAAAACTGCGCAGAAATCATCAGGGATGTAAGGAG 2291
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Qy       2352 GCACCCCGTTAACACTCTGTACATTGATGAGGCATTTGCCTGCCATGCAGGGACGCTGCT 2411
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Qy       2892 GACGCTAGCTGGTGATCCCTGGATAAAGACACTTACAGCTAAATATCCCGGGGATTTCAC 2951
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Qy       3132 ATTCAAGCATGACAGAGCGTACTCACCTGAAATGGCACTGAACTTCTTTTGCACCAGGTT 3191
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Qy       3252 GGATCAGCACTGGGATAACTCGCCAGGGAAGAACATGTATGGGCTTAATAGAGAGGTAGC 3311
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Qy       3492 CGGATTCCTATCTAAGATGAAGGGCAAATCTGTGTTGGTGATCGGCGATCCTATCAGCAT 3551
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RESULT 3
WEEVNS
LOCUS       WEEVNS                  4498 bp    RNA     linear   VRL 14-FEB-2003
DEFINITION  Western equine encephalomyelitis virus partial gene for
            nonstructural polyprotein, genomic RNA.
ACCESSION   X74892
VERSION     X74892.1  GI:398206
KEYWORDS    nonstructural polyprotein; NSP1; NSP2; NSP3; NSP4.
SOURCE      Western equine encephalomyelitis virus
  ORGANISM  Western equine encephalomyelitis virus
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REFERENCE   1
  AUTHORS   Yuferov,V.P., Volchkov,V.E., Netesov,S.V., Safronov,P.F. and
            Uryvaev,L.V.
  TITLE     Nucleotide sequence of the 26S mRNA and genes of nonstructureal
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  JOURNAL   Virusologia 28, 86-98 (1992)
REFERENCE   2  (bases 1 to 4498)
  AUTHORS   Uryvaev,L.V., Volchkov,V.E., Iuferov,V.P., Samokhvalov,E.I.,
            Lebedev,A.I., Safronov,P.F. and Netesov,S.V.
  TITLE     Primary structure of proteins of the nsP2 and nsP3 polymerase
            complex confirm the recombinant nature of western encephalitis
            virus
  JOURNAL   Dokl. Akad. Nauk SSSR 335, 813-818 (1994)
REFERENCE   3  (bases 1 to 4498)
  AUTHORS   Volchkov,V.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-1993) V.E. Volchkov, All-Union Institute of
            Molecular, Biology of NPO Vector, Koltsovo, Novosibirsk region,
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FEATURES             Location/Qualifiers
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ORIGIN
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Qy       1392 CGGGCTCGATATGGGCTTCCGCCGTAGGCTCAAGCTGCTGCTTGAACCAACTGTCAAACC 1451
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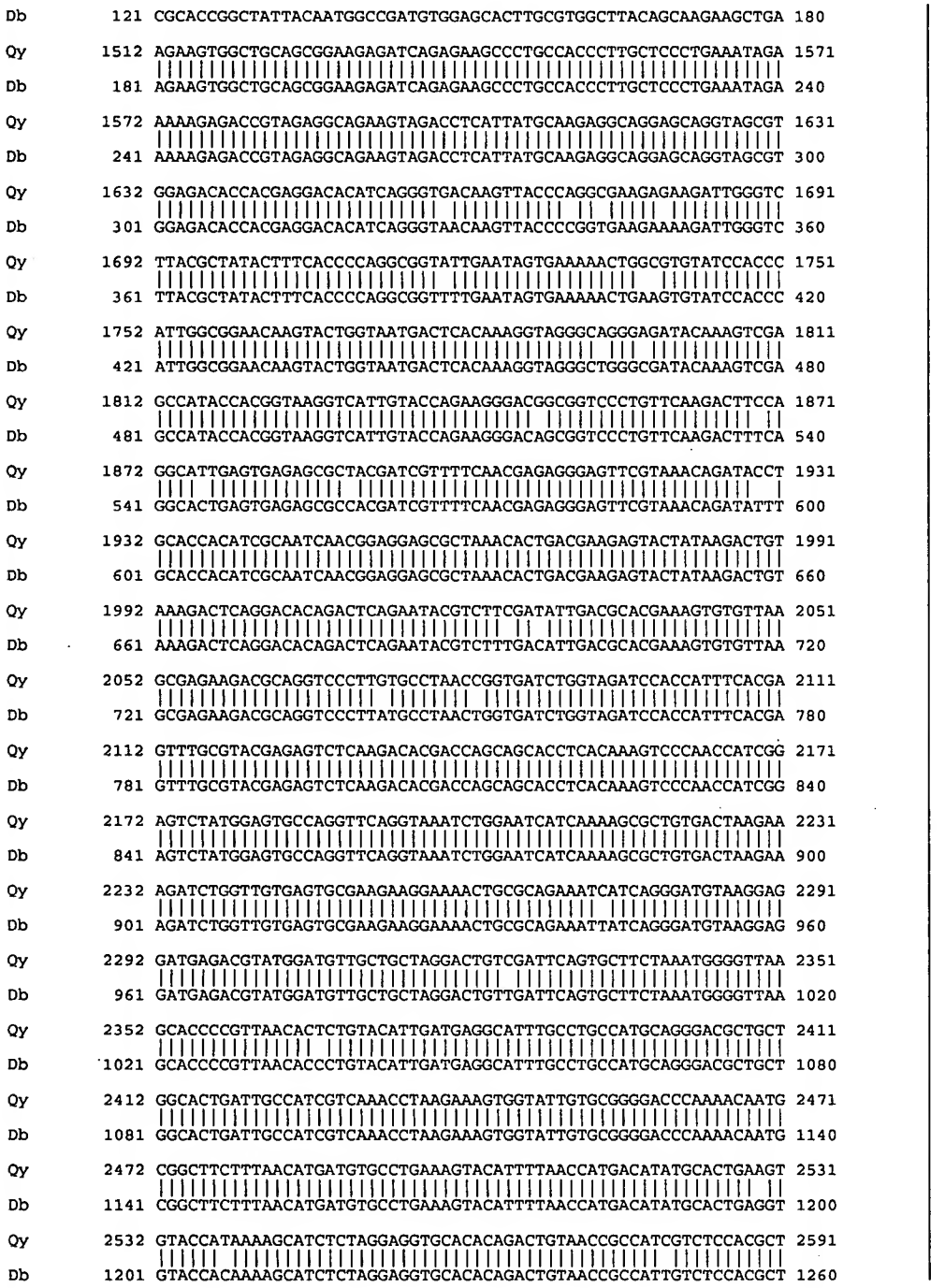
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RESULT 4
U01034

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LOCUS       U01034                 11678 bp    RNA     linear   VRL 02-MAR-2000
DEFINITION  Eastern equine encephalomyelitis virus North American antigenic
            variety nonstructural polyprotein and structural polyprotein genes,
            complete cds.
ACCESSION   U01034
VERSION     U01034.1  GI:393006
KEYWORDS    nsP1; nsP2; nsP3; nsP4; capsid; E3; E2; 6K; E1.
SOURCE      Eastern equine encephalitis virus
  ORGANISM  Eastern equine encephalitis virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
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REFERENCE   1  (bases 1 to 11678)
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            Holland,J.J.
  TITLE     A comparison of the nucleotide sequences of eastern and western
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  JOURNAL   Virology 197 (1), 375-390 (1993)
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  TITLE     Direct Submission
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Query Match 55.3%; Score 2766; DB 14; Length 11678;
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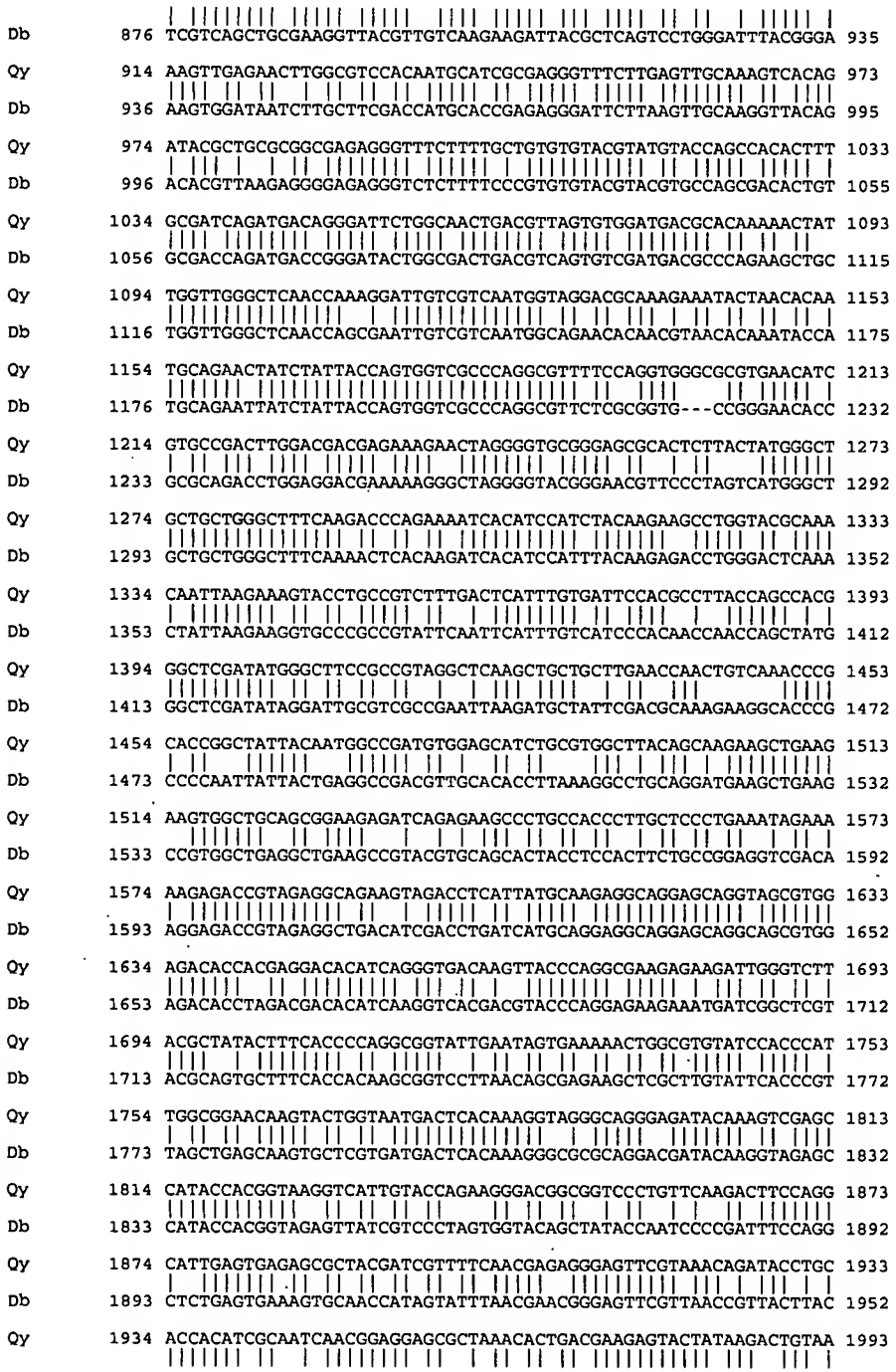
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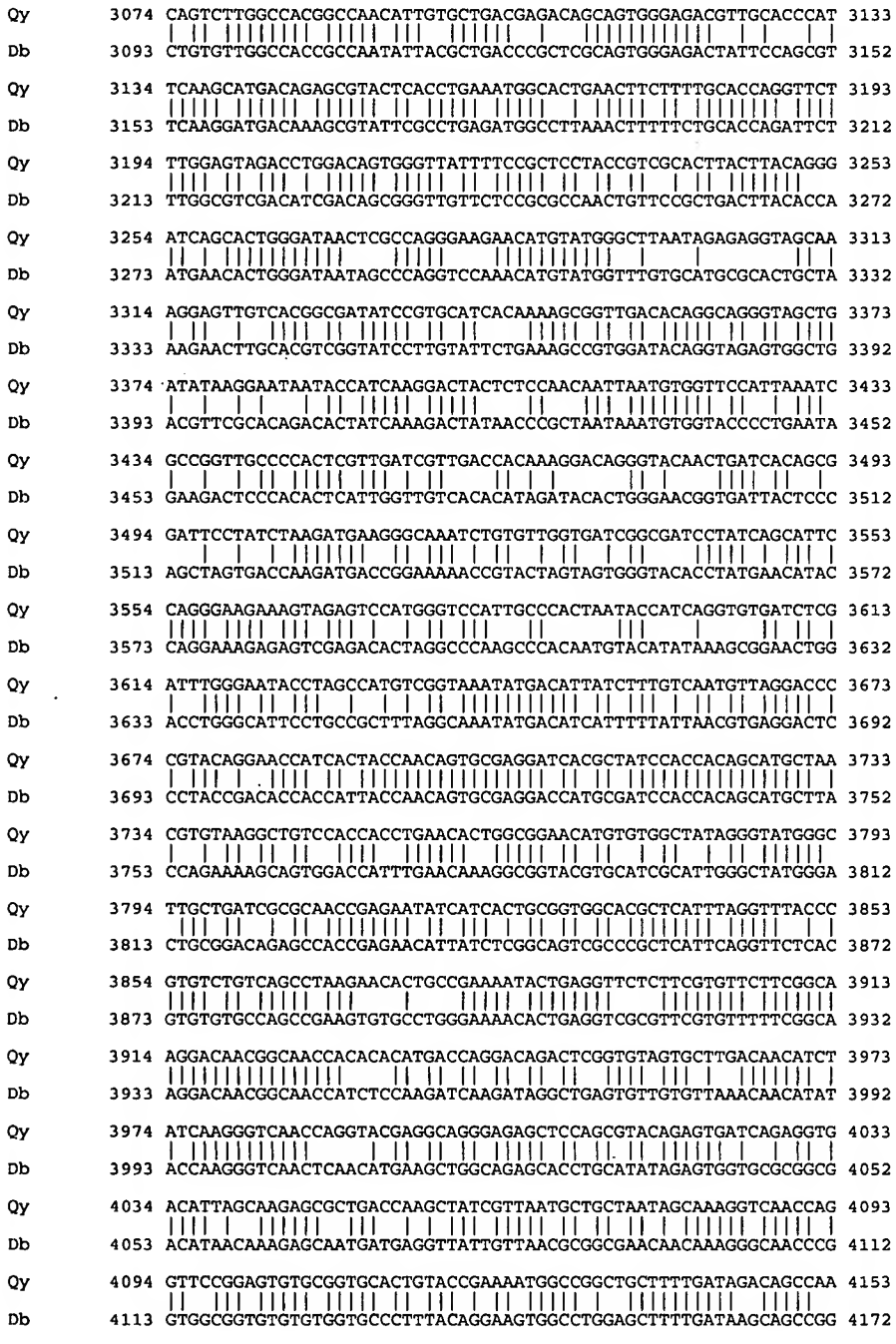

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VERSION X63135.1 GI:59185
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ORGANISM Eastern equine encephalitis virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
Alphavirus; EEEV complex.
REFERENCE 1 (bases 1 to 11675)
AUTHORS Volchkov,V.E., Volchkova,V.A. and Netesov,S.V.
TITLE Complete nucleotide sequence of the Eastern equine
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JOURNAL Mol. Gen. Mikrobiol. Virusol. 5, 8-15 (1991)

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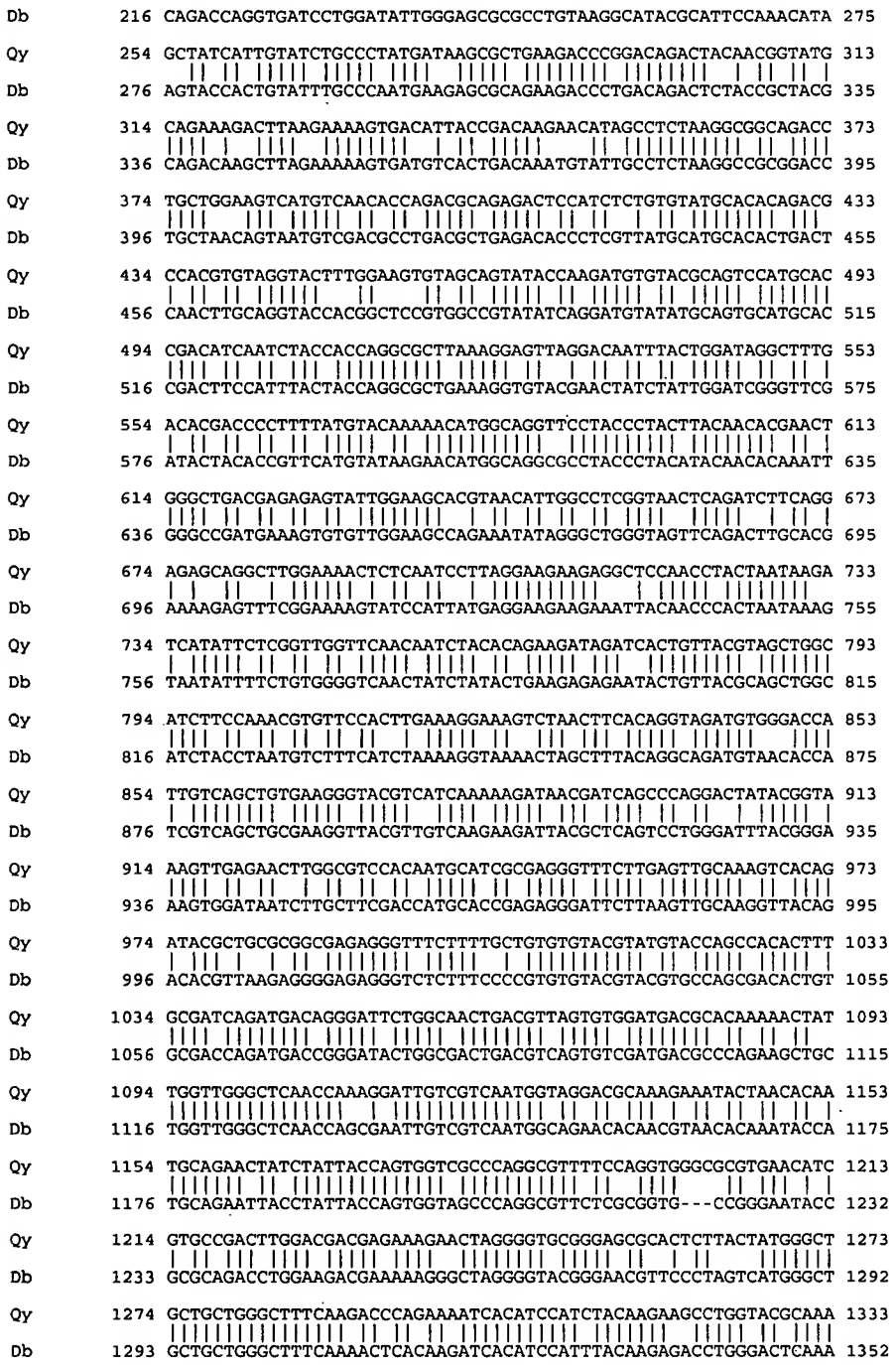
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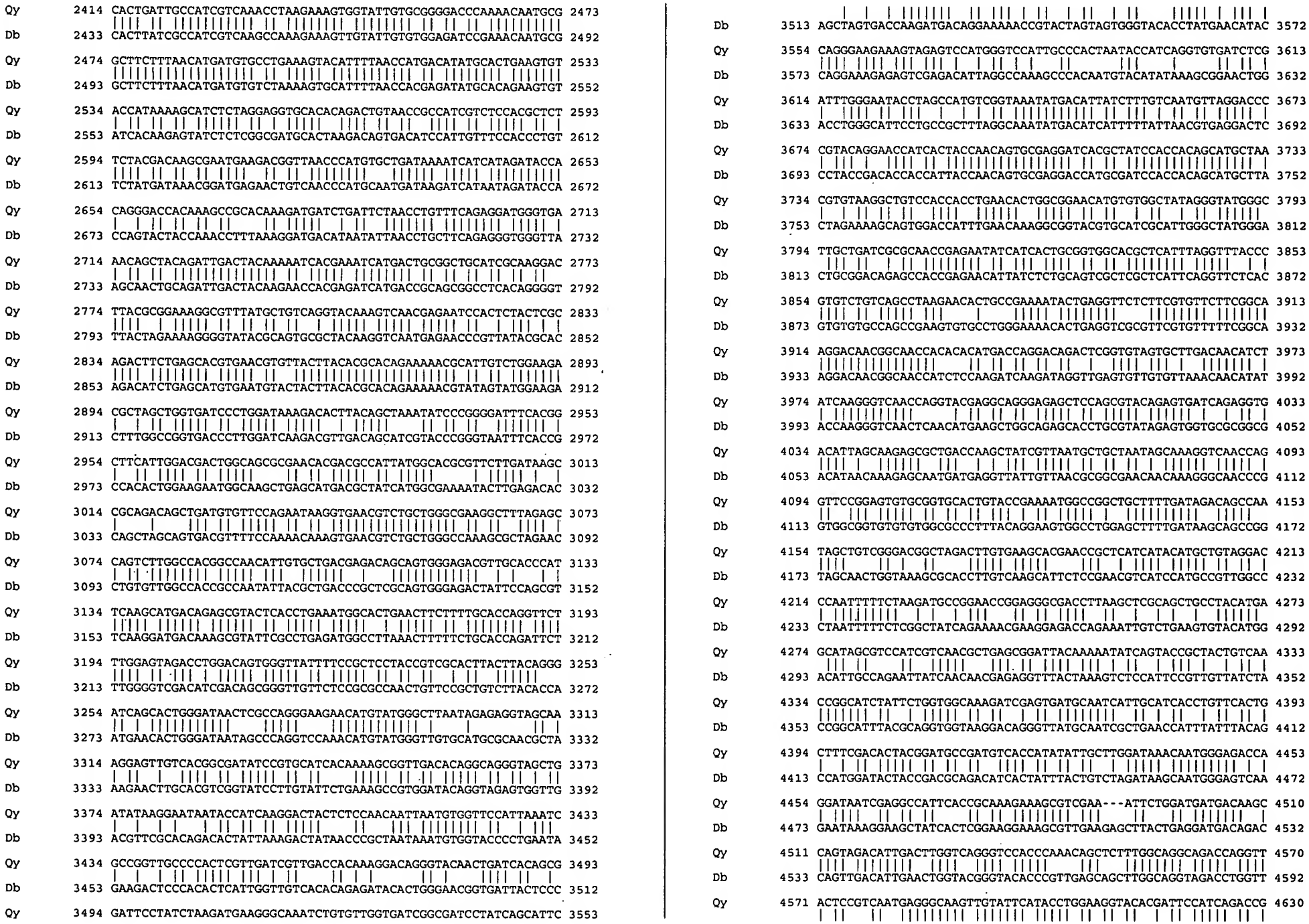

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RESULT 6
VEU55362
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DEFINITION Venezuelan equine encephalitis virus strain 83U434, complete genome.
ACCESSION U55362
VERSION U55362.2 GI:5442471
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SOURCE Venezuelan equine encephalitis virus
ORGANISM Venezuelan equine encephalitis virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae; Alphavirus; VEEV complex.
REFERENCE 1 (bases 8387 to 10063)
AUTHORS Weaver,S.C., Salas,R., Rico-Hesse,R., Ludwig,G.V., Oberste,M.S., Boshell,J. and Tesh,R.B.
TITLE Re-emergence of epidemic Venezuelan equine encephalomyelitis in South America. VEE Study Group
JOURNAL Lancet 348 (9025), 436-440 (1996)
MEDLINE 96332169
PUBMED 8709783
REFERENCE 2 (bases 1 to 11441)
AUTHORS Wang,E., Barrera,R., Boshell,J., Ferro,C., Freier,J.E., Navarro,J.C., Salas,R., Vasquez,C. and Weaver,S.C.
TITLE Genetic and phenotypic changes accompanying the emergence of epizootic subtype IC Venezuelan equine encephalitis viruses from an enzootic subtype ID progenitor
JOURNAL J. Virol. 73 (5), 4266-4271 (1999)
MEDLINE 99214366
PUBMED 10196323
REFERENCE 3 (bases 8387 to 10063)
AUTHORS Weaver,S.C.
TITLE Direct Submission
JOURNAL Submitted (18-APR-1996) Pathology, Univ. TX Med. Branch, 301 University Ave., Galveston, TX 77555-0609, USA
REFERENCE 4 (bases 8387 to 10063)
AUTHORS Weaver,S.C.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-1997) Pathology, Univ. TX Med. Branch, 301 University Ave., Galveston, TX 77555-0609, USA
REMARK Nucleotide and amino acid sequences updated by submitter
REFERENCE 5 (bases 1 to 11441)
AUTHORS Wang,E. and Weaver,S.C.
TITLE Direct Submission
JOURNAL Submitted (12-JUL-1999) Pathology, Univ. TX Med. Branch, 301 University Ave., Galveston, TX 77555-0609, USA
REMARK Sequence update by submitter
COMMENT On Jul 12, 1999 this sequence version replaced gi:3849808.
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ORIGIN

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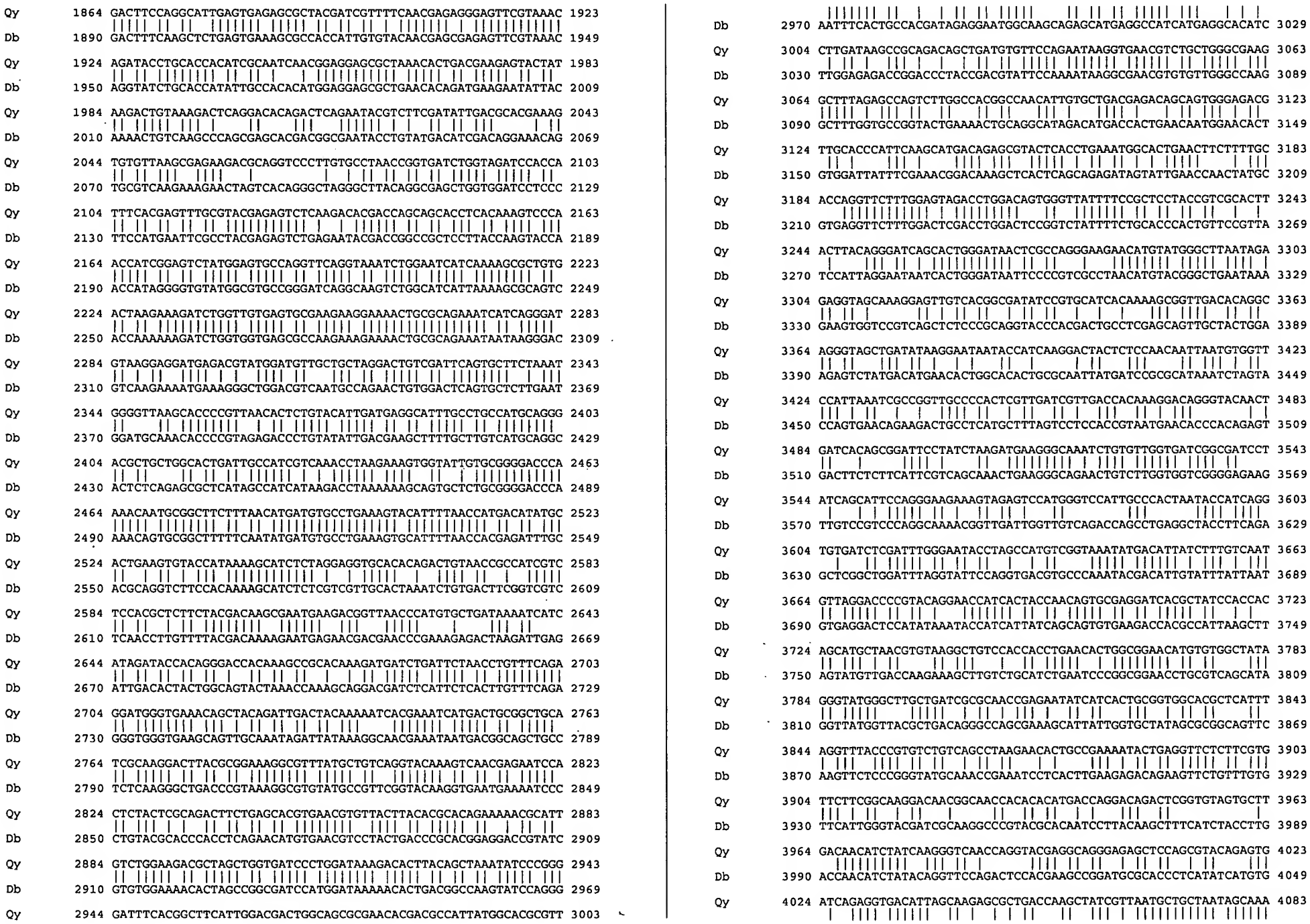

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VERSION     AF004472.2  GI:5442461
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REFERENCE   1  (bases 8366 to 10039)
  AUTHORS   Powers,A.M., Oberste,M.S., Brault,A.C., Rico-Hesse,R.,
            Schmura,S.M., Smith,J.F., Kang,W., Sweeney,W.P. and Weaver,S.C.
  TITLE     Repeated emergence of epidemic/epizootic Venezuelan equine
            encephalitis from a single genotype of enzootic subtype ID virus
  JOURNAL   J. Virol. 71 (9), 6697-6705 (1997)
  MEDLINE   97404681
   PUBMED   9261393
REFERENCE   2  (bases 1 to 11420)
  AUTHORS   Wang,E., Barrera,R., Boshell,J., Ferro,C., Freier,J.E.,
            Navarro,J.C., Salas,R., Vasquez,C. and Weaver,S.C.
  TITLE     Genetic and phenotypic changes accompanying the emergence of
            epizootic subtype IC Venezuelan equine encephalitis viruses from an
            enzootic subtype ID progenitor
  JOURNAL   J. Virol. 73 (5), 4266-4271 (1999)
  MEDLINE   99214366
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REFERENCE   3  (bases 8366 to 10039)
  AUTHORS   Powers,A.M., Oberste,M.S., Brault,A.C., Rico-Hesse,R.,
            Schmura,S.M., Smith,J.F., Kang,W., Sweeney,W.P. and Weaver,S.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-MAY-1997) Pathology, Univ. Texas Med. Branch,
            Galveston, TX 77555-0609, USA
REFERENCE   4  (bases 1 to 11420)
  AUTHORS   Wang,E. and Weaver,S.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JUL-1999) Pathology, Univ. Texas Med. Branch,
            Galveston, TX 77555-0609, USA
  REMARK    Sequence update by submitter
COMMENT     On Jul 12, 1999 this sequence version replaced gi:3849802.
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ORIGIN

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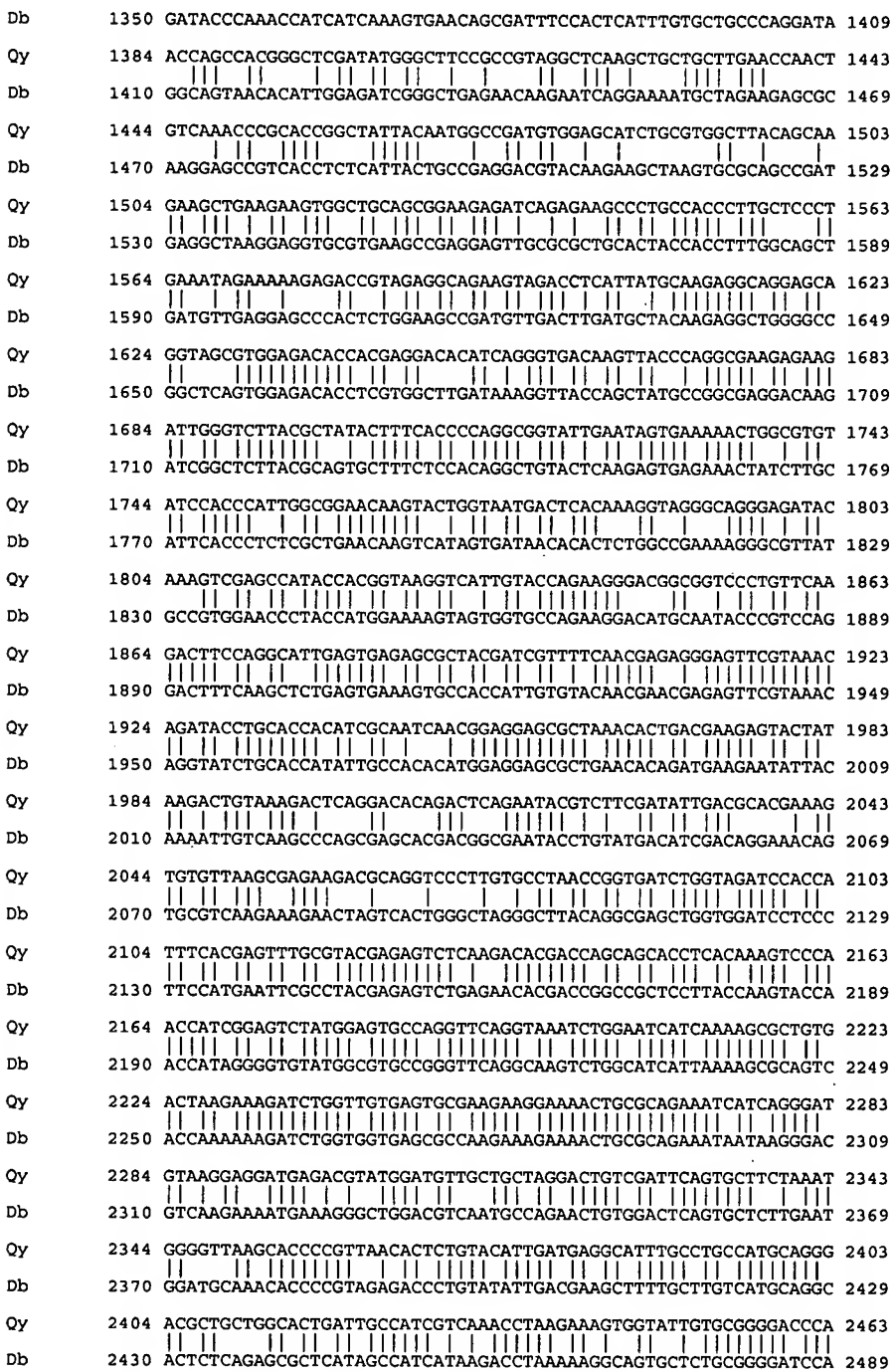
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LOCUS       AF004458               11420 bp    RNA     linear   VRL 12-JUL-1999
DEFINITION  Venezuelan equine encephalitis virus strain 66637, complete genome.
ACCESSION   AF004458
VERSION     AF004458.2  GI:5442458
KEYWORDS    .
SOURCE      Venezuelan equine encephalitis virus
  ORGANISM  Venezuelan equine encephalitis virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
            Alphavirus; VEEV complex.
REFERENCE   1  (bases 8366 to 9182)
  AUTHORS   Powers,A.M., Oberste,M.S., Brault,A.C., Rico-Hesse,R.,
            Schmura,S.M., Smith,J.F., Kang,W., Sweeney,W.P. and Weaver,S.C.
  TITLE     Repeated emergence of epidemic/epizootic Venezuelan equine
            encephalitis from a single genotype of enzootic subtype ID virus
  JOURNAL   J. Virol. 71 (9), 6697-6705 (1997)
  MEDLINE   97404681
   PUBMED   9261393
REFERENCE   2  (bases 1 to 11420)
  AUTHORS   Wang,E., Barrera,R., Boshell,J., Ferro,C., Freier,J.E.,
            Navarro,J.C., Salas,R., Vasquez,C. and Weaver,S.C.
  TITLE     Genetic and phenotypic changes accompanying the emergence of
            epizootic subtype IC Venezuelan equine encephalitis viruses from an
            enzootic subtype ID progenitor
  JOURNAL   J. Virol. 73 (5), 4266-4271 (1999)
  MEDLINE   99214366
   PUBMED   10196323
REFERENCE   3  (bases 8366 to 9182)
  AUTHORS   Powers,A.M., Oberste,M.S., Brault,A.C., Rico-Hesse,R.,
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  TITLE     Direct Submission
  JOURNAL   Submitted (16-MAY-1997) Pathology, Univ. Texas Med. Branch,
            Galveston, TX 77555-0609, USA
REFERENCE   4  (bases 1 to 11420)
  AUTHORS   Wang,E. and Weaver,S.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JUL-1999) Pathology, Univ. Texas Med. Branch,
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  REMARK    Sequence update by submitter
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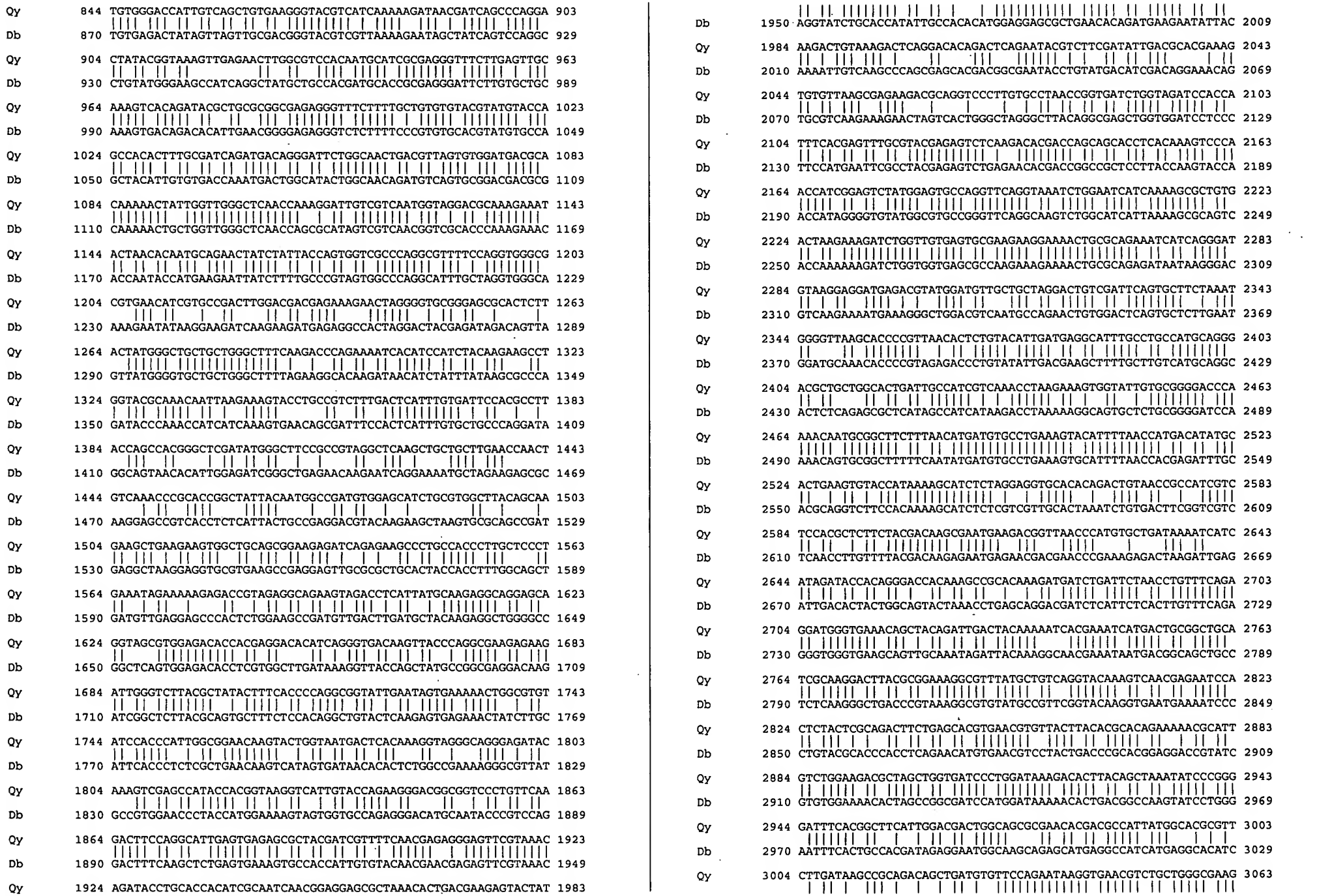

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RESULT 9
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DEFINITION  Venezuelan equine encephalitis virus, complete genome.
ACCESSION   L04653 L00931
VERSION     L04653.1  GI:290609
KEYWORDS    .
SOURCE      Venezuelan equine encephalitis virus
  ORGANISM  Venezuelan equine encephalitis virus
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REFERENCE   1  (bases 1 to 11444)
  AUTHORS   Kinney,R.M., Tsuchiya,K.R., Sneider,J.M. and Trent,D.W.
  TITLE     Genetic evidence that epizootic Venezuelan equine encephalitis
            (VEE) viruses may have evolved from enzootic VEE subtype I-D virus
  JOURNAL   Virology 191 (2), 569-580 (1992)
  MEDLINE   93079859
   PUBMED   1448915
REFERENCE   2  (bases 1 to 11444)
  AUTHORS   Kinney,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUL-1993) Molecular Virology, Centers for Disease
            Control and Prevention, PO Box 2087, Fort Collins, CO 80522, USA
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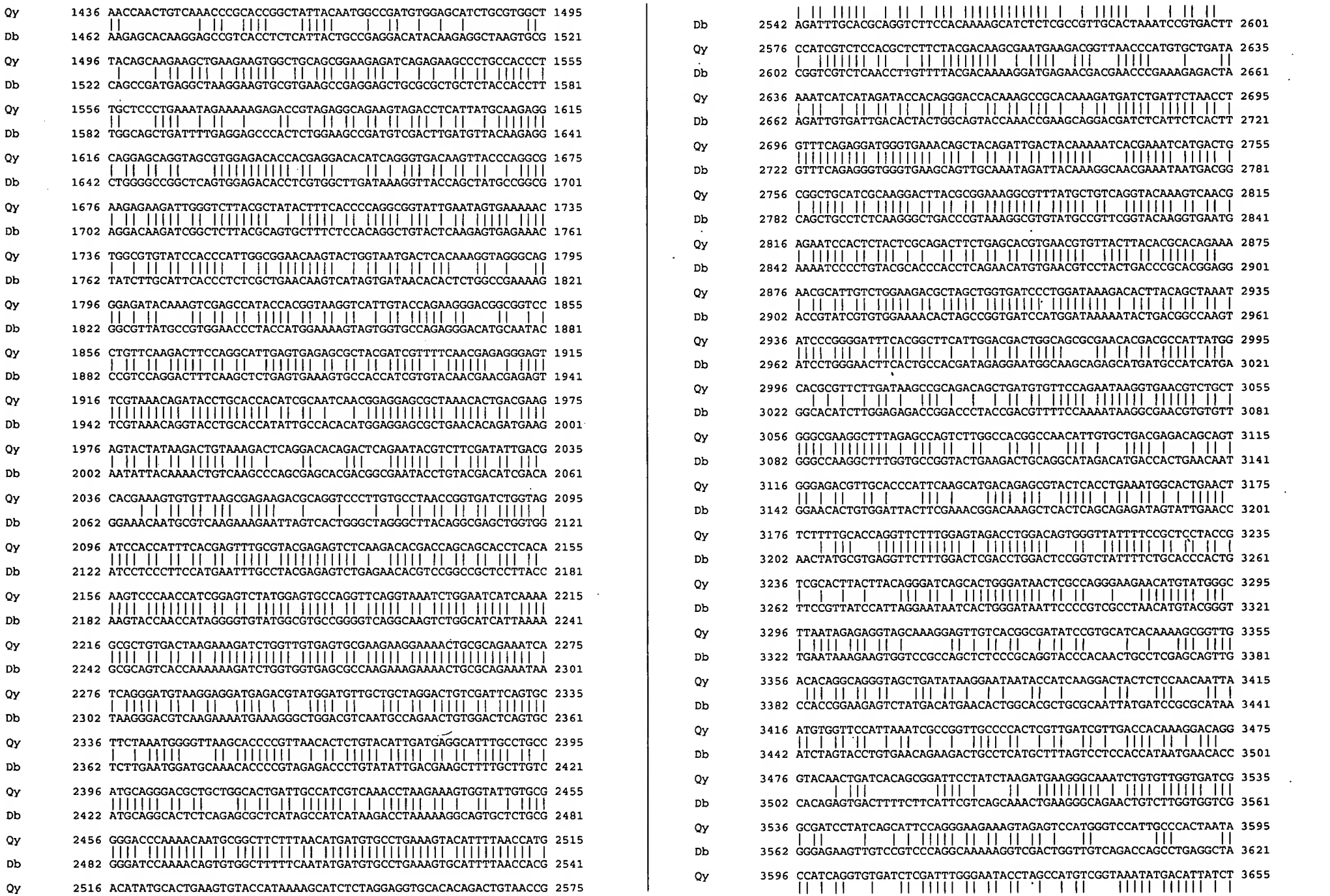

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DEFINITION Venezuelan equine encephalitis virus strain 6119 nonstructural polyprotein and structural polyprotein genes, complete cds.
ACCESSION U55347
VERSION U55347.2 GI:20800451
KEYWORDS .
SOURCE Venezuelan equine encephalitis virus
ORGANISM Venezuelan equine encephalitis virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae; Alphavirus; VEEV complex.
REFERENCE 1 (bases 1 to 11423)
AUTHORS Weaver,S.C., Salas,R., Rico-Hesse,R., Ludwig,G.V., Oberste,M.S., Boshell,J. and Tesh,R.B.
TITLE Re-emergence of epidemic Venezuelan equine encephalomyelitis in South America. VEE Study Group
JOURNAL Lancet 348 (9025), 436-440 (1996)
MEDLINE 96332169
PUBMED 8709783
REFERENCE 2 (bases 1 to 11423)
AUTHORS Weaver,S.C.
TITLE Direct Submission
JOURNAL Submitted (18-APR-1996) Scott C. Weaver, Pathology, Univ. TX Med. Branch, 301 University Ave., Galveston, TX 77555-0609, USA
REFERENCE 3 (bases 1 to 11423)
AUTHORS Weaver,S.C.
TITLE Direct Submission
JOURNAL Submitted (01-MAY-2001) Scott C. Weaver, Pathology, Univ. TX Med. Branch, 301 University Ave., Galveston, TX 77555-0609, USA
REMARK Sequence update by submitter
COMMENT On May 15, 2002 this sequence version replaced gi:2335117.
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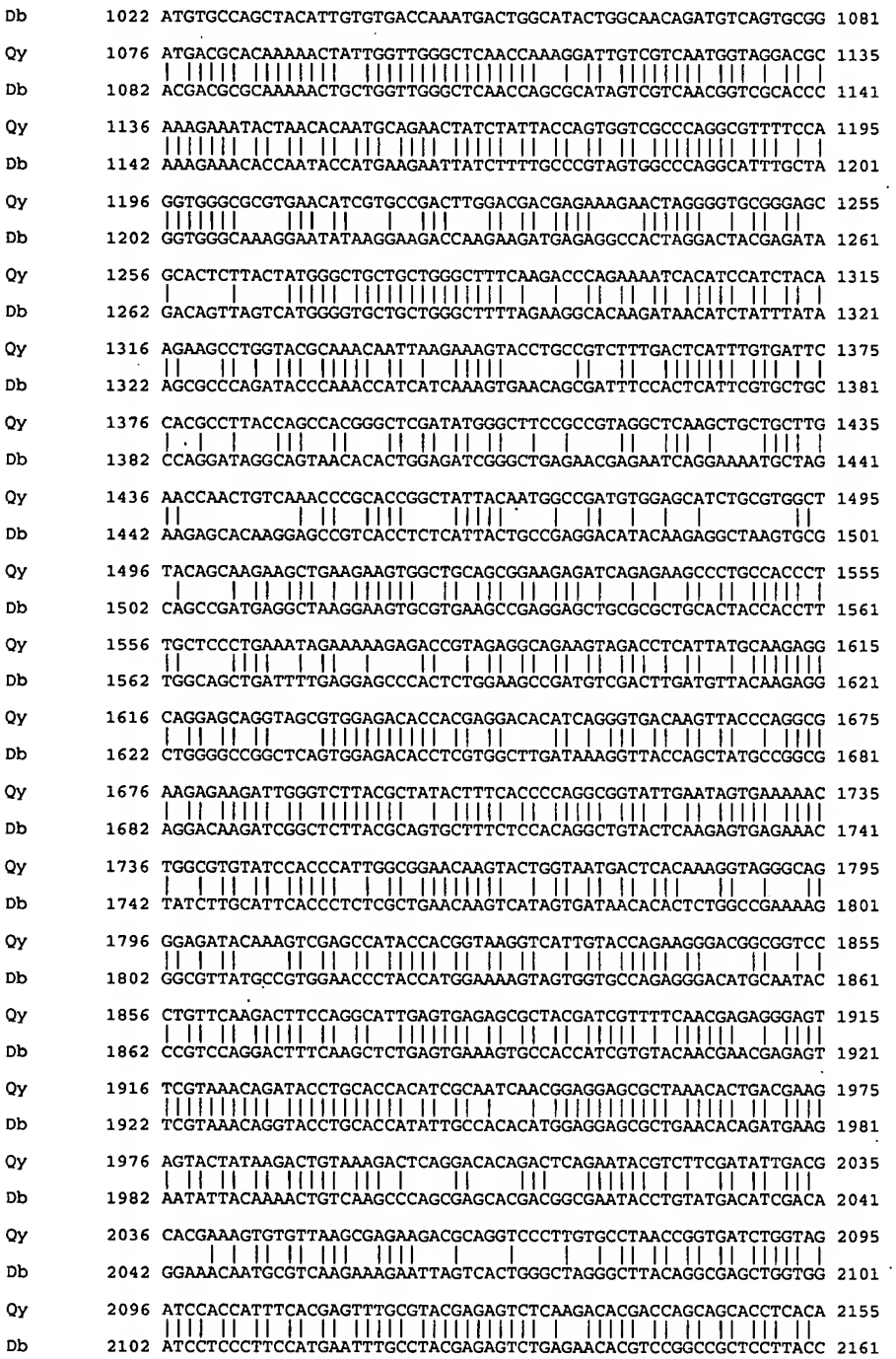
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RESULT 11
EEVNSPEPA
LOCUS       EEVNSPEPA              11447 bp ss-RNA     linear   VRL 25-MAY-1999
DEFINITION  Venezuelan equine encephalitis virus, complete genome.
ACCESSION   L01442
VERSION     L01442.2  GI:4887231
KEYWORDS    .
SOURCE      Venezuelan equine encephalitis virus
  ORGANISM  Venezuelan equine encephalitis virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
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REFERENCE   1  (bases 1 to 11447)
  AUTHORS   Kinney,R.M., Johnson,B.J., Brown,V.L. and Trent,D.W.
  TITLE     Nucleotide sequence of the 26 S mRNA of the virulent Trinidad
            donkey strain of Venezuelan equine encephalitis virus and deduced
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  JOURNAL   Virology 152 (2), 400-413 (1986)
  MEDLINE   86263392
   PUBMED   3088830
REFERENCE   2  (bases 1 to 11447)
  AUTHORS   Johnson,B.J., Kinney,R.M., Kost,C.L. and Trent,D.W.
  TITLE     Molecular determinants of alphavirus neurovirulence: nucleotide and
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  JOURNAL   J. Gen. Virol. 67 (Pt 9), 1951-1960 (1986)
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  MEDLINE   86306669
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REFERENCE   3  (bases 1 to 11447)
  AUTHORS   Kinney,R.M., Johnson,B.J., Welch,J.B., Tsuchiya,K.R. and Trent,D.W.
  TITLE     The full-length nucleotide sequences of the virulent Trinidad
            donkey strain of Venezuelan equine encephalitis virus and its
            attenuated vaccine derivative, strain TC-83
  JOURNAL   Virology 170 (1), 19-30 (1989)
  MEDLINE   89243175
   PUBMED   2524126
REFERENCE   4  (bases 1 to 11447)
  AUTHORS   Kinney,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-1993) Molecular Virology, Centers for Disease
            Control and Prevention, PO Box 2087, Fort Collins, CO 80522, USA
REFERENCE   5  (bases 1 to 11447)
  AUTHORS   Kinney,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-MAY-1999) Molecular Virology, Centers for Disease
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COMMENT     On May 25, 1999 this sequence version replaced gi:323711.
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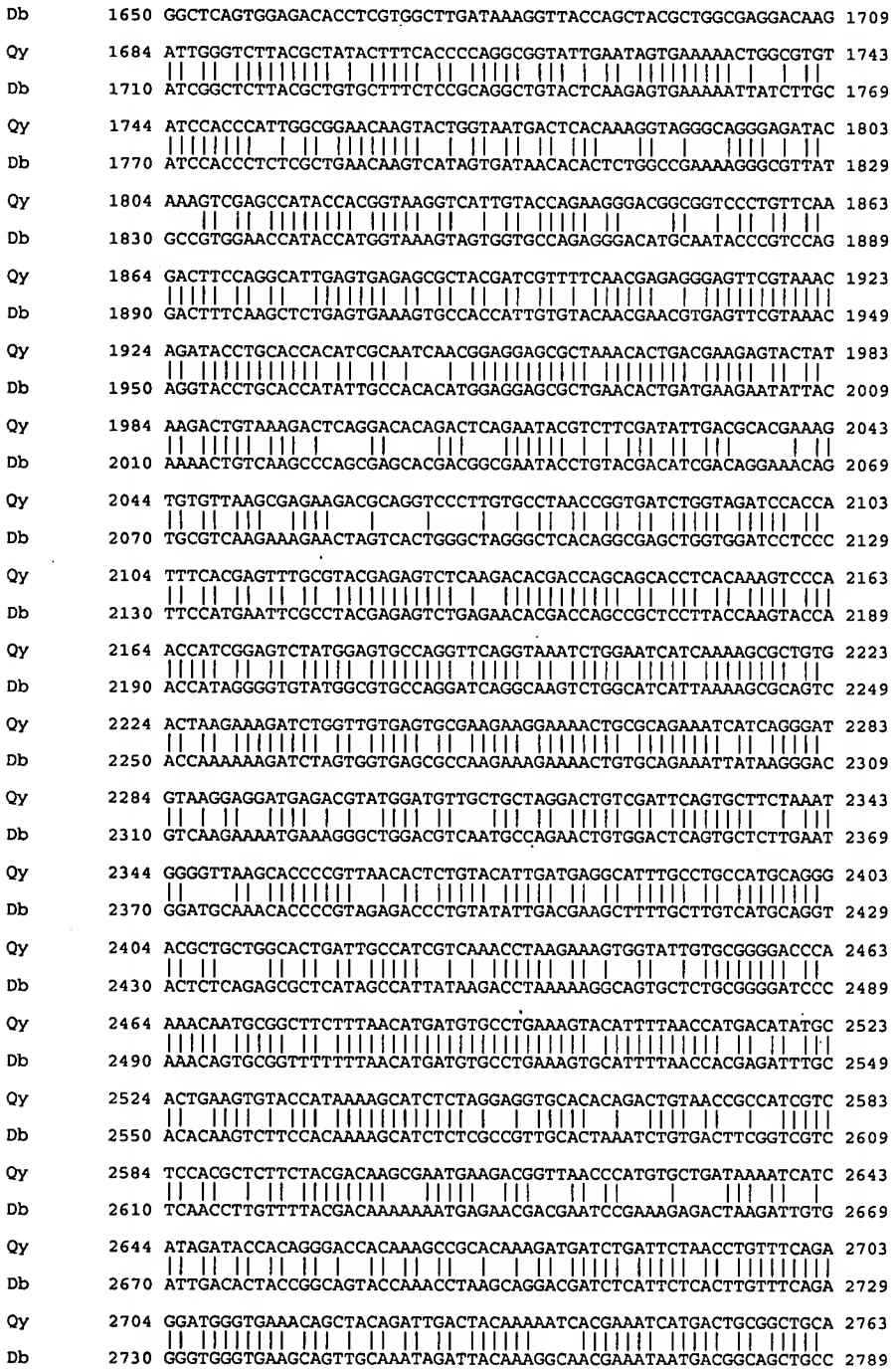
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RESULT 12
AF004459

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DEFINITION  Venezuelan equine encephalitis virus strain 243937, complete
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ACCESSION   AF004459
VERSION     AF004459.2  GI:5442464
KEYWORDS    .
SOURCE      Venezuelan equine encephalitis virus
  ORGANISM  Venezuelan equine encephalitis virus
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REFERENCE   1  (bases 8366 to 9182)
  AUTHORS   Powers,A.M., Oberste,M.S., Brault,A.C., Rico-Hesse,R.,
            Schmura,S.M., Smith,J.F., Kang,W., Sweeney,W.P. and Weaver,S.C.
  TITLE     Repeated emergence of epidemic/epizootic Venezuelan equine
            encephalitis from a single genotype of enzootic subtype ID virus
  JOURNAL   J. Virol. 71 (9), 6697-6705 (1997)
  MEDLINE   97404681
   PUBMED   9261393
REFERENCE   2  (bases 1 to 11420)
  AUTHORS   Wang,E., Barrera,R., Boshell,J., Ferro,C., Freier,J.E.,
            Navarro,J.C., Salas,R., Vasquez,C. and Weaver,S.C.
  TITLE     Genetic and phenotypic changes accompanying the emergence of
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  JOURNAL   J. Virol. 73 (5), 4266-4271 (1999)
  MEDLINE   99214366
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REFERENCE   3  (bases 8366 to 9182)
  AUTHORS   Powers,A.M., Oberste,M.S., Brault,A.C., Rico-Hesse,R.,
            Schmura,S.M., Smith,J.F., Kang,W., Sweeney,W.P. and Weaver,S.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-MAY-1997) Pathology, Univ. Texas Med. Branch,
            Galveston, TX 77555-0609, USA
REFERENCE   4  (bases 1 to 11420)
  AUTHORS   Wang,E. and Weaver,S.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JUL-1999) Pathology, Univ. Texas Med. Branch,
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  REMARK    Sequence update by submitter
COMMENT     On Jul 12, 1999 this sequence version replaced gi:3849804.
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ORIGIN

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Db         90 AGAGCTTTGCAACGGAGCTTCCCGCAGTTTGAGGTAGAAGCCAAGCAGGTCACTGATAAT 149

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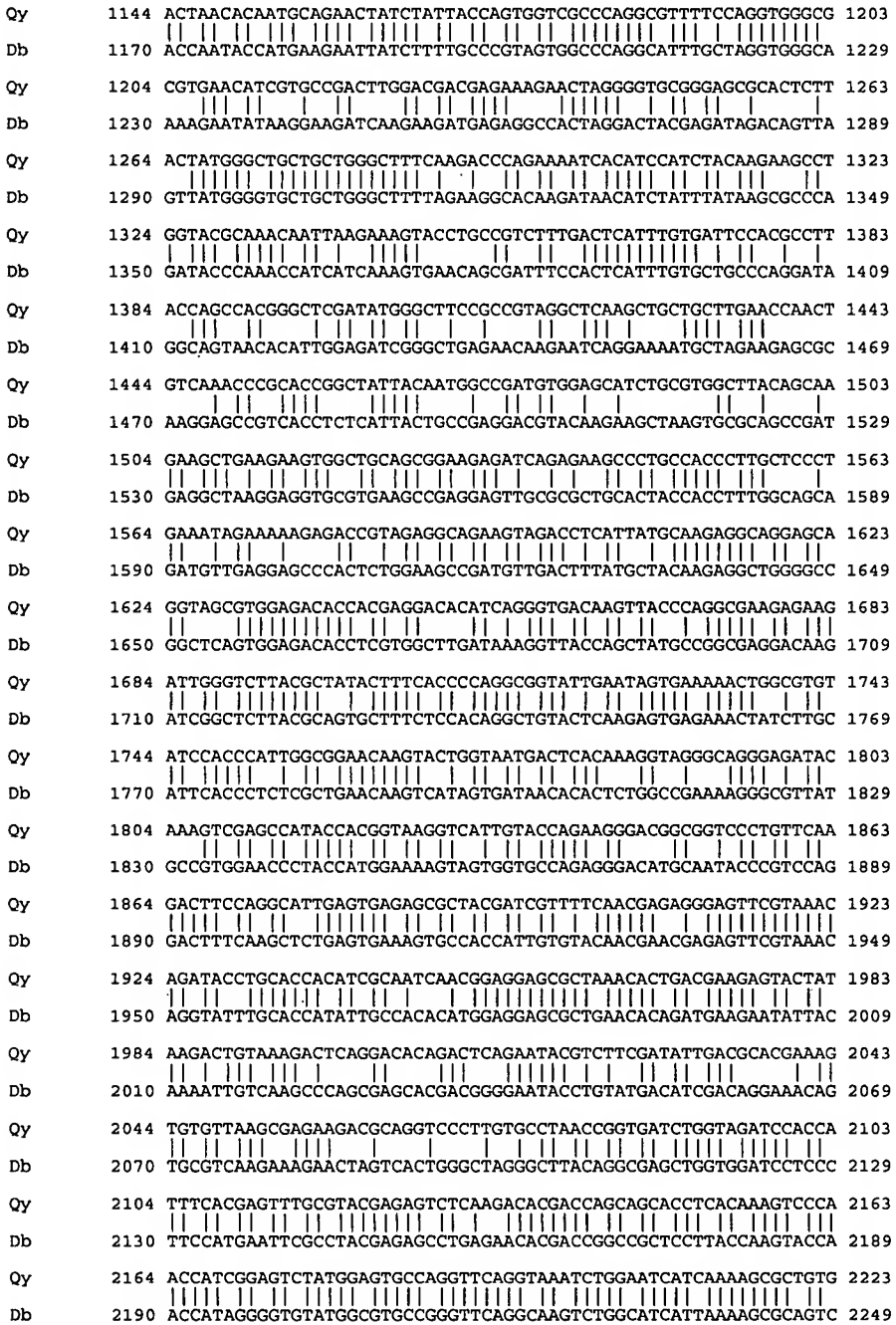

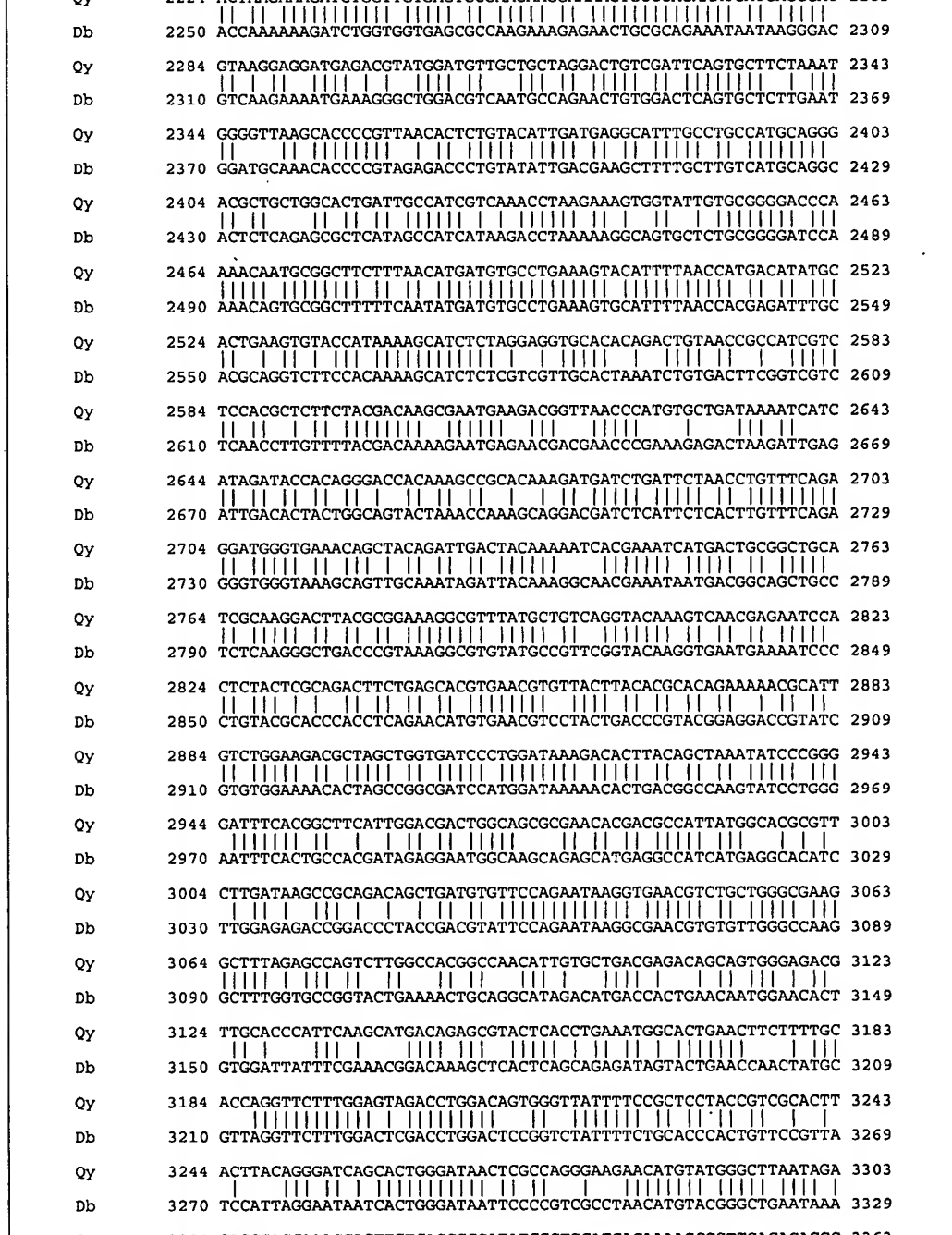

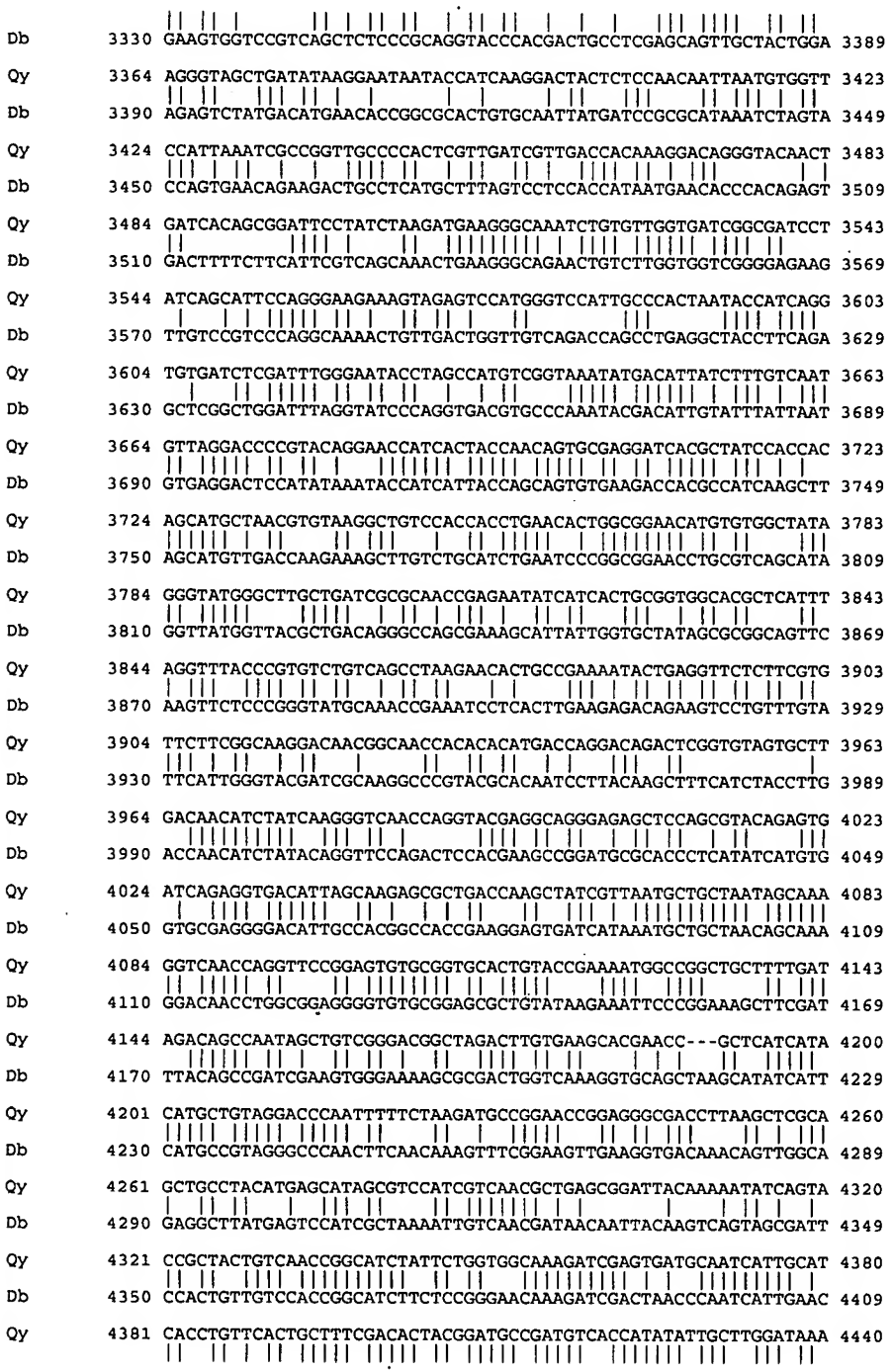

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VERSION U55360.2 GI:5442468
KEYWORDS .
SOURCE Venezuelan equine encephalitis virus
ORGANISM Venezuelan equine encephalitis virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae; Alphavirus; VEEV complex.
REFERENCE 1 (bases 8366 to 10042)
AUTHORS Weaver,S.C., Salas,R., Rico-Hesse,R., Ludwig,G.V., Oberste,M.S., Boshell,J. and Tesh,R.B.
TITLE Re-emergence of epidemic Venezuelan equine encephalomyelitis in South America. VEE Study Group
JOURNAL Lancet 348 (9025), 436-440 (1996)
MEDLINE 96332169
PUBMED 8709783
REFERENCE 2 (bases 1 to 11420)
AUTHORS Wang,E., Barrera,R., Boshell,J., Ferro,C., Freier,J.E., Navarro,J.C., Salas,R., Vasquez,C. and Weaver,S.C.
TITLE Genetic and phenotypic changes accompanying the emergence of epizootic subtype IC Venezuelan equine encephalitis viruses from an enzootic subtype ID progenitor
JOURNAL J. Virol. 73 (5), 4266-4271 (1999)
MEDLINE 99214366
PUBMED 10196323
REFERENCE 3 (bases 8366 to 10042)
AUTHORS Weaver,S.C.

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  TITLE     Direct Submission
  JOURNAL   Submitted (18-APR-1996) Pathology, Univ. TX Med. Branch, 301
            University Ave., Galveston, TX 77555-0609, USA
REFERENCE   4  (bases 1 to 11420)
  AUTHORS   Wang,E. and Weaver,S.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JUL-1999) Pathology, Univ. TX Med. Branch, 301
            University Ave., Galveston, TX 77555-0609, USA
  REMARK    Sequence update by submitter
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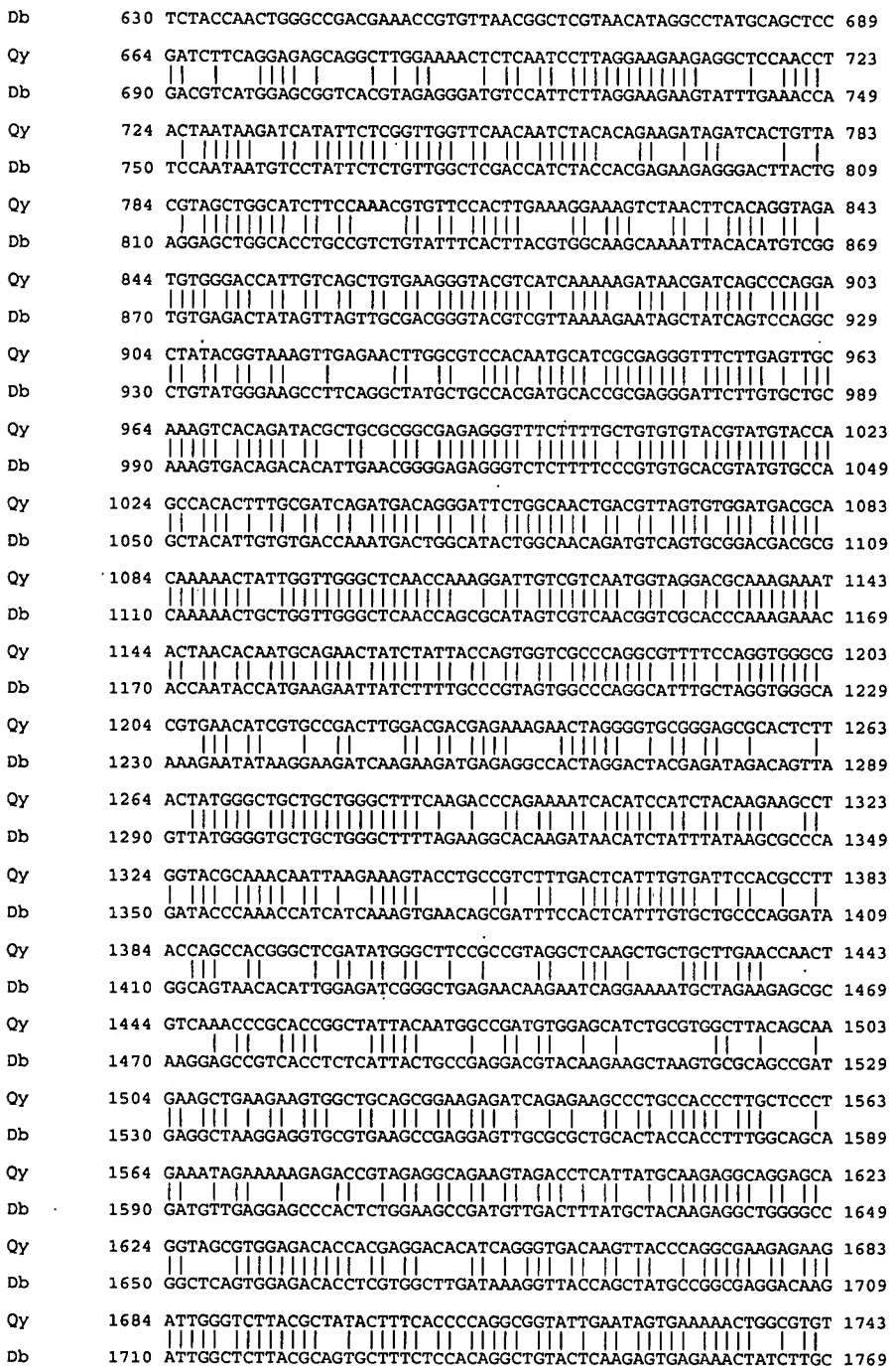
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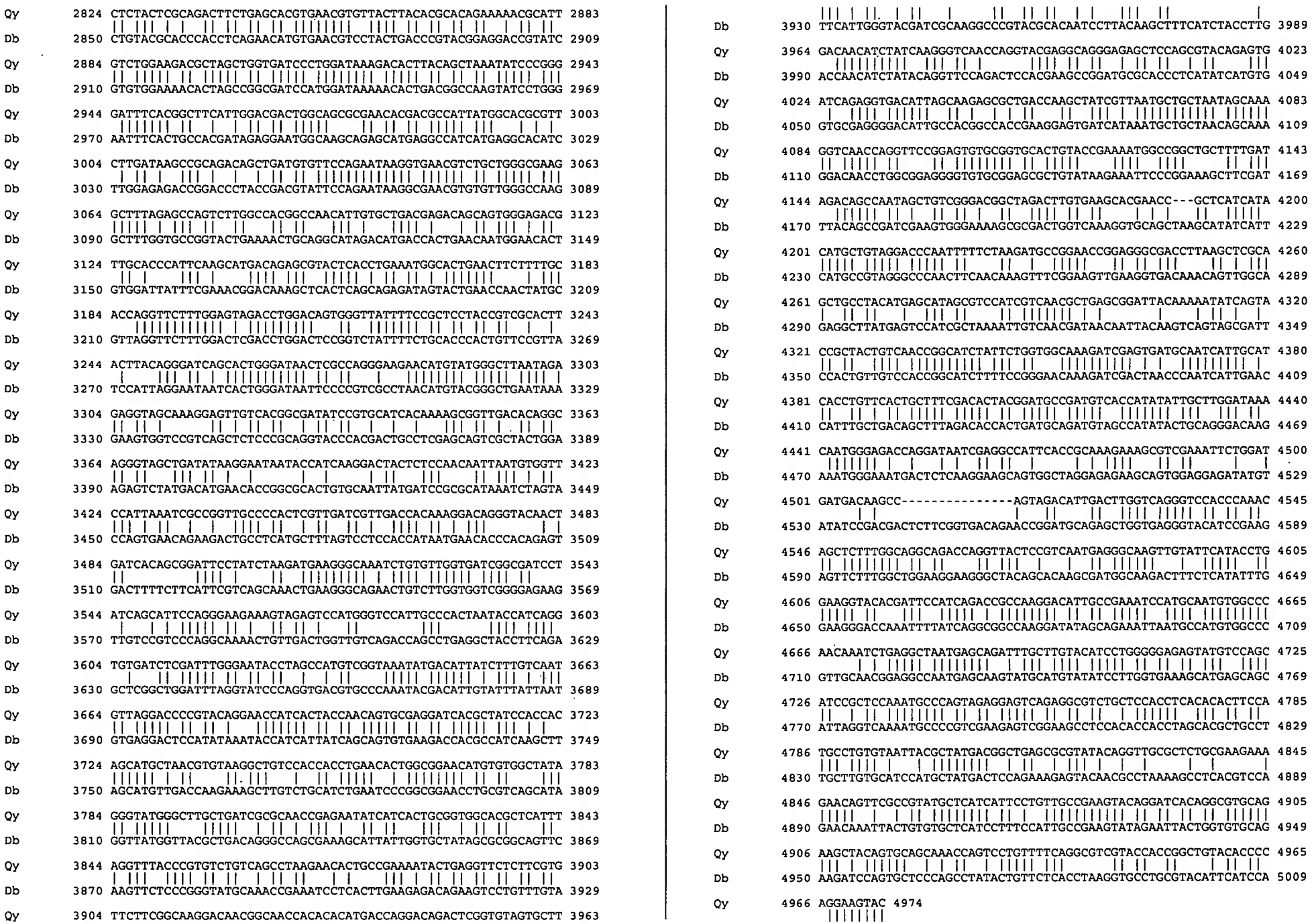

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RESULT 14
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DEFINITION  Venezuelan equine encephalitis virus nonstructural polyprotein and
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ACCESSION   AF375051
VERSION     AF375051.1  GI:14549692
KEYWORDS    .
SOURCE      Venezuelan equine encephalitis virus
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  AUTHORS   Brault,A.C., Powers,A.M., Medina,G., Wang,E., Kang,W., Salas,R.A.,
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  TITLE     Potential sources of the 1995 Venezuelan equine encephalitis
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  JOURNAL   J. Virol. 75 (13), 5823-5832 (2001)
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  TITLE     Direct Submission
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ORIGIN

  Query Match           42.4%;  Score 2119;  DB 14;  Length 11423;
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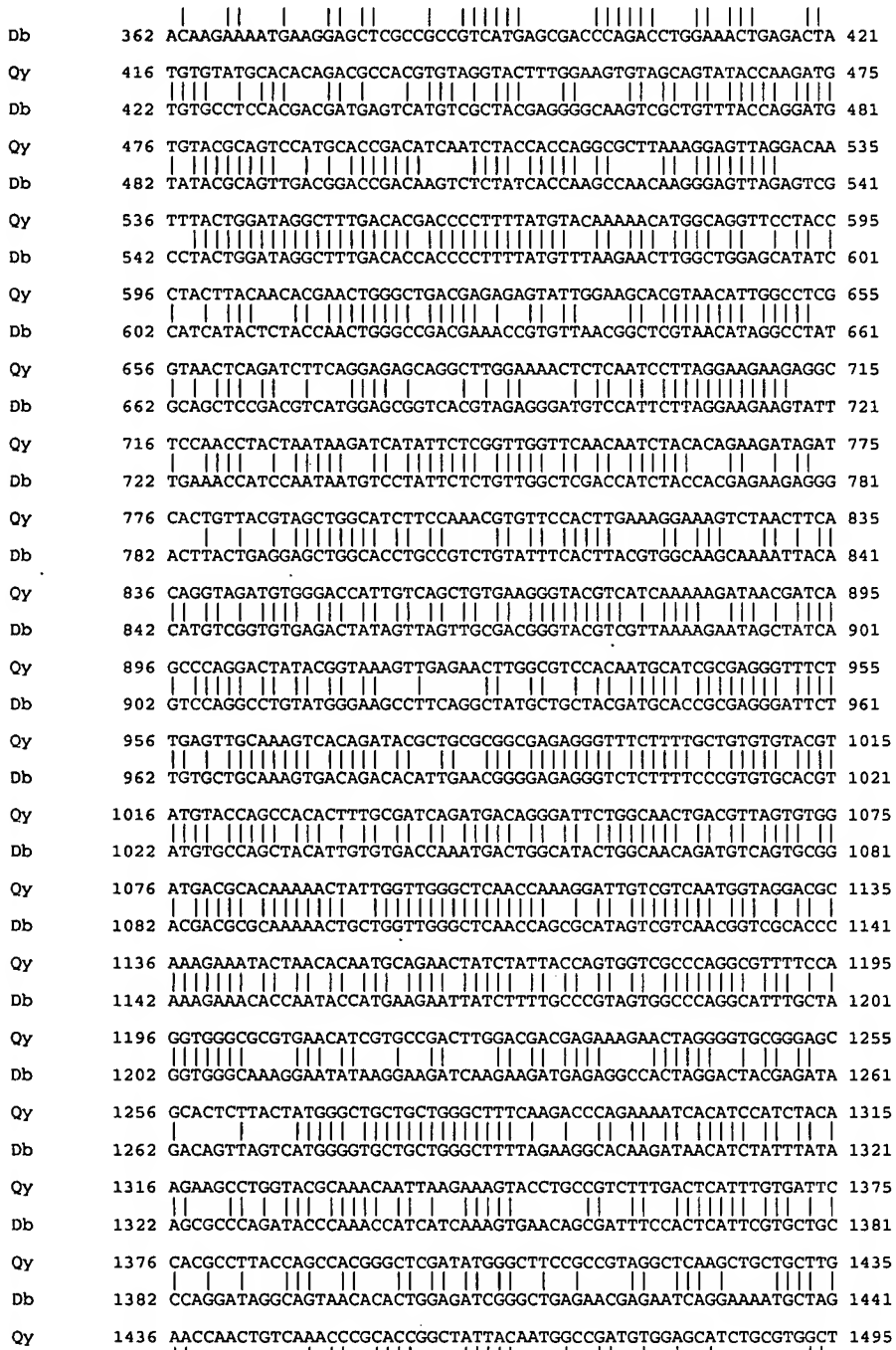
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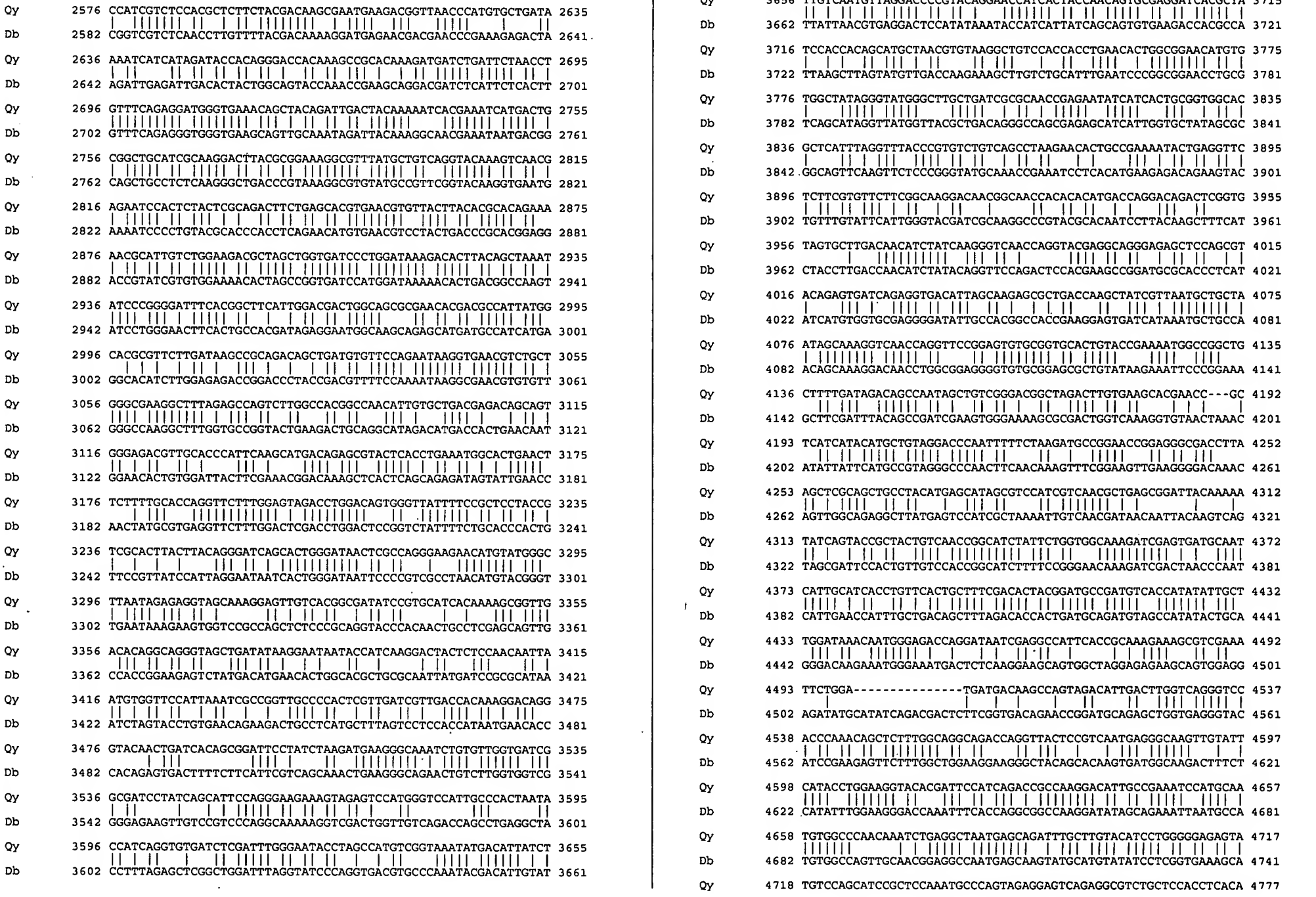

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RESULT 15
VEU55342
LOCUS       VEU55342               11423 bp    RNA     linear   VRL 15-JAN-2002
DEFINITION  Venezuelan equine encephalitis virus nonstructural polyprotein and
            structural polyprotein genes, complete cds.
ACCESSION   U55342
VERSION     U55342.2  GI:18152933
KEYWORDS    .
SOURCE      Venezuelan equine encephalitis virus
  ORGANISM  Venezuelan equine encephalitis virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
            Alphavirus; VEEV complex.
REFERENCE   1  (bases 1 to 11423)
  AUTHORS   Weaver,S.C., Salas,R., Rico-Hesse,R., Ludwig,G.V., Oberste,M.S.,
            Boshell,J. and Tesh,R.B.
  TITLE     Re-emergence of epidemic Venezuelan equine encephalomyelitis in
            South America. VEE Study Group
  JOURNAL   Lancet 348 (9025), 436-440 (1996)
  MEDLINE   96332169
   PUBMED   8709783
REFERENCE   2  (bases 1 to 11423)
  AUTHORS   Weaver,S.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-APR-1996) Scott C. Weaver, Pathology, Univ. TX Med.
            Branch, 301 University Ave., Galveston, TX 77555-0609, USA
REFERENCE   3  (bases 1 to 11423)
  AUTHORS   Weaver,S.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-MAY-2001) Scott C. Weaver, Pathology, Univ. TX Med.
            Branch, 301 University Ave., Galveston, TX 77555-0609, USA
  REMARK    Sequence update by submitter
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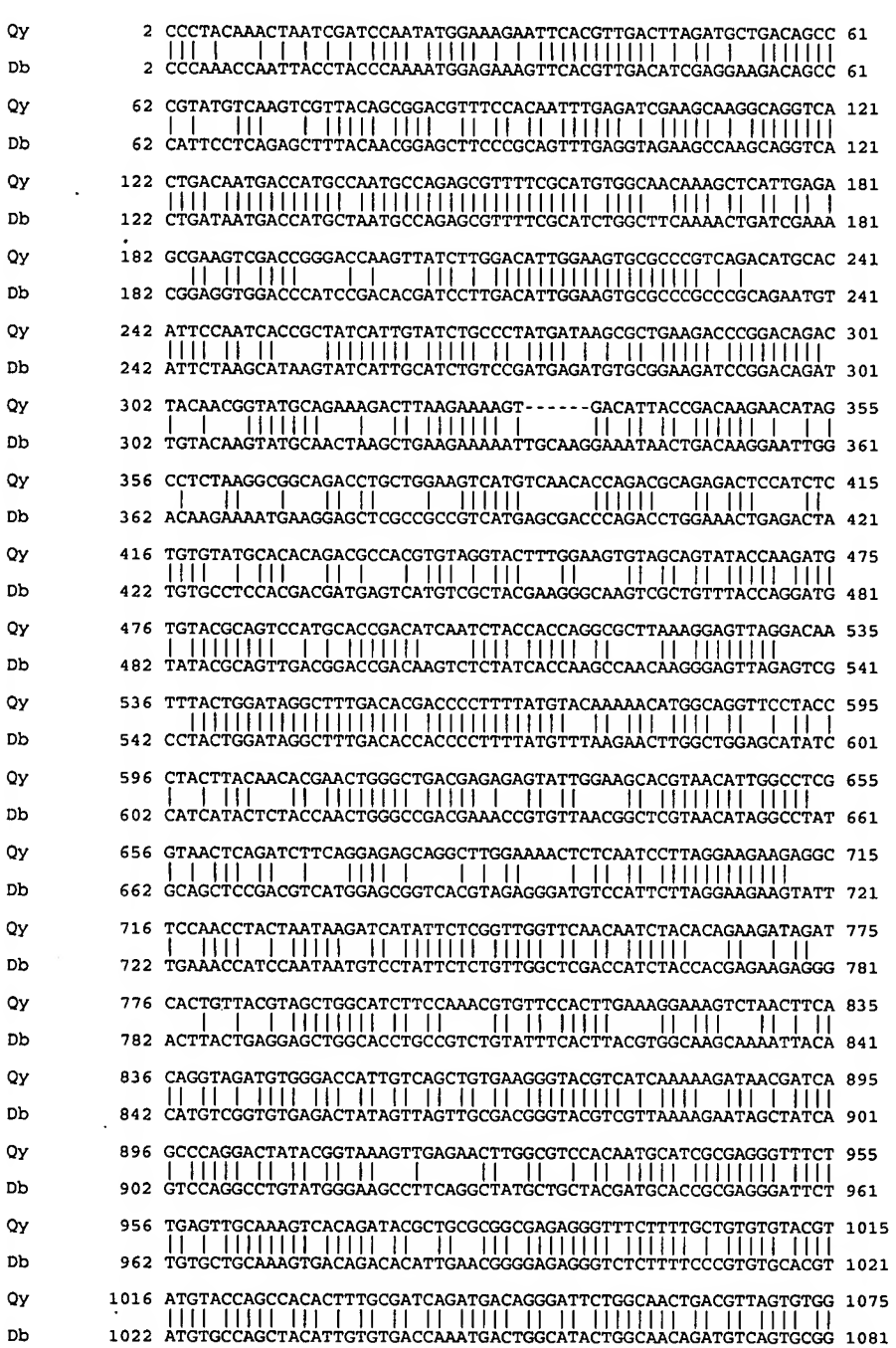
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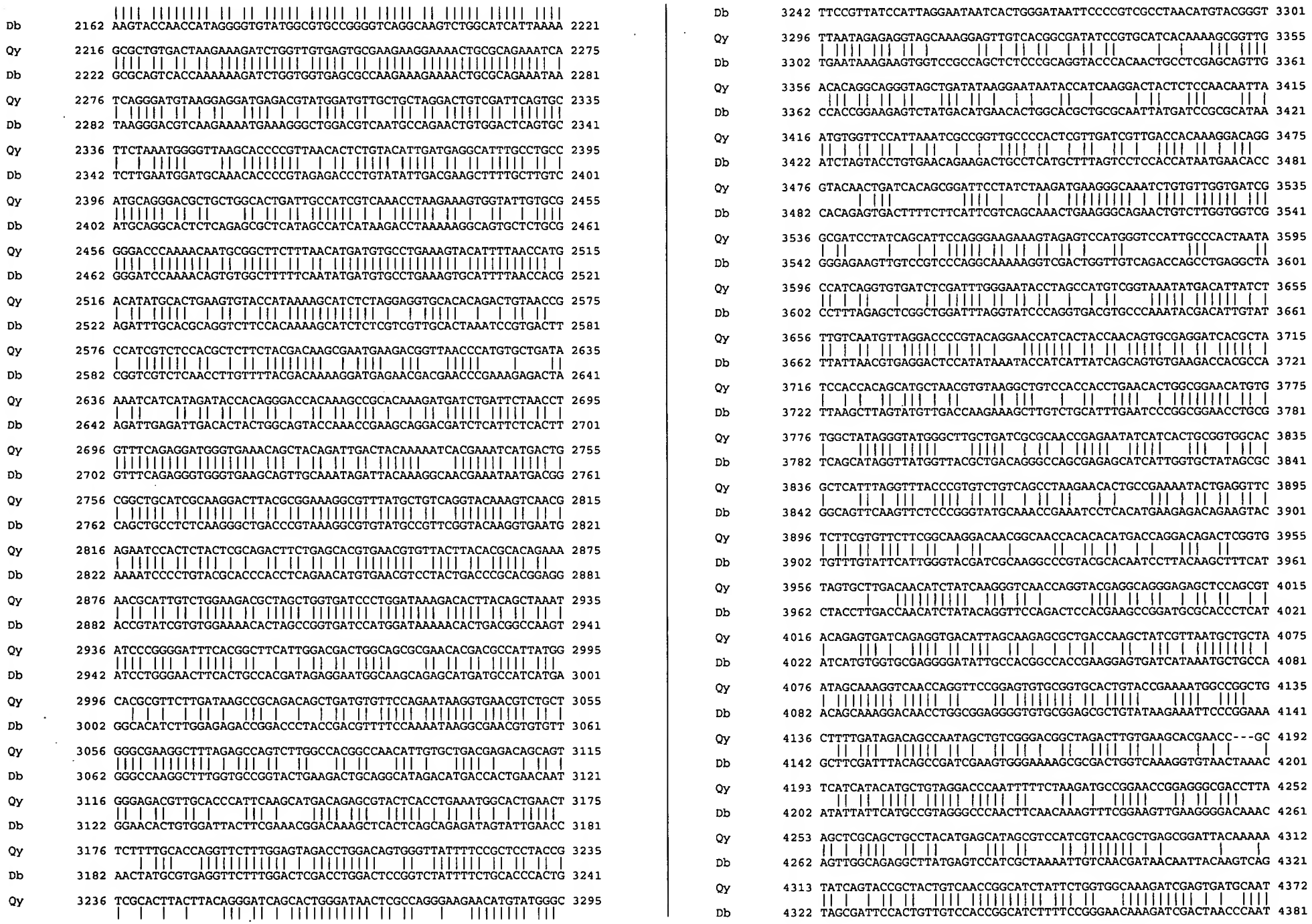

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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31	2369.2	36.5	16656	6	AR183758	AR183758 Sequence
32	2365.6	36.5	11708	14	SINOCK82	M69205 Ockelbo vir
33	2340.2	36.1	11569	14	AF429428	AF429428 Sindbis v
34	2329.4	35.9	11626	14	AF103728	AF103728 Sindbis v
35	2322.4	35.8	16958	6	AX665480	AX665480 Sequence
36	2227.4	34.3	11678	14	U01034	U01034 Eastern equ
37	2225.2	34.3	11687	6	AX286761	AX286761 Sequence
38	2214.2	34.1	11675	14	EEEVIRNA	X63135 Eastern Equ
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41	2150.8	33.2	4525	14	AF339475	AF339475 Fort Morg
42	2122.6	32.7	13905	6	AR137241	AR137241 Sequence
43	2122.6	32.7	13905	6	AR282856	AR282856 Sequence
44	1880	29.0	11824	14	AF126284	AF126284 Aura viru
45	1825.2	28.1	4676	14	AF339477	AF339477 Babanki v

ALIGNMENTS

RESULT 1
AF214040
LOCUS AF214040 11484 bp RNA linear VRL 27-JAN-2000
DEFINITION Western equine encephalomyelitis virus strain 71V-1658 nonstructural polyprotein and structural polyprotein genes, complete cds.
ACCESSION AF214040 AF143811
VERSION AF214040.1 GI:6760410
KEYWORDS .
SOURCE Western equine encephalomyelitis virus
ORGANISM Western equine encephalomyelitis virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae; Alphavirus; WEEV complex.
REFERENCE 1 (bases 1 to 11484)
AUTHORS Netolitzky,D.J., Schmaltz,F.L., Parker,M.D., Rayner,G.A.,

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          Fisher,G.R., Trent,D.W., Bader,D.E. and Nagata,L.P.
  TITLE   Complete genomic RNA sequence of western equine encephalitis virus
          and expression of the structural genes
  JOURNAL J. Gen. Virol. 81 (Pt 1), 151-159 (2000)
  MEDLINE 20109043
   PUBMED 10640553
REFERENCE 2  (bases 1 to 11484)
  AUTHORS Netolitzky,D.J., Schmaltz,F.L., Parker,M.D., Rayner,G.A.,
          Fisher,G.R., Trent,D.W., Bader,D.E. and Nagata,L.P.
  TITLE   Direct Submission
  JOURNAL Submitted (08-DEC-1999) Medical Countermeasures Section, Defence
          Research Establishment Suffield, P.O. Box 4000, Stn Main, Medicine
          Hat, Alberta T1A 8K6, Canada
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BASE COUNT     3251 a    2842 c    2808 g    2583 t
ORIGIN

  Query Match           100.0%;  Score 6485;  DB 14;  Length 11484;
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  Matches 6485;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      7460 ACCCACCGGCAGAATGTTTCCATACCCTCAGCTGAACTTTCCACCAGTTTACCCTACAAA 7519

Qy      2521 TCCGATGGCTTACCGAGATCCAAACCCTCCTAGGCGCCGCTGGAGGCCGTTTCGGCCCCC 2580
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7520 TCCGATGGCTTACCGAGATCCAAACCCTCCTAGGCGCCGCTGGAGGCCGTTTCGGCCCCC 7579

Qy      2581 GCTGGCTGCTCAAATCGAAGATCTTAGGAGGTCGATAGTCAACTTGACTTTCAAACAACG 2640
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7580 GCTGGCTGCTCAAATCGAAGATCTTAGGAGGTCGATAGTCAACTTGACTTTCAAACAACG 7639

Qy      2641 ATCACCTAATCCGCCGCCAGGTCCACCGCCAAAGAAGAAGAAGAGTGCTCCTAAGCCAAA 2700
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7640 ATCACCTAATCCGCCGCCAGGTCCACCGCCAAAGAAGAAGAAGAGTGCTCCTAAGCCAAA 7699

Qy      2701 ACCTACTCAGCCTAAAAAGAAGAAGCAGCAAGCCAAGAGGACGAAACGCAAGCCTAAACC 2760
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Db       7700 ACCTACTCAGCCTAAAAAGAAGAAGCAGCAAGCCAAGAGGACGAAACGCAAGCCTAAACC 7759
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Qy       2821 GAACGGCCAAGTGAATGGATATGCCTGCGTTGTCGGAGGAAGGCTGATGAAACCACTCCA 2880
Db       7820 GAACGGCCAAGTGAATGGATATGCCTGCGTTGTCGGAGGAAGGCTGATGAAACCACTCCA 7879
Qy       2881 CGTTGAAGGAAAAATTGATAATGAGCAATTAGCGGCCGTGAAATTGAAGAAGGCTAGCAT 2940
Db       7880 CGTTGAAGGAAAAATTGATAATGAGCAATTAGCGGCCGTGAAATTGAAGAAGGCTAGCAT 7939
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Qy       3001 CAGCGACAAACCACCGGGCTTCTACAACTGGCACCACGGCGCAGTCCAGTATGAGAATGG 3060
Db       8000 CAGCGACAAACCACCGGGCTTCTACAACTGGCACCACGGCGCAGTCCAGTATGAGAATGG 8059
Qy       3061 GAGATTTACCGTACCGAGAGGAGTGGGCGGGAAAGGCGACAGCGGAAGACCGATCCTGGA 3120
Db       8060 GAGATTTACCGTACCGAGAGGAGTGGGCGGGAAAGGCGACAGCGGAAGACCGATCCTGGA 8119
Qy       3121 CAACAGAGGCAGAGTTGTGGCTATTGTTCTAGGAGGTGCAAATGAGGGCACGCGTACGGC 3180
Db       8120 CAACAGAGGCAGAGTTGTGGCTATTGTTCTAGGAGGTGCAAATGAGGGCACGCGTACGGC 8179
Qy       3181 GCTTTCAGTGGTCACTTGGAACCAGAAAGGGGTGACCATTAGGGATACCCCCGAAGGTTC 3240
Db       8180 GCTTTCAGTGGTCACTTGGAACCAGAAAGGGGTGACCATTAGGGATACCCCCGAAGGTTC 8239
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Db       8240 TGAACCGTGGTCACTAGTTACAGCGCTATGCGTGCTTTCGAATGTCACGTTCCCATGCGA 8299
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Qy       3361 CGTCGACAATCCAAATTACGACACGCTGCTGGAGAACGTCTTGAAATGTCCATCACGCCG 3420
Db       8360 CGTCGACAATCCAAATTACGACACGCTGCTGGAGAACGTCTTGAAATGTCCATCACGCCG 8419
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Db       8540 ATCTGATGATGGATCGATTAGAATCCAGGTCTCGGCACAATTCGGCTACAATCAGGCAGG 8599
Qy       3601 CACTGCGGATGTCACCAAATTCCGTTACATGTCTTTCGACCACGACCATGACATCAAGGA 3660
Db       8600 CACTGCGGATGTCACCAAATTCCGTTACATGTCTTTCGACCACGACCATGACATCAAGGA 8659
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Db       8660 AGACAGTATGGAGAAAATAGCTATCAGCACATCTGGACCCTGCCGTCGTCTTGGCCACAA 8719
Qy       3721 AGGGTACTTCCTGTTAGCTCAATGTCCTCCAGGTGACAGTGTAACCGTCAGTATCACGAG 3780
Db       8720 AGGGTACTTCCTGTTAGCTCAATGTCCTCCAGGTGACAGTGTAACCGTCAGTATCACGAG 8779
Qy       3781 CGGAGCATCTGAGAATTCATGCACCGTGGAGAAAAAGATCAGGAGGAAGTTTGTCGGTAG 3840
Db       8780 CGGAGCATCTGAGAATTCATGCACCGTGGAGAAAAAGATCAGGAGGAAGTTTGTCGGTAG 8839

Qy       3841 AGAGGAGTACTTGTTCCCACCCGTCCATGGAAAGCTGGTAAAGTGCCACGTTTACGATCA 3900
Db       8840 AGAGGAGTACTTGTTCCCACCCGTCCATGGAAAGCTGGTAAAGTGCCACGTTTACGATCA 8899
Qy       3901 CTTGAAGGAGACGTCTGCCGGGTACATAACCATGCACAGGCCAGGCCCACACGCGTATAA 3960
Db       8900 CTTGAAGGAGACGTCTGCCGGGTACATAACCATGCACAGGCCAGGCCCACACGCGTATAA 8959
Qy       3961 GTCCTATCTGGAGGAAGCGTCAGGCGAAGTGTACATTAAACCACCTTCTGGCAAGAACGT 4020
Db       8960 GTCCTATCTGGAGGAAGCGTCAGGCGAAGTGTACATTAAACCACCTTCTGGCAAGAACGT 9019
Qy       4021 CACCTACGAATGTAAGTGTGGCGACTACAGCACAGGTATCGTGAGCACGCGAACGAAGAT 4080
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Qy       4141 CTTCAACTCGCCGGATCTTATTAGGCACACAGACCACTCAGTGCAAGGTAAATTGCACAT 4200
Db       9140 CTTCAACTCGCCGGATCTTATTAGGCACACAGACCACTCAGTGCAAGGTAAATTGCACAT 9199
Qy       4201 TCCATTCCGCTTGACACCGACAGTCTGCCCGGTTCCGTTAGCTCACACGCCTACAGTCAC 4260
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Qy       4261 GAAGTGGTTCAAAGGCATCACCCTCCACCTGACTGCAATGCGACCAACATTGCTGACAAC 4320
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Qy       4321 GAGAAAATTGGGGCTGCGAGCAGACGCAACAGCAGAATGGATTACAGGGTCTACATCCAG 4380
Db       9320 GAGAAAATTGGGGCTGCGAGCAGACGCAACAGCAGAATGGATTACAGGGTCTACATCCAG 9379
Qy       4381 GAATTTTTCTGTGGGGCGAGAAGGGCTGGAGTACGTATGGGGTAACCATGAACCAGTCAG 4440
Db       9380 GAATTTTTCTGTGGGGCGAGAAGGGCTGGAGTACGTATGGGGTAACCATGAACCAGTCAG 9439
Qy       4441 AGTCTGGGCCCAGGAGTCGGCACCAGGCGACCCACATGGATGGCCGCATGAGATCATCAT 4500
Db       9440 AGTCTGGGCCCAGGAGTCGGCACCAGGCGACCCACATGGATGGCCGCATGAGATCATCAT 9499
Qy       4501 CCACTATTATCATCGGCATCCAGTCTACACTGTCATTGTGCTGTGTGGTGTCGCTCTTGC 4560
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Qy       4561 TATCCTGGTAGGCACTGCATCATCAGCAGCTTGCATCGCCAAAGCAAGAAGAGACTGCCT 4620
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Qy       4621 GACGCCATACGCGCTTGCACCGAACGCAACGGTACCCACAGCATTAGCGGTTTTGTGCTG 4680
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Qy       4741 CCAACCGTTTCTCTGGGCACAGTTGTGCATTCCTCTGGCAGCGCTTGTTATTCTGTTCCG 4800
Db       9740 CCAACCGTTTCTCTGGGCACAGTTGTGCATTCCTCTGGCAGCGCTTGTTATTCTGTTCCG 9799
Qy       4801 CTGCTTTTCATGCTGCATGCCTTTTTTATTGGTTGCAGGCGTCTGCCTGGGGAAGGTAGA 4860
Db       9800 CTGCTTTTCATGCTGCATGCCTTTTTTATTGGTTGCAGGCGTCTGCCTGGGGAAGGTAGA 9859
Qy       4861 CGCCTTCGAACATGCGACCACTGTGCCAAATGTTCCGGGGATCCCGTATAAGGCGTTGGT 4920
Db       9860 CGCCTTCGAACATGCGACCACTGTGCCAAATGTTCCGGGGATCCCGTATAAGGCGTTGGT 9919
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Qy       4921 CGAACGCGCAGGTTACGCGCCACTTAACCTGGAGATCACGGTCGTCTCATCGGAATTAAC 4980
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Qy       4981 ACCTTCAACTAACAAGGAGTACGTGACCTGCAAATTCCACACAGTCATTCCTTCACCACA 5040
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Qy       5041 AGTTAAATGCTGCGGGTCCCTCGAGTGCAAGGCATCCTCAAAGGCGGATTACACATGCCG 5100
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Qy       5101 CGTTTTTGGCGGTGTGTACCCTTTCATGTGGGGAGGCGCACAATGCTTCTGTGACAGTGA 5160
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Db       10100 CGTTTTTGGCGGTGTGTACCCTTTCATGTGGGGAGGCGCACAATGCTTCTGTGACAGTGA 10159

Qy       5161 GAACACACAACTGAGTGAGGCGTACGTCGAGTTCGCTCCAGACTGCACTATAGATCACGC 5220
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Db       10160 GAACACACAACTGAGTGAGGCGTACGTCGAGTTCGCTCCAGACTGCACTATAGATCACGC 10219

Qy       5221 AGTCGCACTAAAAGTTCACACAGCTGCTCTGAAAGTCGGCCTGCGTATAGTATACGGCAA 5280
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Db       10220 AGTCGCACTAAAAGTTCACACAGCTGCTCTGAAAGTCGGCCTGCGTATAGTATACGGCAA 10279

Qy       5281 CACCACCGCGCACCTGGATACGTTTGTCAATGGCGTCACGCCAGGTTCCTCACGGGACCT 5340
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Db       10280 CACCACCGCGCACCTGGATACGTTTGTCAATGGCGTCACGCCAGGTTCCTCACGGGACCT 10339

Qy       5341 GAAGGTCATAGCAGGGCCGATATCAGCCGCTTTTTCACCCTTTGACCATAAGGTCGTCAT 5400
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Qy       5401 CAGAAAGGGGCTTGTTTACAACTACGACTTCCCTGAGTATGGAGCTATGAAACCAGGAGC 5460
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Qy       5461 GTTCGGCGATATTCAAGCATCCTCGCTTGATGCTACAGACATAGTAGCCCGCACTGACAT 5520
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Db       10460 GTTCGGCGATATTCAAGCATCCTCGCTTGATGCTACAGACATAGTAGCCCGCACTGACAT 10519

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Qy       5701 GATTGACATCCCTGATGCAGCTTTTGTGAGATCATCAGAATCACCAACAATTTTAGAAGT 5760
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Db       10700 GATTGACATCCCTGATGCAGCTTTTGTGAGATCATCAGAATCACCAACAATTTTAGAAGT 10759

Qy       5761 TAGCTGCACAGTAGCAGACTGCATTTATTCTGCAGACTTTGGTGGTTCTCTAACATTACA 5820
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Qy       5821 GTACAAAGCTGACAGGGAGGGACATTGTCCAGTTCACTCCCACTCCACGACAGCTGTTTT 5880
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Db       10880 GAAGGAAGCGACCACACATGTGACTGCCGTAGGCAGCATAACACTACATTTTAGCACATC 10939

Qy       5941 GAGCCCACAAGCAAATTTTATAGTTTCGCTATGCGGCAAGAAGTCCACCTGCAATGCTGA 6000
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Qy       6121 CCTCATTGTTGTAGGACTTATAGTGTTGGTCTGCAGCTCTATGCTTATAAACACACGTAG 6180
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Qy       6181 ATGACTGAGCGCGGACACTGACATAGCGGTAAAACTCGATGTACTTCCGAGGAAGCGTGG 6240
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Qy       6241 TGCATAATGCCACGCGCCGCTTGACACTAAAACTCGATGTATTTCCGAGGAAGCACAGTG 6300
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Qy       6361 CACTTTTATGAGACTCACTATGGGTCTCTAATATACACTACACATATTTTACTTAAAAAC 6420
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Qy       6421 ACTATACACACTTTATAAATTCTTTTATAATTTTTCTTTTGTTTTTATTTTGTTTTTAAA 6480
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Db       11420 ACTATACACACTTTATAAATTCTTTTATAATTTTTCTTTTGTTTTTATTTTGTTTTTAAA 11479

Qy       6481 ATTTC 6485
             |||||
Db       11480 ATTTC 11484
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RESULT 2
EEWSP

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LOCUS       EEWSP                   4170 bp ss-RNA     linear   VRL 02-AUG-1993
DEFINITION  Western equine encephalitis virus RNA encoding structural proteins
            at the 3' end of the genome.
ACCESSION   J03854
VERSION     J03854.1  GI:323728
KEYWORDS    6 kd protein; capsid protein; envelope protein.
SOURCE      Western equine encephalomyelitis virus
  ORGANISM  Western equine encephalomyelitis virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
            Alphavirus; WEEV complex.
REFERENCE   1  (bases 1 to 4170)
  AUTHORS   Hahn,C.S., Lustig,S., Strauss,E.G. and Strauss,J.H.
  TITLE     Western equine encephalitis virus is a recombinant virus
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (16), 5997-6001 (1988)
  MEDLINE   88320369
   PUBMED   3413072
COMMENT     Original source text: Western equine encephalitis virus (strain
            BFS1703) RNA, passed in suckling mice and VERO cells, originally
            from Cx.tarsalis.
FEATURES             Location/Qualifiers
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                     NAETFGETLNHLWFNNQPFLWAQLCIPLAALVILFRCFSCCMPFLLVAGVCLGKVDAF
                     EHATTVPNVPGIPYKALVERAGYAPLNLEITVVSSELTPSTNKEYVTCRFHTVIPSPQ
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BASE COUNT     1157 a   1080 c    992 g    941 t
ORIGIN

  Query Match             62.8%;  Score 4075.6;  DB 14;  Length 4170;
  Best Local Similarity   98.6%;  Pred. No. 0;
  Matches 4111;  Conservative    0;  Mismatches   59;  Indels    0;  Gaps    0;

Qy       2316 TCCAGATACGAGATCATACTGGCAGGCCTGATCATCACGTCTCTGTCCACGTTAGCCGAA 2375
             ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db          1 TCCAGATACGAGATCATACTGGCAGGCCTGATCATCACGTCCCTGTCCACGTTAGCCGAA 60

Qy       2376 AGCGTTAAGAACTTCAAGAGCATAAGAGGGAGCCCAATCACCCTCTACGGCTGACCTAAA 2435
             ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db         61 AGCGTTAAGAACTTCAAGAGCATAAGAGGGAACCCAATCACCCTCTACGGCTGACCTAAA 120

Qy       2436 TAGGTGACGTAGTAGACACGCACCTACCCACCGGCAGAATGTTTCCATACCCTCAGCTGA 2495
             |||||||||||||||||||||||||||||||| || ||||||||||||||||||||||||||
Db        121 TAGGTGACGTAGTAGACACGCACCTACCCACCGCCAAAATGTTTCCATACCCTCAGCTGA 180

Qy       2496 ACTTTCCACCAGTTTACCCTACAAATCCGATGGCTTACCGAGATCCAAACCCTCCTAGGC 2555
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Db        181 ACTTTCCACCAGTTTACCCTACAAATCCGATGGCTTACCGAGATCCAAACCCTCCTAGGT 240

Qy       2556 GCCGCTGGAGGCCGTTTCGGCCCCCGCTGGCTGCTCAAATCGAAGATCTTAGGAGGTCGA 2615
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Db        241 GCCGCTGGAGGCCGTTTCGGCCCCCGCTGGCTGCTCAAATCGAAGATCTTAGGAGGTCGA 300

Qy       2616 TAGTCAACTTGACTTTCAAACAACGATCACCTAATCCGCCGCCAGGTCCACCGCCAAAGA 2675
             ||| |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TAGCCAACTTAACTTTCAAACAACGATCACCTAATCCGCCGCCAGGTCCACCGCCAAAGA 360

Qy       2676 AGAAGAAGAGTGCTCCTAAGCCAAAACCTACTCAGCCTAAAAAGAAGAAGCAGCAAGCCA 2735
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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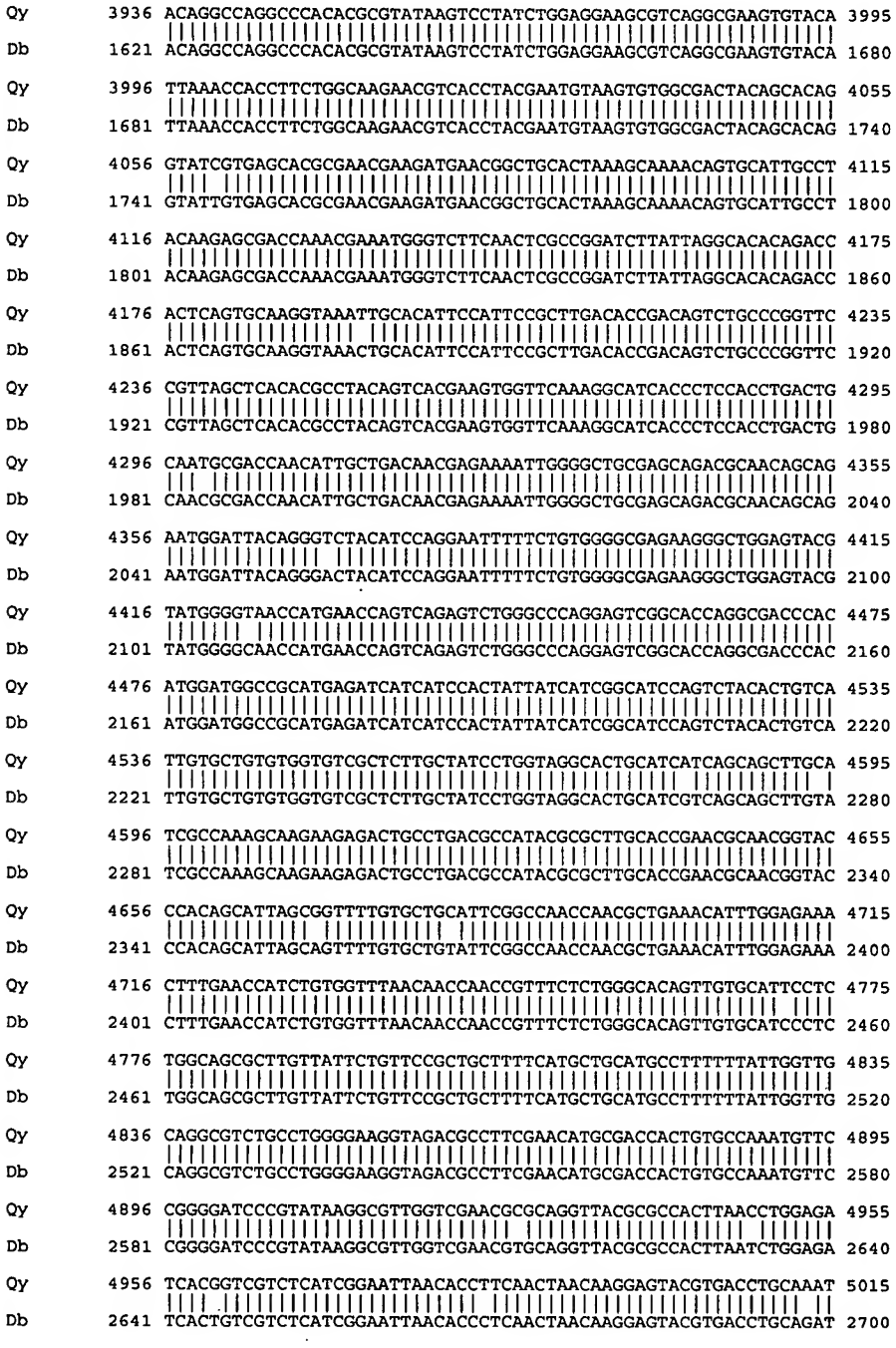
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RESULT 3
AF229608
LOCUS       AF229608                4047 bp    RNA     linear   VRL 27-MAR-2000
DEFINITION  Western equine encephalomyelitis virus structural polyprotein gene,
            complete cds.
ACCESSION   AF229608
VERSION     AF229608.1  GI:7330240
KEYWORDS    .
SOURCE      Western equine encephalomyelitis virus
  ORGANISM  Western equine encephalomyelitis virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
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REFERENCE   1  (bases 40 to 816)
  AUTHORS   Uryvaev,L.V., Lebedev,A.Iu., Sokolova,T.M. and Iuferov,V.P.
  TITLE     Primary structure of the nucleocapsid gene C and the protein coded
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  JOURNAL   Dokl. Akad. Nauk. 344 (3), 397-401 (1995)
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REFERENCE   2  (bases 40 to 816)
  AUTHORS   Uryvaev,L.V. and Lebedev,A.Iu.
  TITLE     Comparative analysis of primary structure of nucleocapsid protein
            from Western equine encephalomyelitis virus and other alphaviruses
  JOURNAL   Vopr. Virusol. 41 (6), 252-259 (1996)
  MEDLINE   97130212
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REFERENCE   3  (bases 997 to 2265)
  AUTHORS   Uryvaev,L.V., Lebedev,A.Iu., Sokolova,T.M. and Iuferov,V.P.
  TITLE     Capsid glycoprotein of E2 Encephalitis Virus, Western Equine:
            primary structure of gene and its product
  JOURNAL   Dokl. Akad. Nauk. 357 (1), 134-139 (1997)
  MEDLINE   98100973
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REFERENCE   4  (bases 1 to 4047)
  AUTHORS   Uryvaev,L.V.
  TITLE     Primary structure of WEEV 26S RNA
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  AUTHORS   Uryvaev,L.V.
  TITLE     Direct Submission
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ORIGIN

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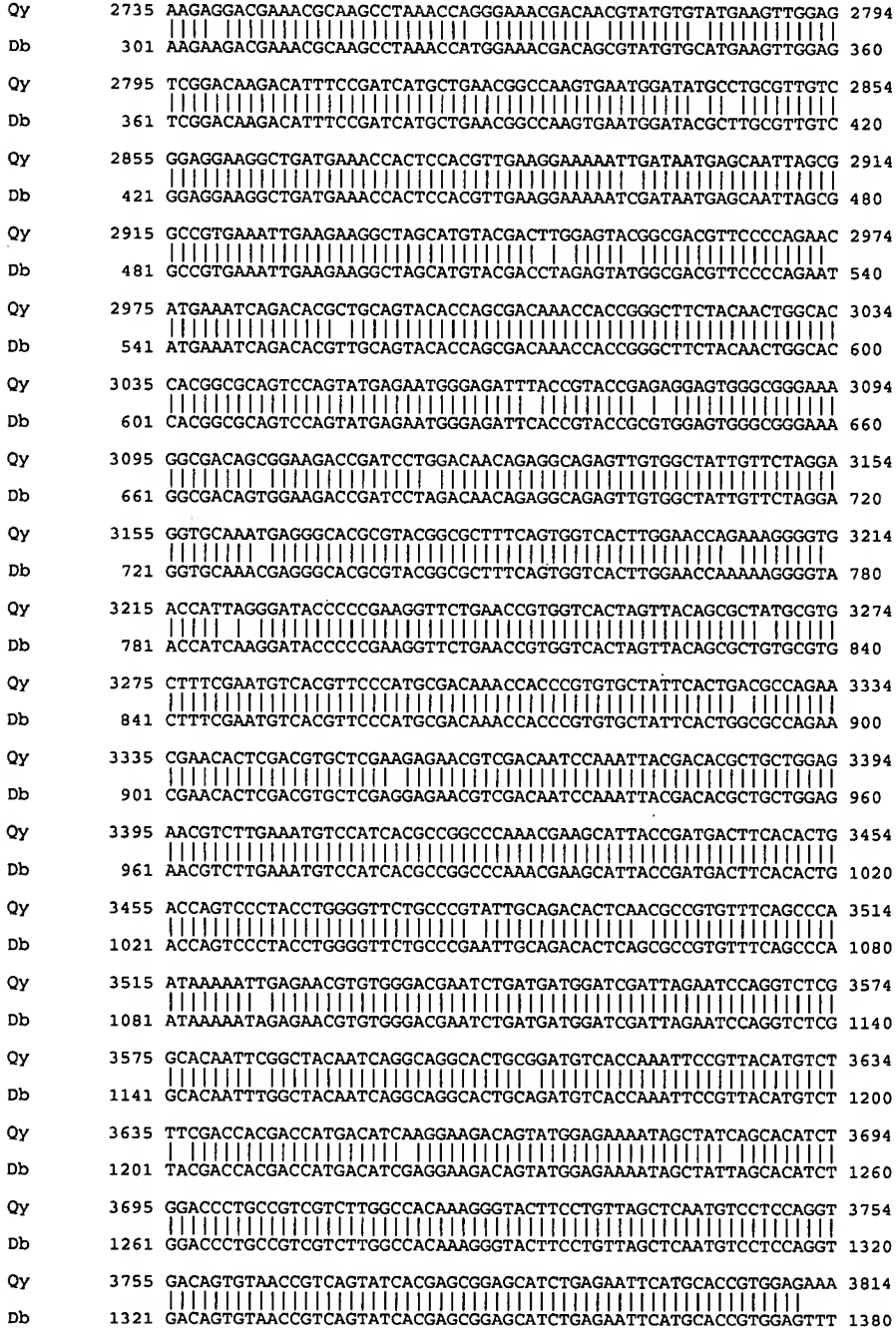
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  JOURNAL   Unpublished
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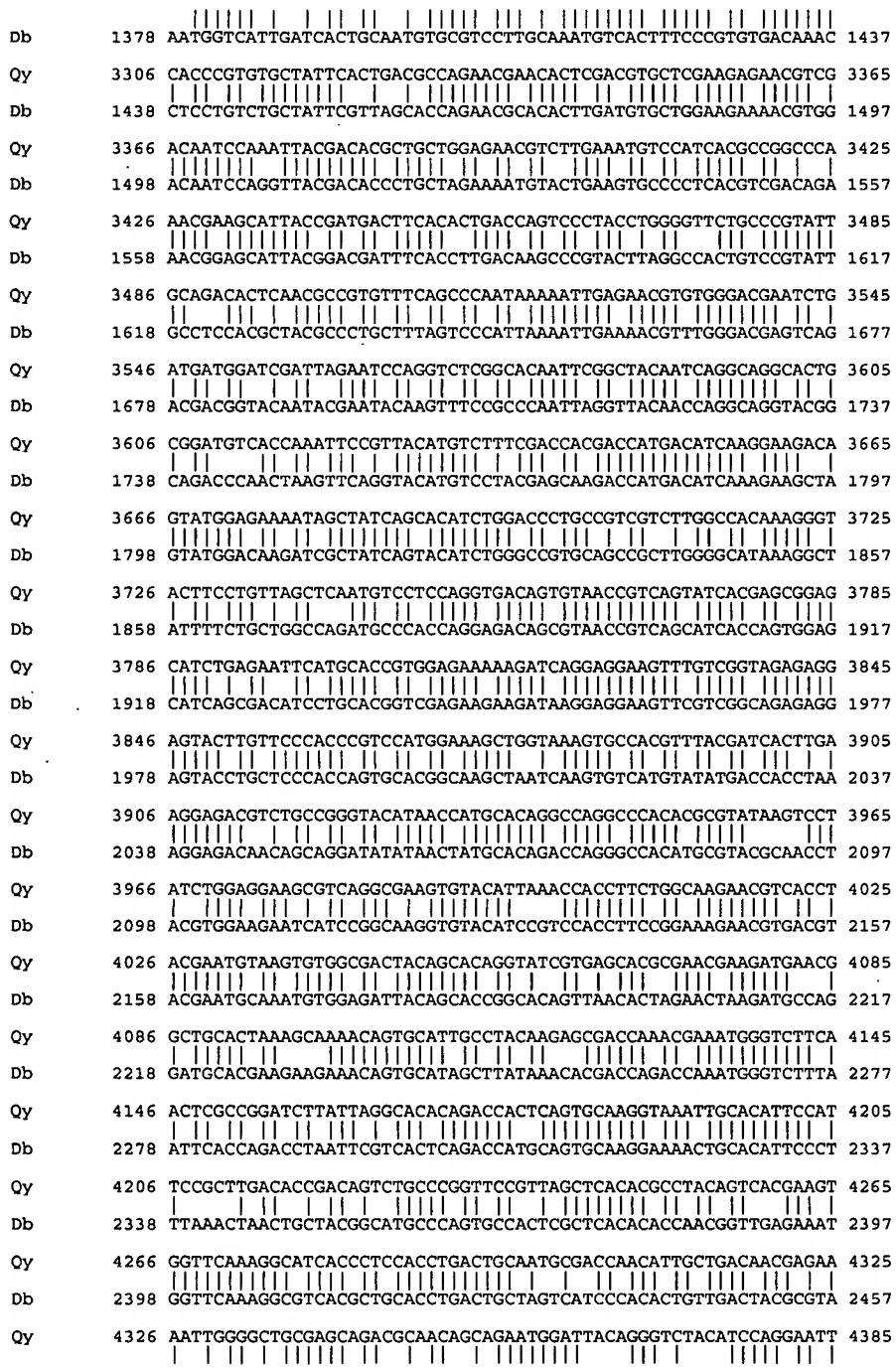
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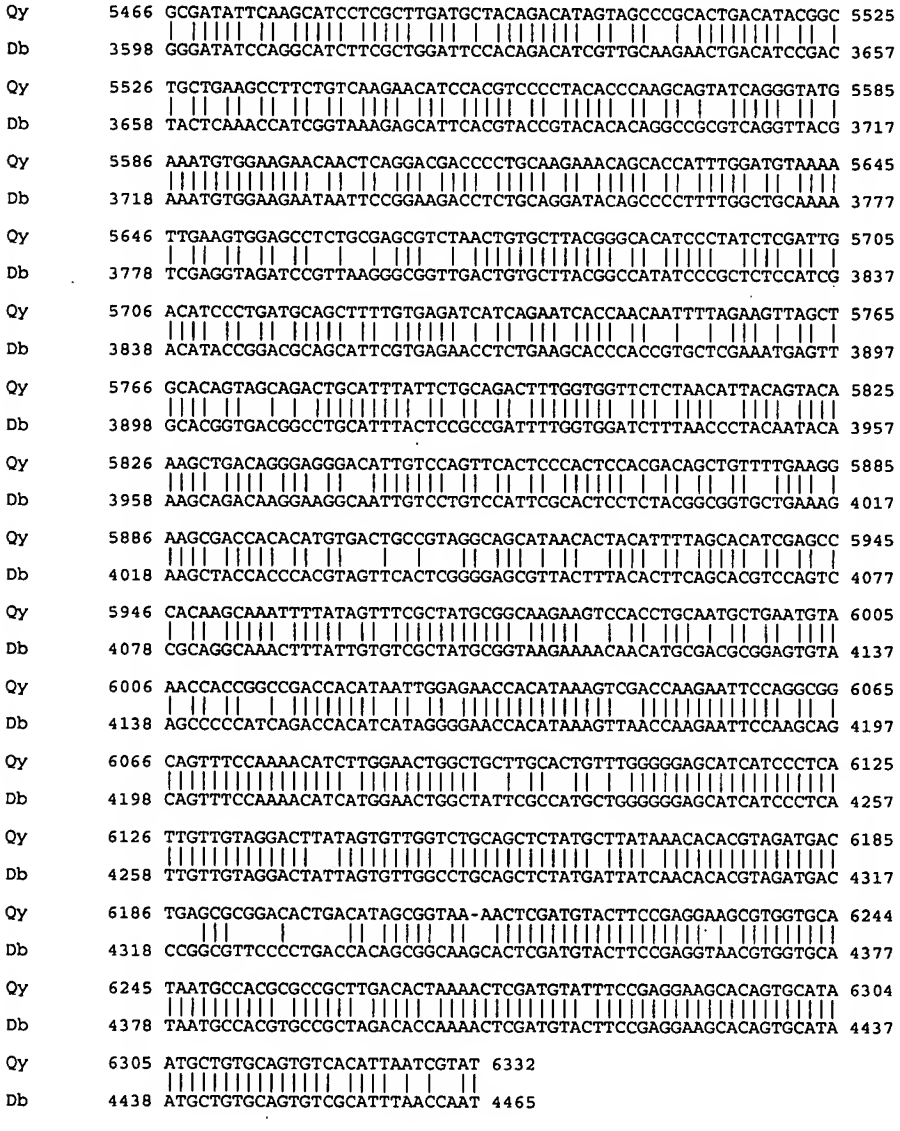

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  AUTHORS   Johnston,R.E., Davis,N.L. and Simpson,D.A.
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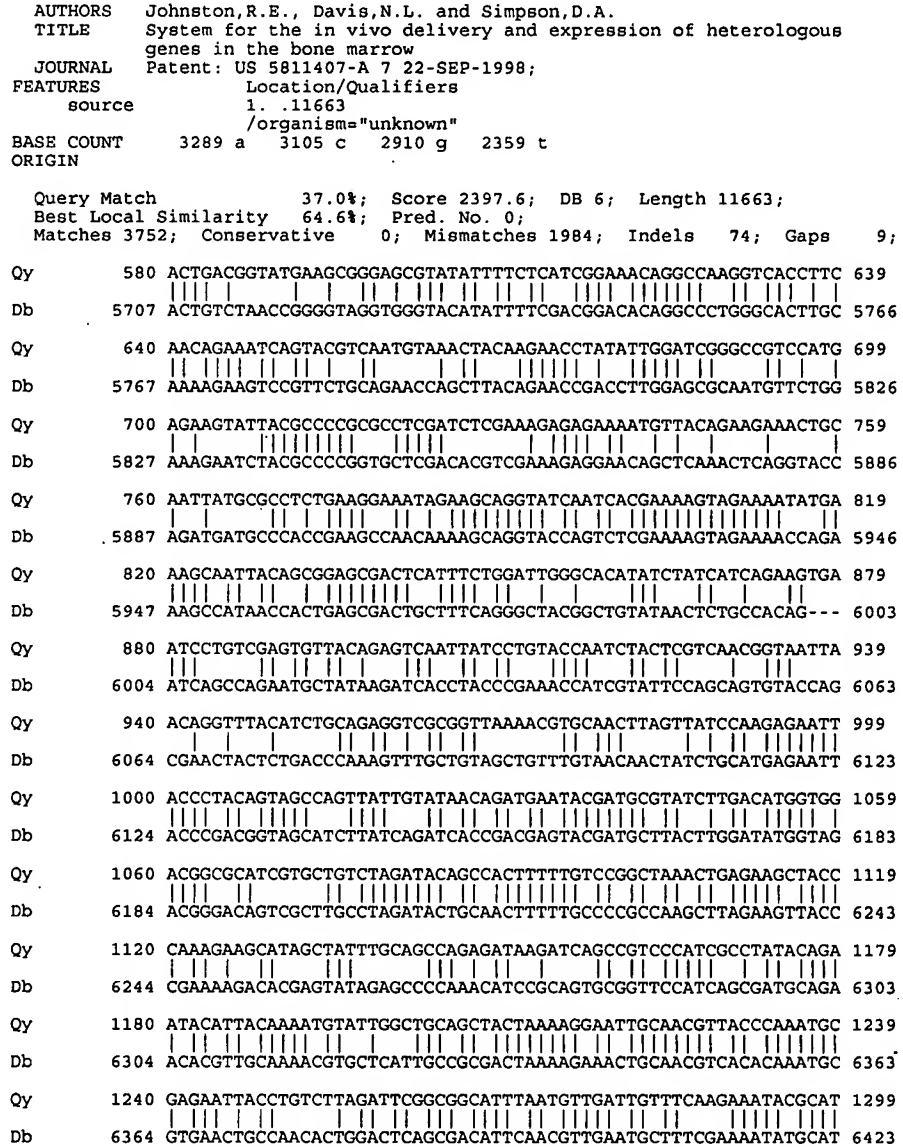

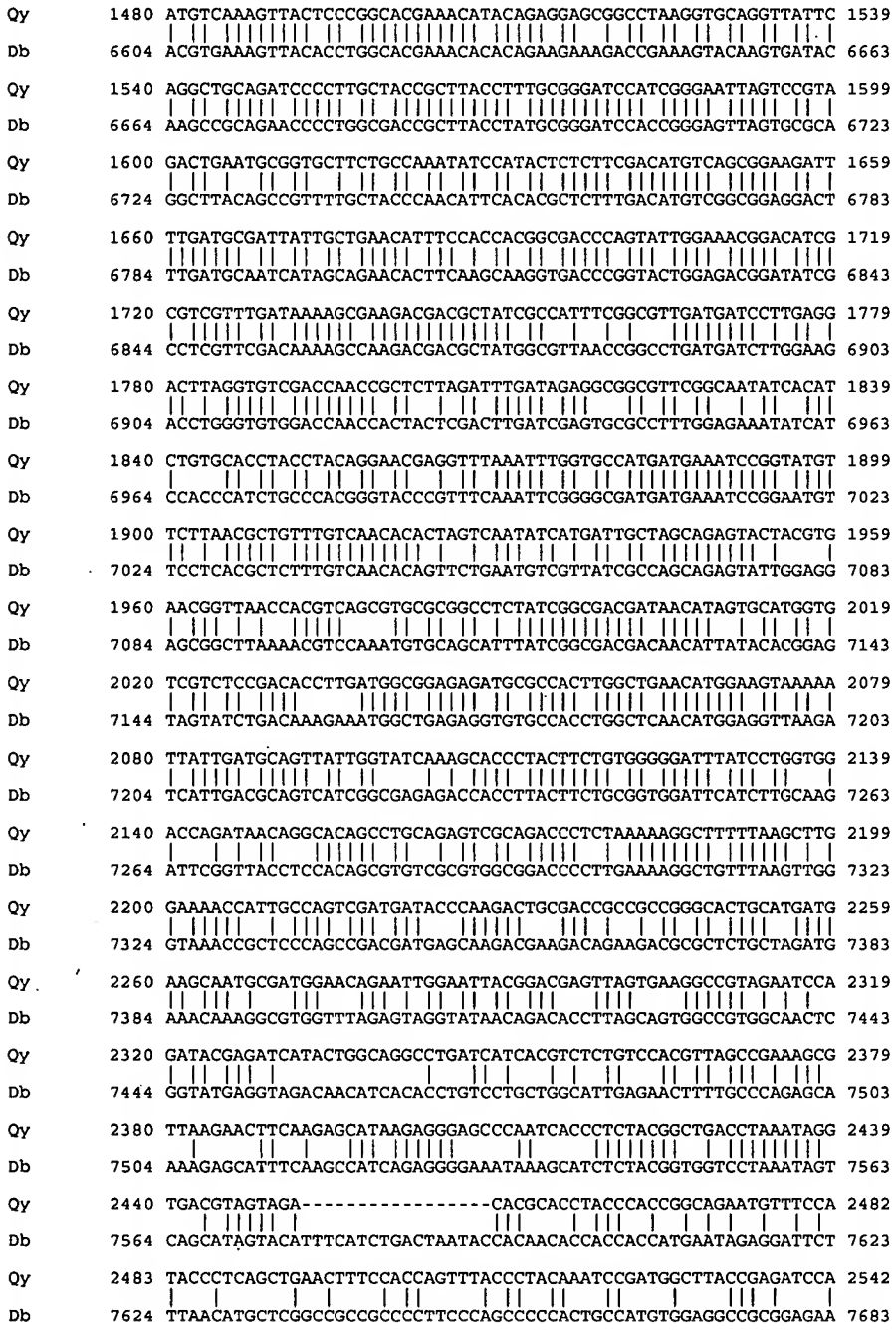

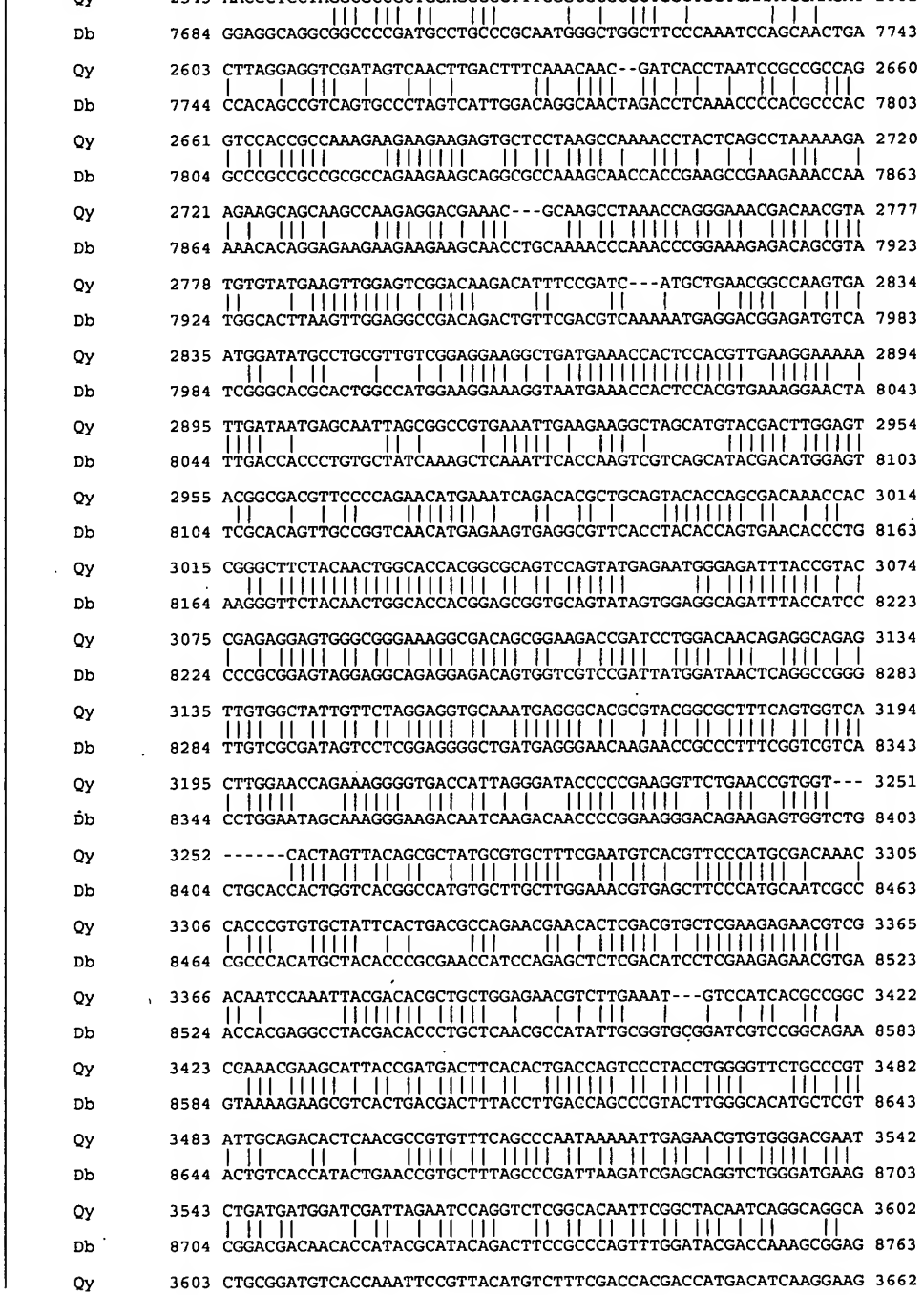

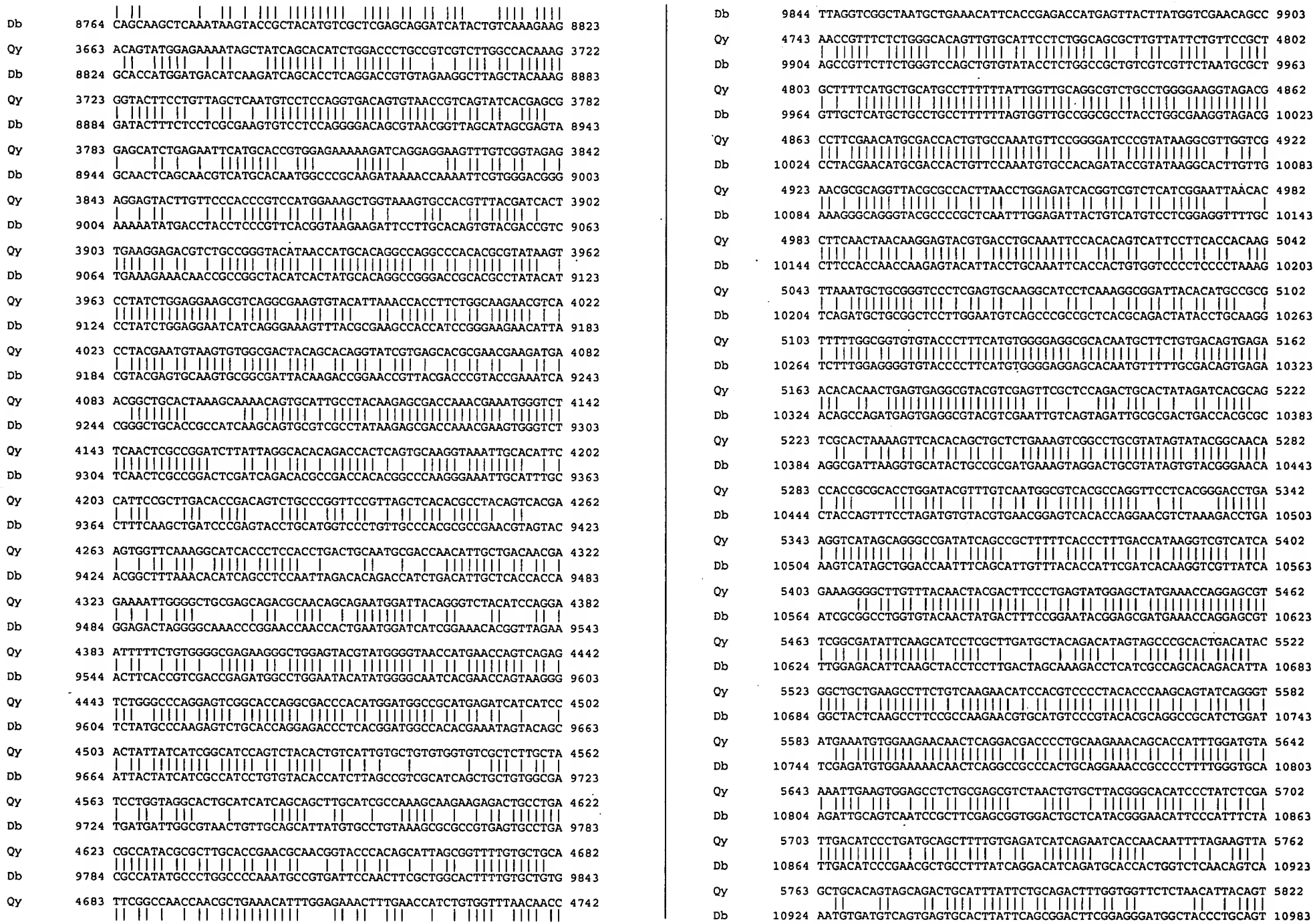

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VERSION AR096557.1 GI:10025467
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 11663)
AUTHORS Johnston,R.E., Davis,N.L. and Simpson,D.A.
TITLE System for the in vivo delivery and expression of heterologous genes in the bone marrow
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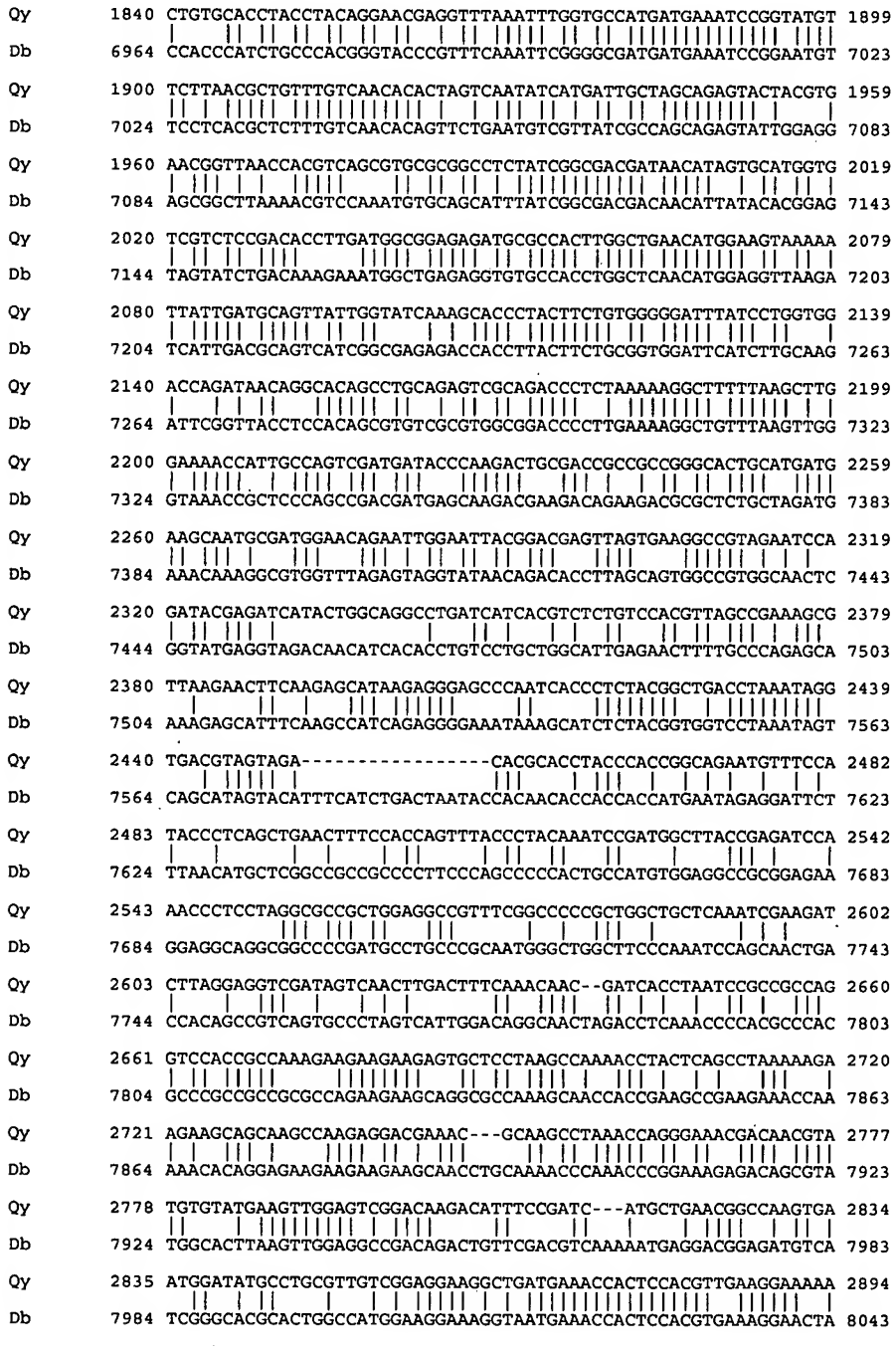

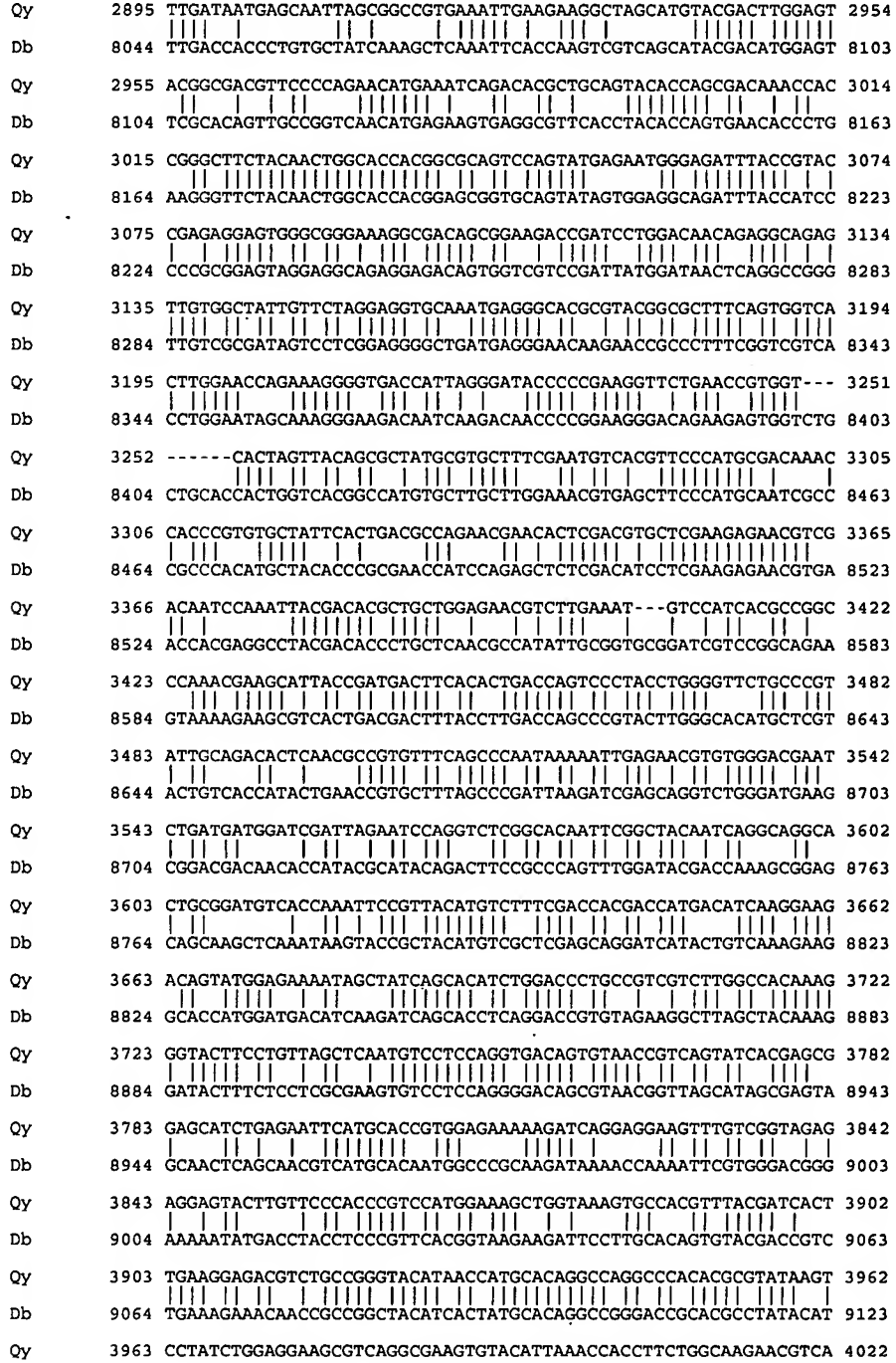

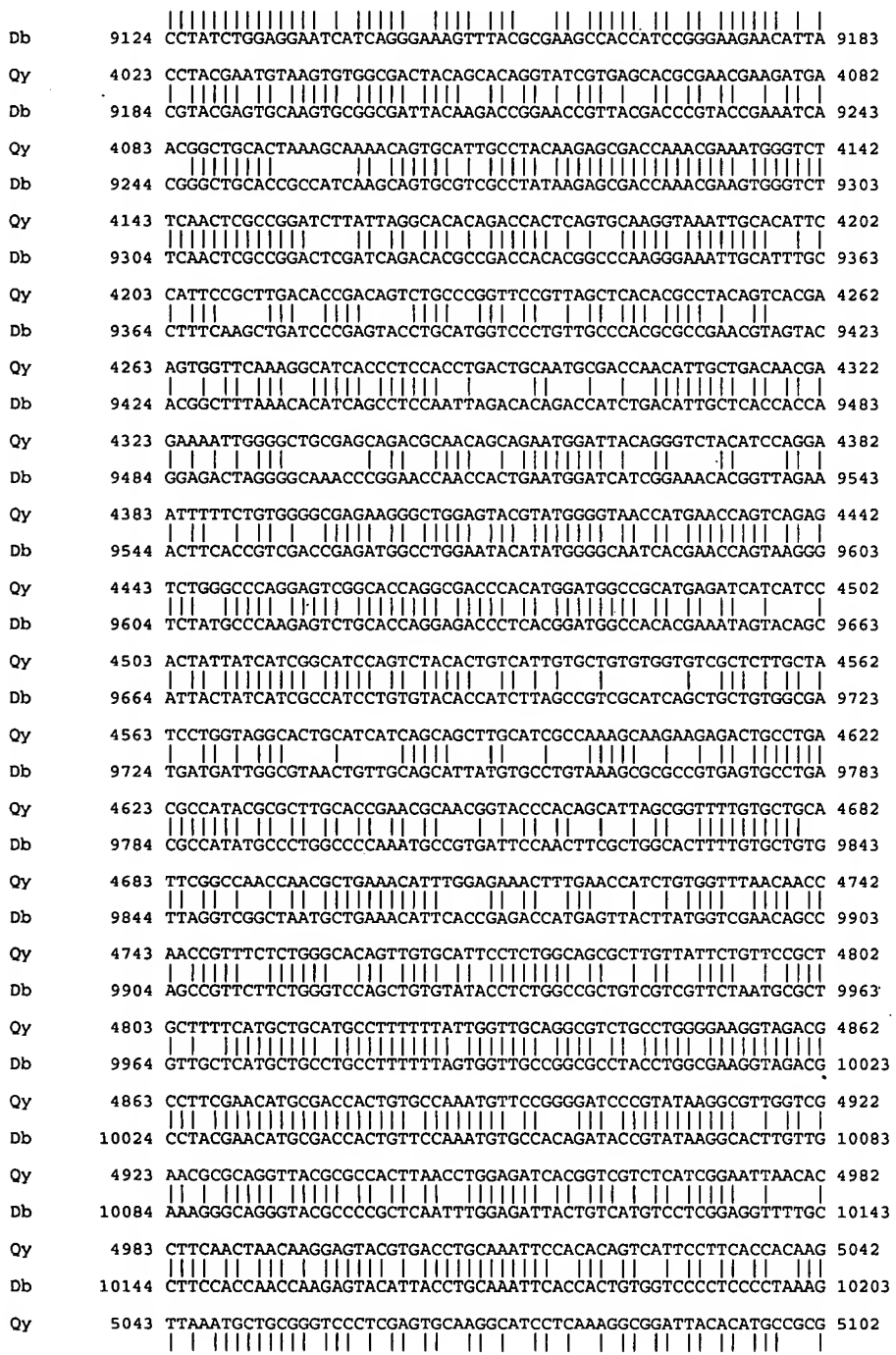
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RESULT 7
BD071122
LOCUS       BD071122               11663 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  System for the in vivo delivery and expression of heterologous
            genes in the bone marrow.
ACCESSION   BD071122
VERSION     BD071122.1  GI:22616725
KEYWORDS    JP 2001515348-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 11663)
  AUTHORS   Johnston,R.E., Davis,N.L. and Simpson,D.A.
  TITLE     System for the in vivo delivery and expression of heterologous
            genes in the bone marrow
  JOURNAL   Patent: JP 2001515348-A 3 18-SEP-2001;
            UNIVERSITY OF NORTH CAROLINA AT CHAPEL HILL
COMMENT     OS   Girdwood S.A.
            PN   JP 2001515348-A/3
            PD   18-SEP-2001
            PF   18-FEB-1998 JP 1998536760
            PR   19-FEB-1997 US    08/801263
            PI   ROBERT E JOHNSTON,NANCY L DAVIS,DENNIS A SIMPSON PC
            C12N15/86,C12N15/33,C12N7/01,C12N5/10,A61K39/12,A61K48/00 CC
            System for the in vivo delivery and expression of heterologous
            CC          genes in
            CC   the bone marrow
            FH   Key             Location/Qualifiers
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FEATURES             Location/Qualifiers
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  Matches 3752;  Conservative    0;  Mismatches 1984;  Indels   74;  Gaps    9;

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Qy        640 AACAGAAATCAGTACGTCAATGTAAACTACAAGAACCTATATTGGATCGGGCCGTCCATG 699
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Qy        820 AAGCAATTACAGCGGAGCGACTCATTTCTGGATTGGGCACATATCTATCATCAGAAGTGA 879

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Qy       1780 ACTTAGGTGTCGACCAACCGCTCTTAGATTTGATAGAGGCGGCGTTCGGCAATATCACAT 1839
Db       6904 ACCTGGGTGTGGACCAACCACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCAT 6963

Qy       1840 CTGTGCACCTACCTACAGGAACGAGGTTTAAATTTGGTGCCATGATGAAATCCGGTATGT 1899
Db       6964 CCACCCATCTGCCCACGGGTACCCGTTTCAAATTCGGGGCGATGATGAAATCCGGAATGT 7023

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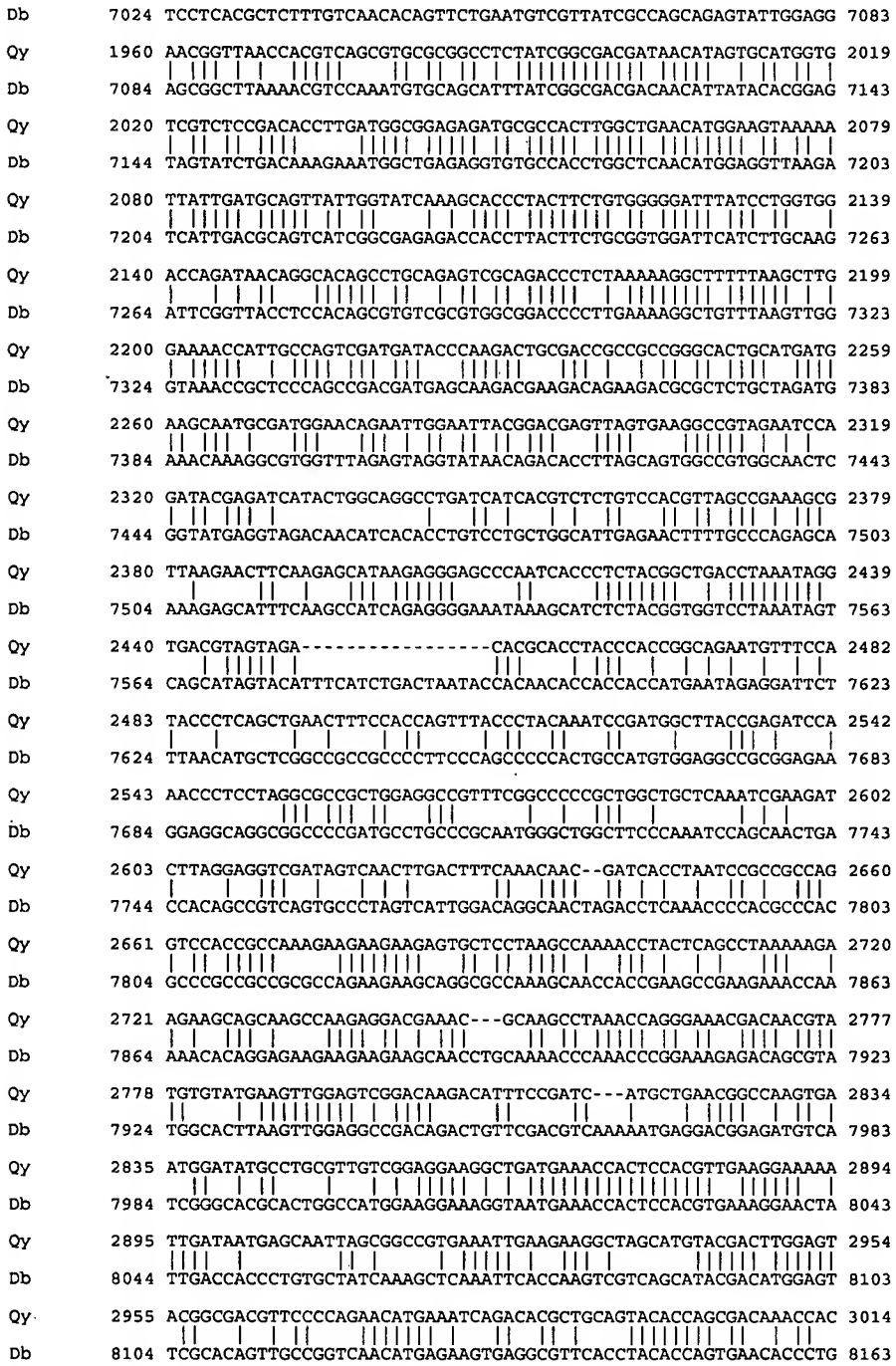

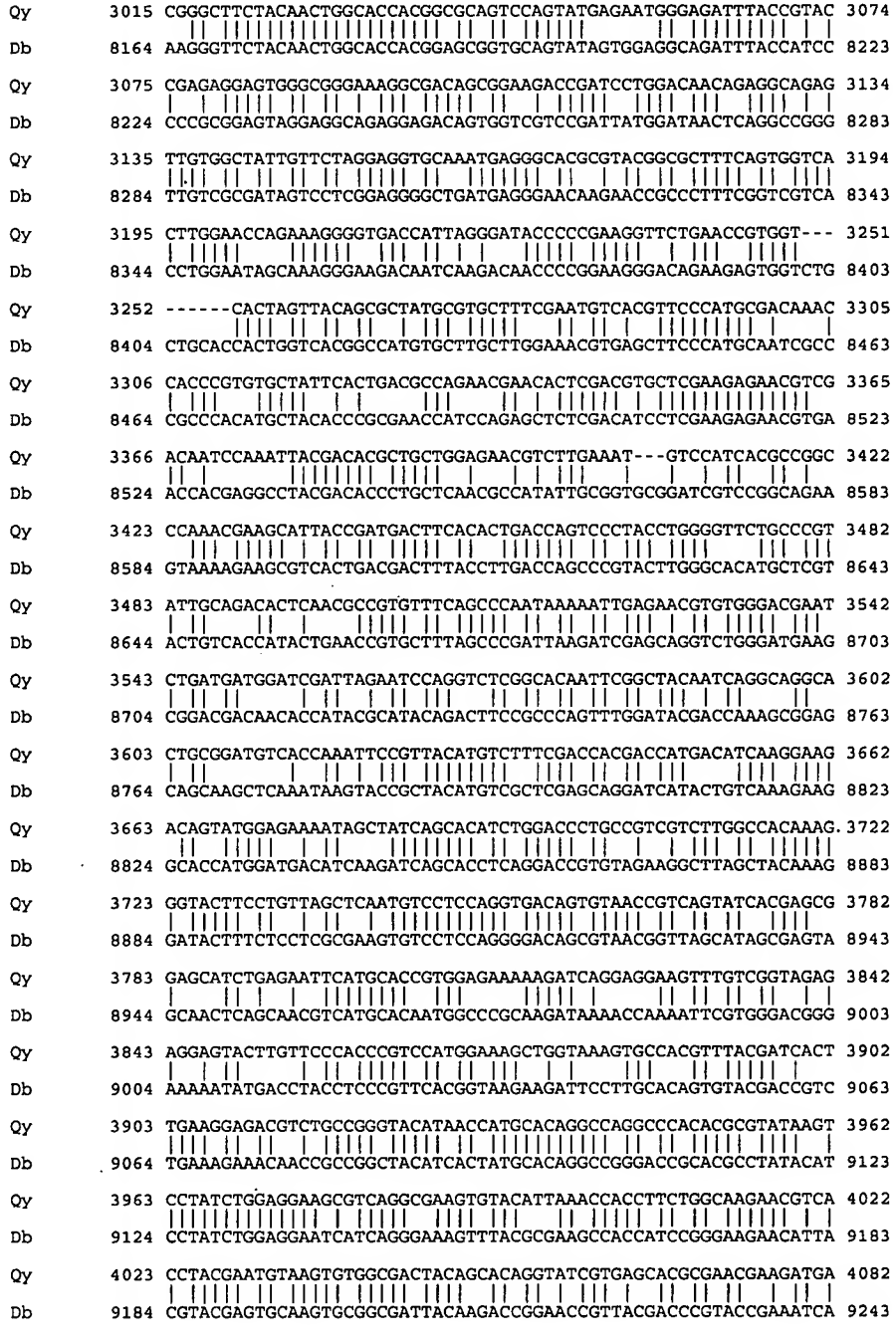

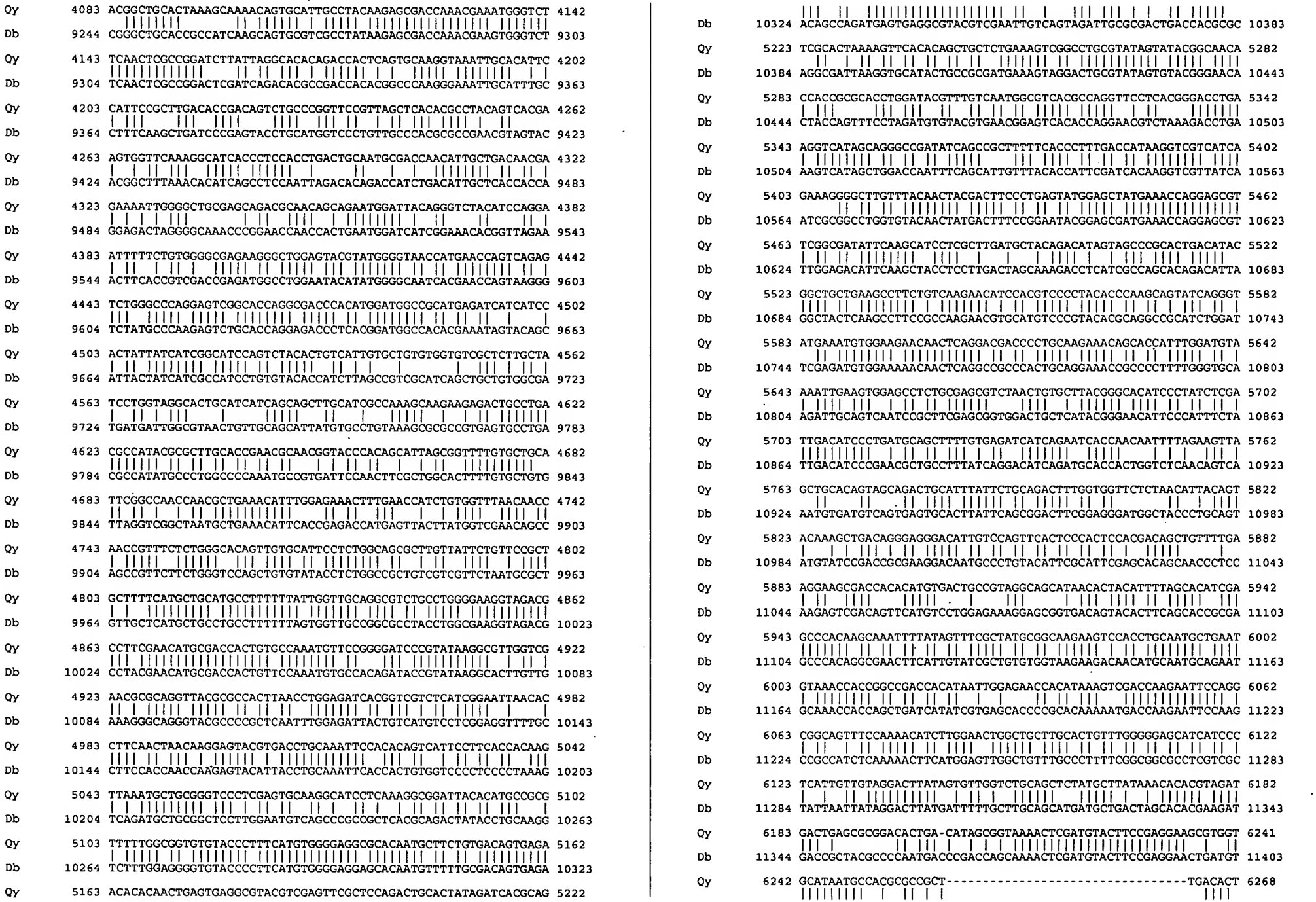

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RESULT 8
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LOCUS       AR042409               11663 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5811407.
ACCESSION   AR042409
VERSION     AR042409.1  GI:5962905
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11663)
  AUTHORS   Johnston,R.E., Davis,N.L. and Simpson,D.A.
  TITLE     System for the in vivo delivery and expression of heterologous
            genes in the bone marrow
  JOURNAL   Patent: US 5811407-A 1 22-SEP-1998;
FEATURES             Location/Qualifiers
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Qy        580 ACTGACGGTATGAAGCGGGAGCGTATATTTTCTCATCGGAAACAGGCCAAGGTCACCTTC 639
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Db       5827 AAAGAATCTACGCCCCGGTGCTCGACACGTCGAAAGAGGAACAGCTCAAACTCAGGTACC 5886

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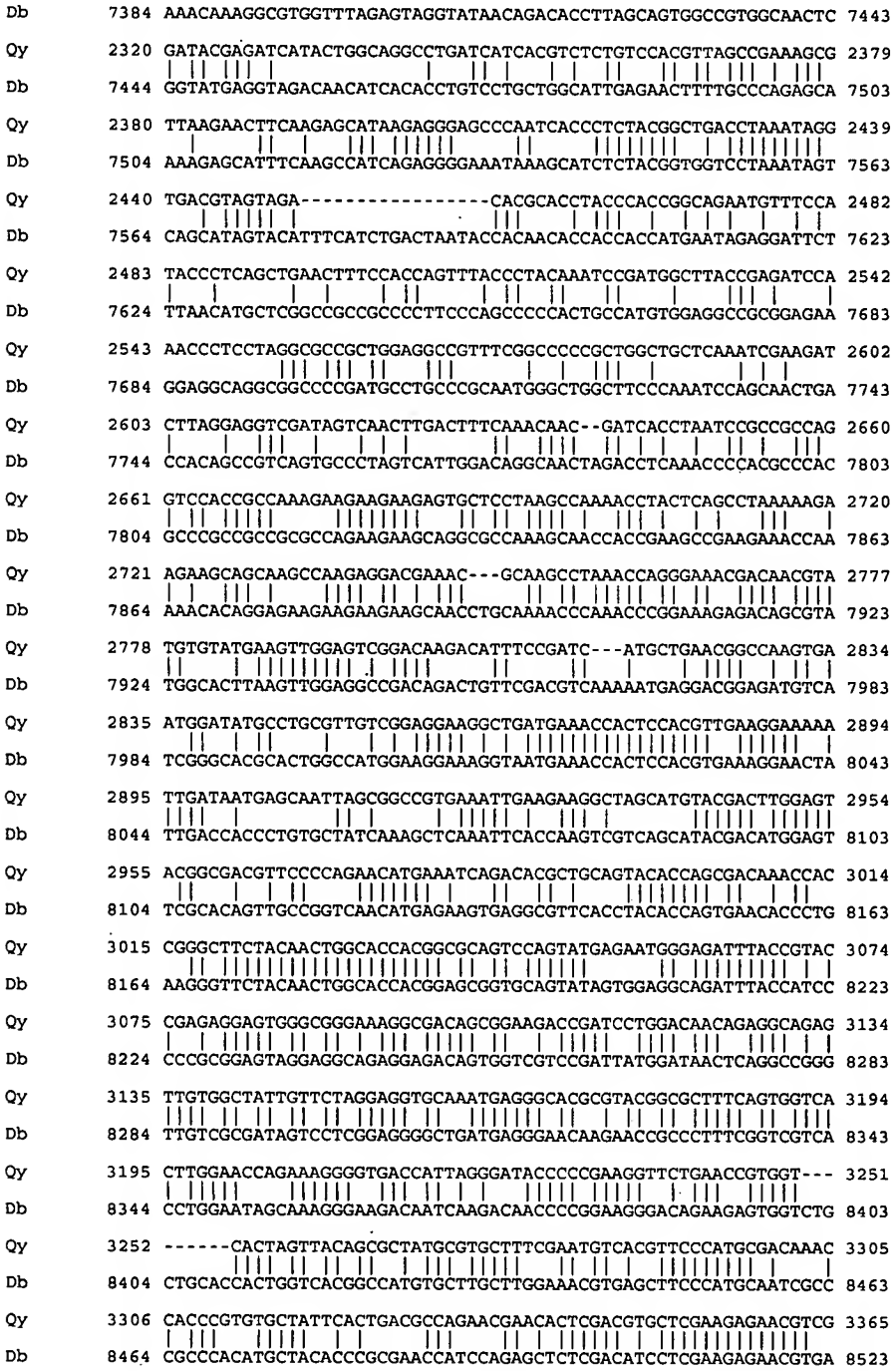

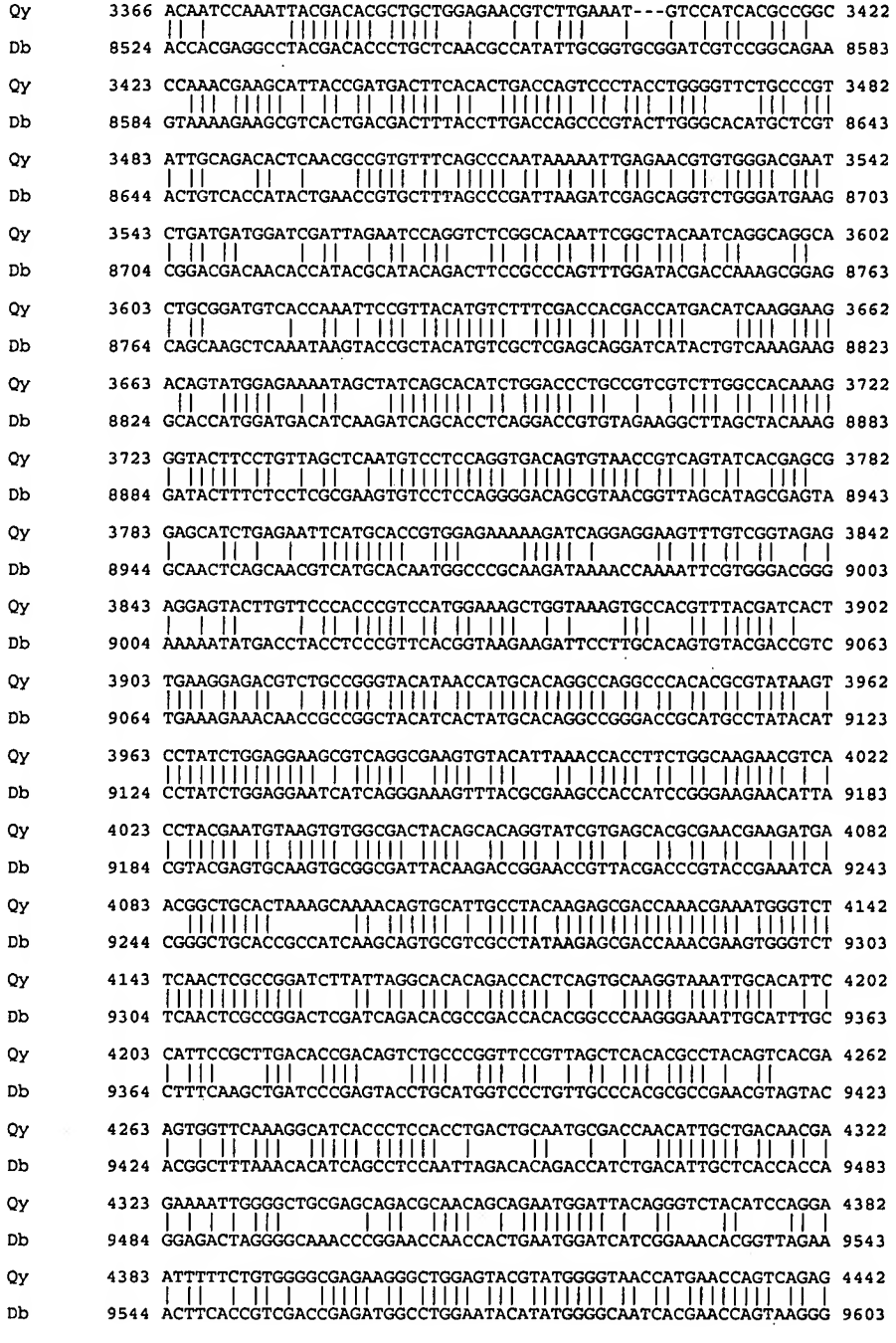

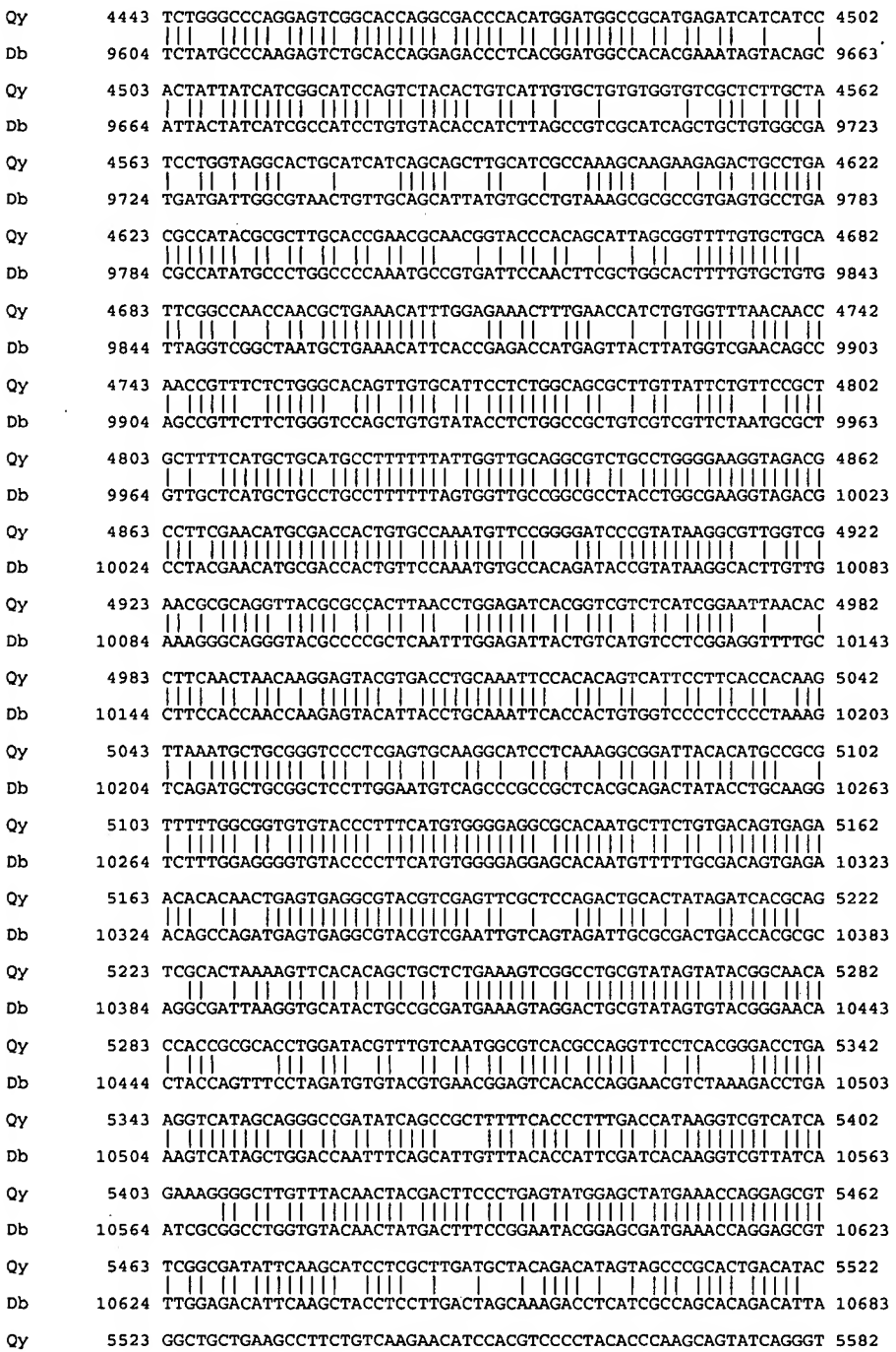

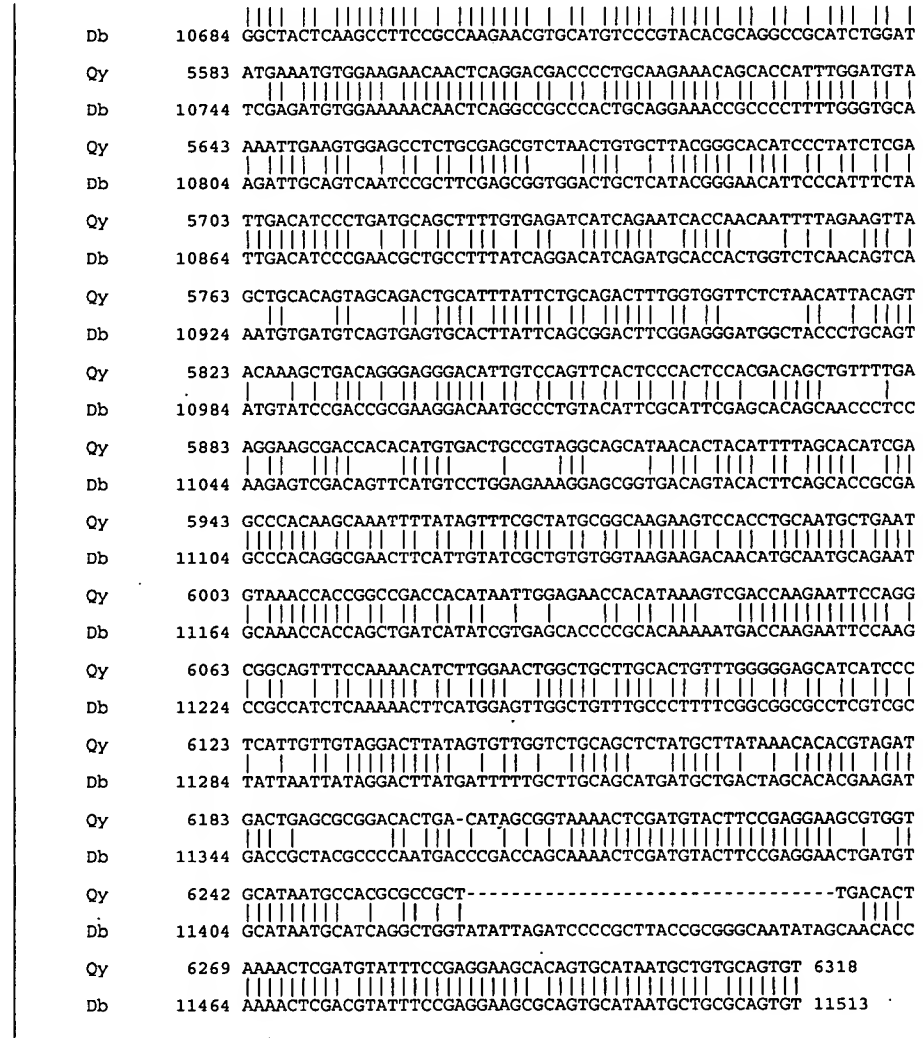

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VERSION     AR096555.1  GI:10025463
KEYWORDS    .
SOURCE      Unknown.
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REFERENCE   1  (bases 1 to 11663)
  AUTHORS   Johnston,R.E., Davis,N.L. and Simpson,D.A.
  TITLE     System for the in vivo delivery and expression of heterologous
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Db       5827 AAAGAATCTACGCCCCGGTGCTCGACACGTCGAAAGAGGAACAGCTCAAACTCAGGTACC 5886

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Db       5887 AGATGATGCCCACCGAAGCCAACAAAAGCAGGTACCAGTCTCGAAAAGTAGAAAACCAGA 5946

Qy        820 AAGCAATTACAGCGGAGCGACTCATTTCTGGATTGGGCACATATCTATCATCAGAAGTGA 879
              |||| || ||  | |||||||||  |||| ||  |  |     |||    ||  |   ||
Db       5947 AAGCCATAACCACTGAGCGACTGCTTTCAGGGCTACGACTGTATAACTCTGCCACAG--- 6003

Qy        880 ATCCTGTCGAGTGTTACAGAGTCAATTATCCTGTACCAATCTACTCGTCAACGGTAATTA 939
              |||      || || || |   |||  || ||    ||||   || ||     |  |||
Db       6004 ATCAGCCAGAATGCTATAAGATCACCTACCCGAAACCATCGTATTCCAGCAGTGTACCAG 6063

Qy        940 ACAGGTTTACATCTGCAGAGGTCGCGGTTAAAACGTGCAACTTAGTTATCCAAGAGAATT 999
                |  |   |     || || | || ||      || |||     | | || |||||||
Db       6064 CGAACTACTCTGACCCAAAGTTTGCTGTAGCTGTTTGTAACAACTATCTGCATGAGAATT 6123

Qy       1000 ACCCTACAGTAGCCAGTTATTGTATAACAGATGAATACGATGCGTATCTTGACATGGTGG 1059
              |||| || |||||   ||||    || || || || |||||||| ||  | || ||||| |
Db       6124 ACCCGACGGTAGCATCTTATCAGATCACCGACGAGTACGATGCTTACTTGGATATGGTAG 6183

Qy       1060 ACGGCGCATCGTGCTGTCTAGATACAGCCACTTTTTGTCCGGCTAAACTGAGAAGCTACC 1119
              ||||  ||      || |||||||| || |||||||| || || || || ||||| ||||
Db       6184 ACGGGACAGTCGCTTGCCTAGATACTGCAACTTTTTGCCCCGCCAAGCTTAGAAGTTACC 6243

Qy       1120 CAAAGAAGCATAGCTATTTGCAGCCAGAGATAAGATCAGCCGTCCCATCGCCTATACAGA 1179
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Db       6244 CGAAAAGACACGAGTATAGAGCCCCAAACATCCGCAGTGCGGTTCCATCAGCGATGCAGA 6303

Qy       1180 ATACATTACAAAATGTATTGGCTGCAGCTACTAAAAGGAATTGCAACGTTACCCAAATGC 1239
              | || || ||||| ||   |   ||| || |||||||| || |||||||| || |||||||
Db       6304 ACACGTTGCAAAACGTGCTCATTGCCGCGACTAAAAGAAACTGCAACGTCACACAAATGC 6363

Qy       1240 GAGAATTACCTGTCTTAGATTCGGCGGCATTTAATGTTGATTGTTTCAAGAAATACGCAT 1299
              | ||| | ||     | || || ||| |||| || ||||| || ||     ||||| ||||
Db       6364 GTGAACTGCCAACACTGGACTCAGCGACATTCAACGTTGAATGCTTTCGAAAATATGCAT 6423

Qy       1300 GCAATGATGAGTACTGGGATACCTTTCGCGATAACCCTATTCGGCTAACTACAGAGAACG 1359
              |||||||  |||||  |||||    |||   |   || || ||| || | |||||  |||   ||
Db       6424 GCAATGACGAGTATTGGGAGGAGTTTGCCCGAAAGCCAATTAGGATCACTACTGAGTTCG 6483

Qy       1360 TTACGCAATATGTGACAAAGCTGAAAGGGCCGAAAGCAGCAGCATTGTTTGCGAATACTC 1419
              ||||   ||| ||| | |  |||||||| || || || ||| |||| || || || | |
Db       6484 TTACCGCATACGTGGCCAGACTGAAAGGCCCTAAGGCCGCCGCACTGTTCGCAAAGACGC 6543

Qy       1420 ATAATCTAAAACCGTTGCAGGAGATACCAATGGATCAATTCGTCATGGATCTAAAGAGAG 1479
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Qy       1480 ATGTCAAAGTTACTCCCGGCACGAAACATACAGAGGAGCGGCCTAAGGTGCAGGTTATTC 1539
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Qy       1540 AGGCTGCAGATCCCCTTGCTACCGCTTACCTTTGCGGGATCCATCGGGAATTAGTCCGTA 1599
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Qy       1660 TTGATGCGATTATTGCTGAACATTTCCACCACGGCGACCCAGTATTGGAAACGGACATCG 1719
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Qy       1780 ACTTAGGTGTCGACCAACCGCTCTTAGATTTGATAGAGGCGGCGTTCGGCAATATCACAT 1839
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Db       6904 ACCTGGGTGTGGACCAACCACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCAT 6963

Qy       1840 CTGTGCACCTACCTACAGGAACGAGGTTTAAATTTGGTGCCATGATGAAATCCGGTATGT 1899
              |    || || || || || ||  | || |||||  || || ||||||||||||||  ||||
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Qy       1960 AACGGTTAACCACGTCAGCGTGCGCGGCCTCTATCGGCGACGATAACATAGTGCATGGTG 2019
              | ||| | |||||    || || | |||||||||||| ||||| | || || | || || |
Db       7084 AGCGGCTTAAAACGTCCAAATGTGCAGCATTTATCGGCGACGACAACATTATACACGGAG 7143

Qy       2020 TCGTCTCCGACACCTTGATGGCGGAGAGATGCGCCACTTGGCTGAACATGGAAGTAAAAA 2079
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Qy       2320 GATACGAGATCATACTGGCAGGCCTGATCATCACGTCTCTGTCCACGTTAGCCGAAAGCG 2379
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Qy       2543 AACCCTCCTAGGCGCCGCTGGAGGCCGTTTCGGCCCCCGCTGGCTGCTCAAATCGAAGAT 2602
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Db       7684 GGAGGCAGGCGGCCCCGATGCCTGCCCGCAATGGGCTGGCTTCCCAAATCCAGCAACTGA 7743

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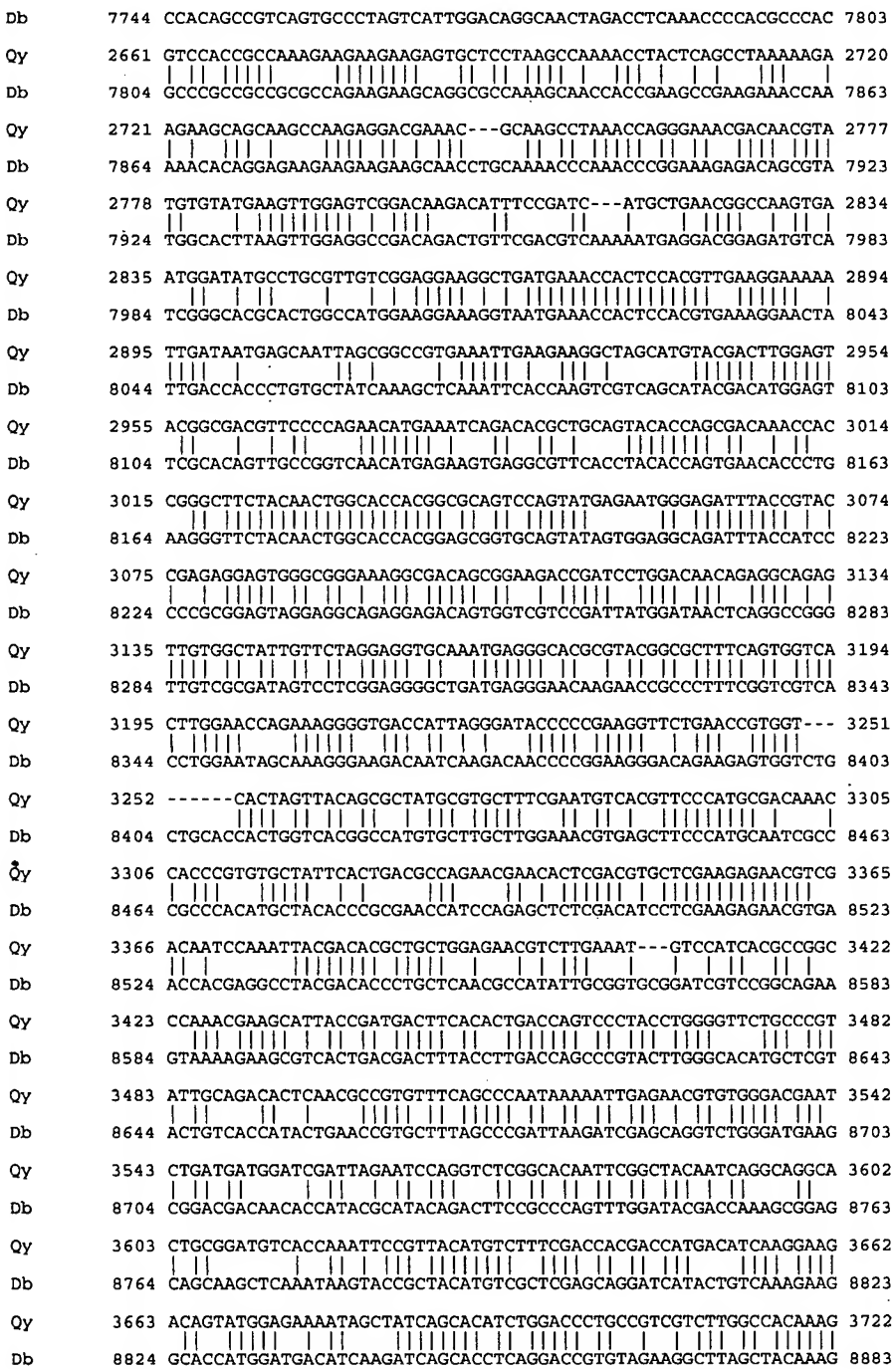
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Qy 2895 TTGATAATGAGCAATTAGCGGCCGTGAAATTGAAGAAGGCTAGCATGTACGACTTGGAGT 2954
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RESULT 10
BD071120

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LOCUS       BD071120               11663 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  System for the in vivo delivery and expression of heterologous
            genes in the bone marrow.
ACCESSION   BD071120
VERSION     BD071120.1  GI:22616723
KEYWORDS    JP 2001515348-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 11663)
  AUTHORS   Johnston,R.E., Davis,N.L. and Simpson,D.A.
  TITLE     System for the in vivo delivery and expression of heterologous
            genes in the bone marrow
  JOURNAL   Patent: JP 2001515348-A.1 18-SEP-2001;
            UNIVERSITY OF NORTH CAROLINA AT CHAPEL HILL
COMMENT     OS   Girdwood S.A.
            PN   JP 2001515348-A/1
            PD   18-SEP-2001
            PF   18-FEB-1998 JP 1998536760
            PR   19-FEB-1997 US    08/801263
            PI   ROBERT E JOHNSTON,NANCY L DAVIS,DENNIS A SIMPSON PC
            C12N15/86,C12N15/33,C12N7/01,C12N5/10,A61K39/12,A61K48/00 CC
            System for the in vivo delivery and expression of heterologous
            CC            genes in
            CC   the bone marrow
            FH   Key             Location/Qualifiers
            FT   CDS             (60). .(7559)
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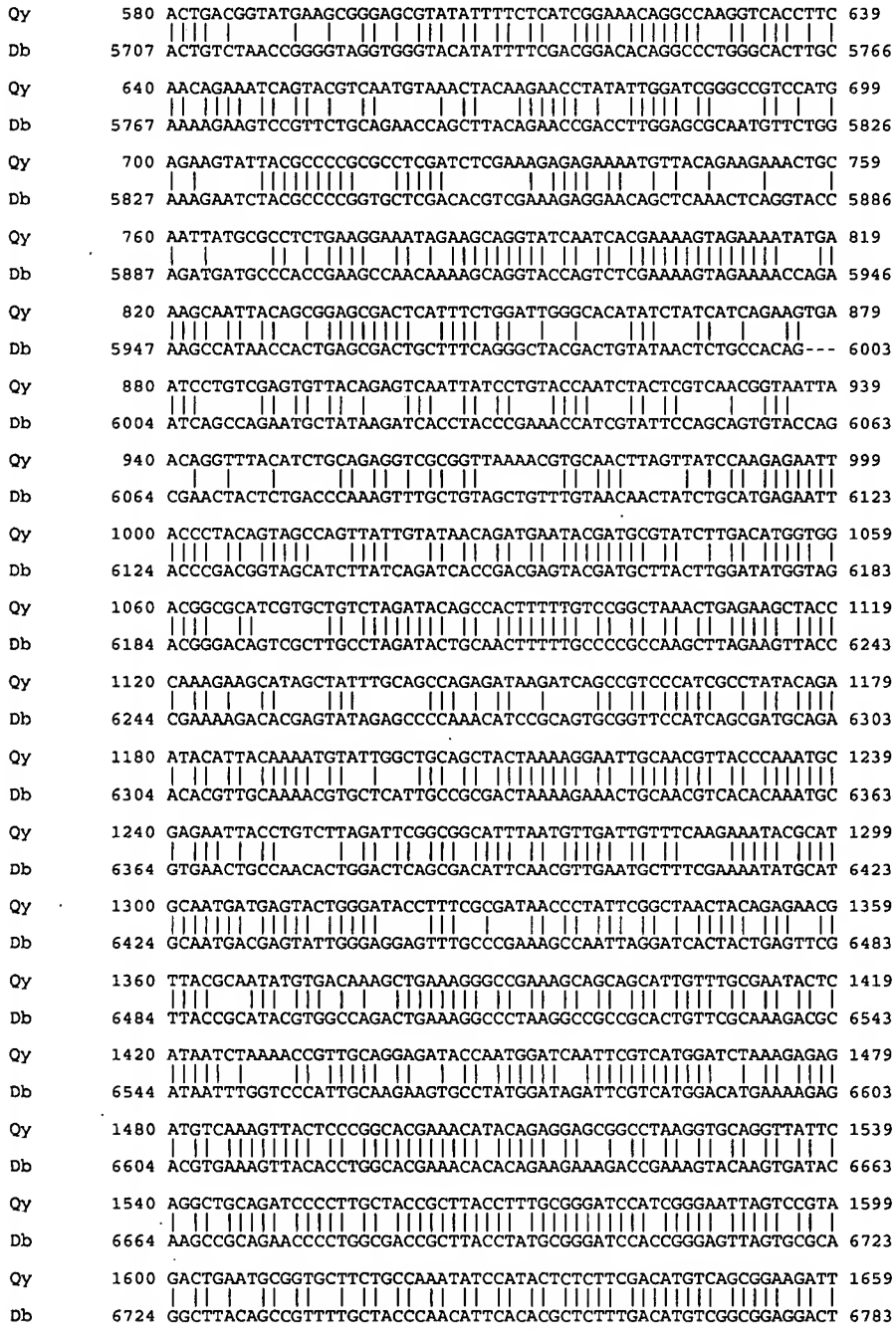

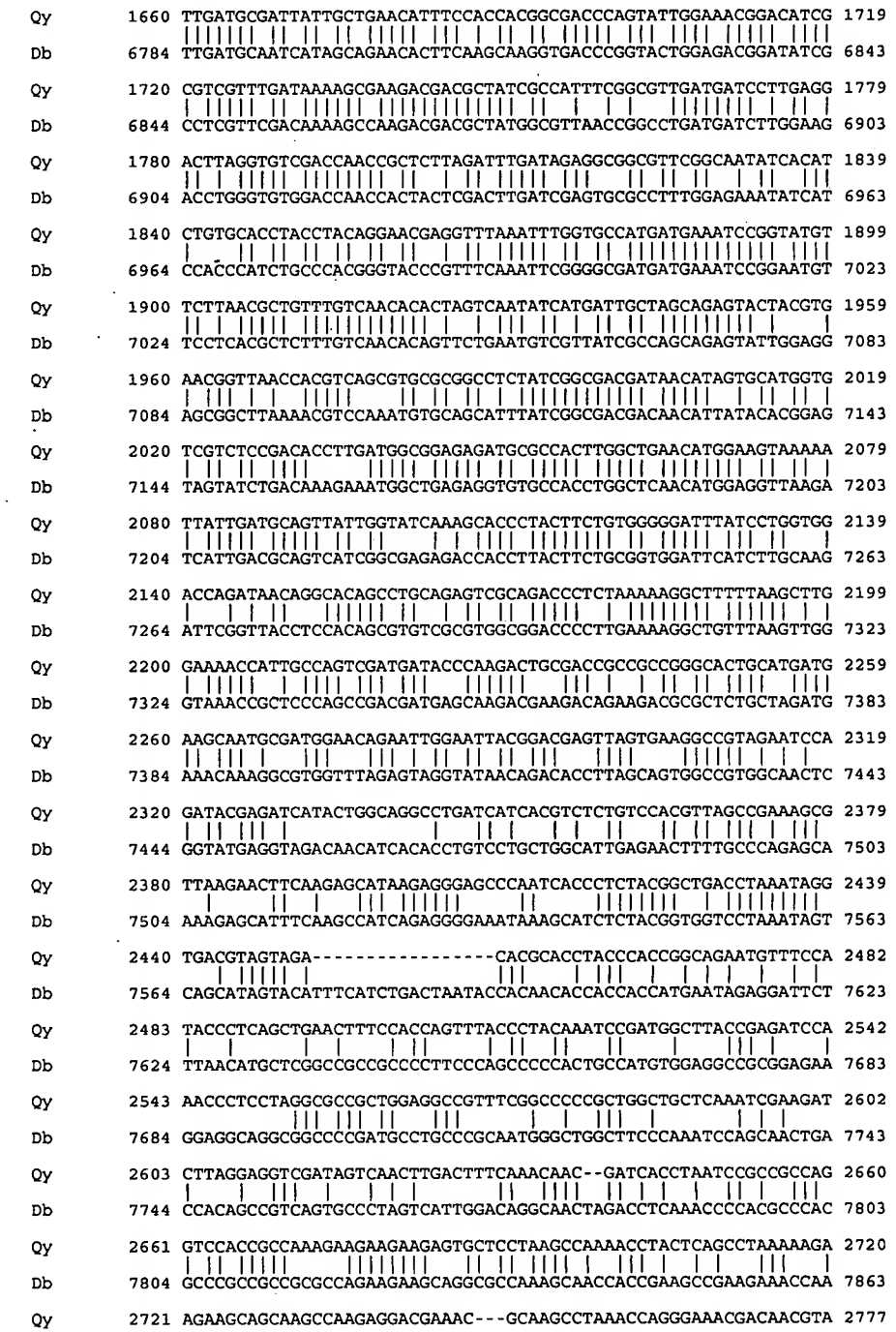

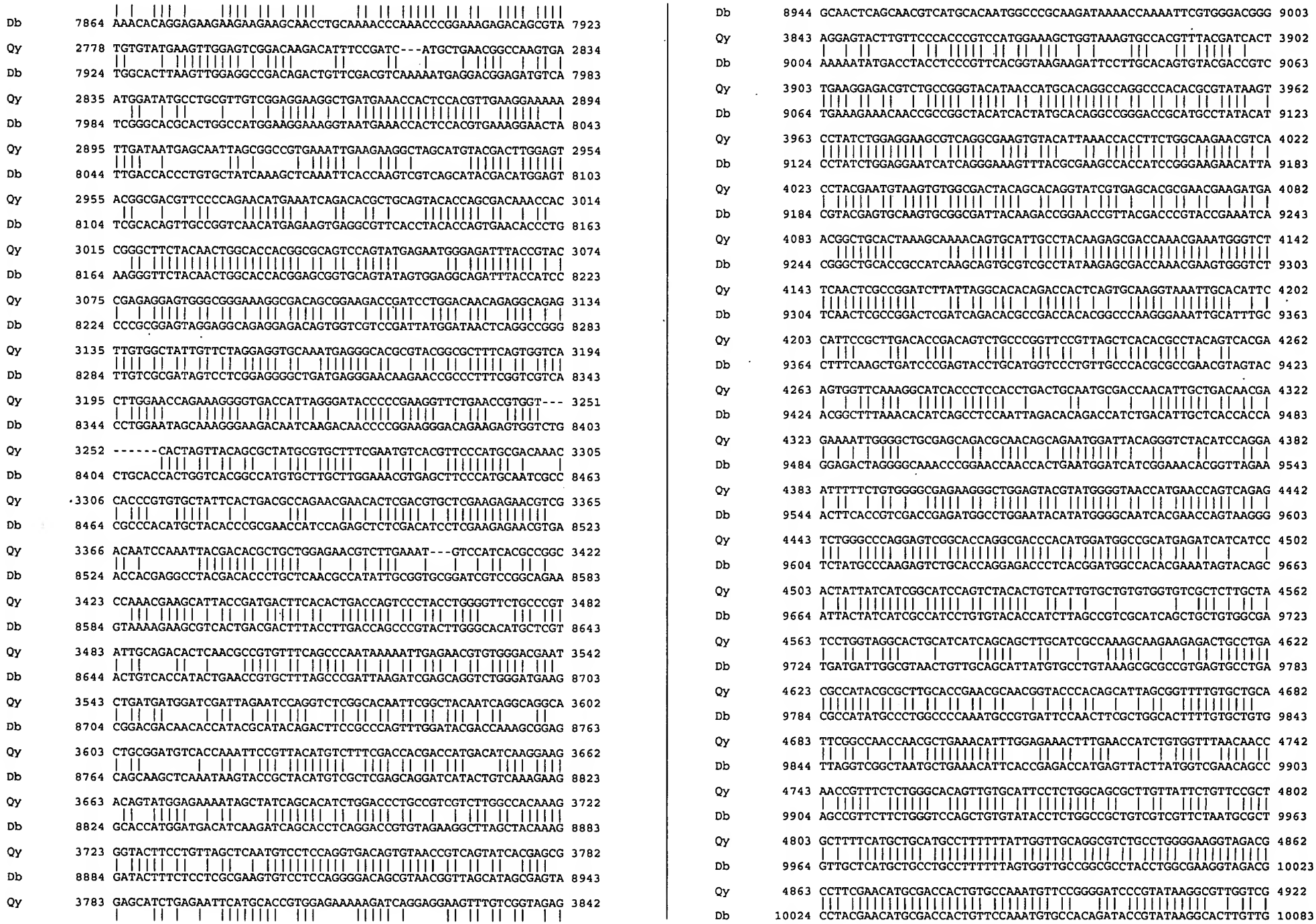

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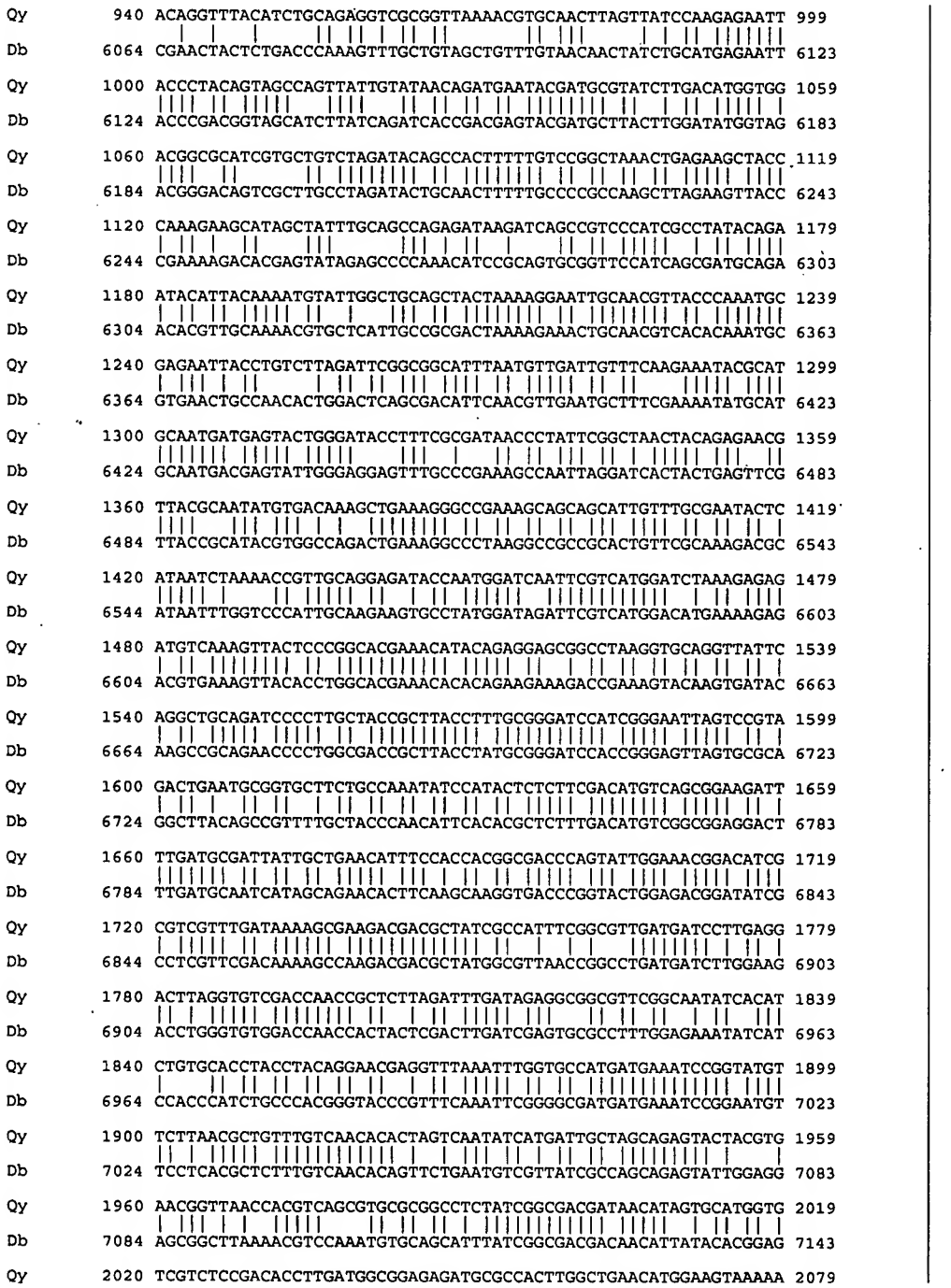
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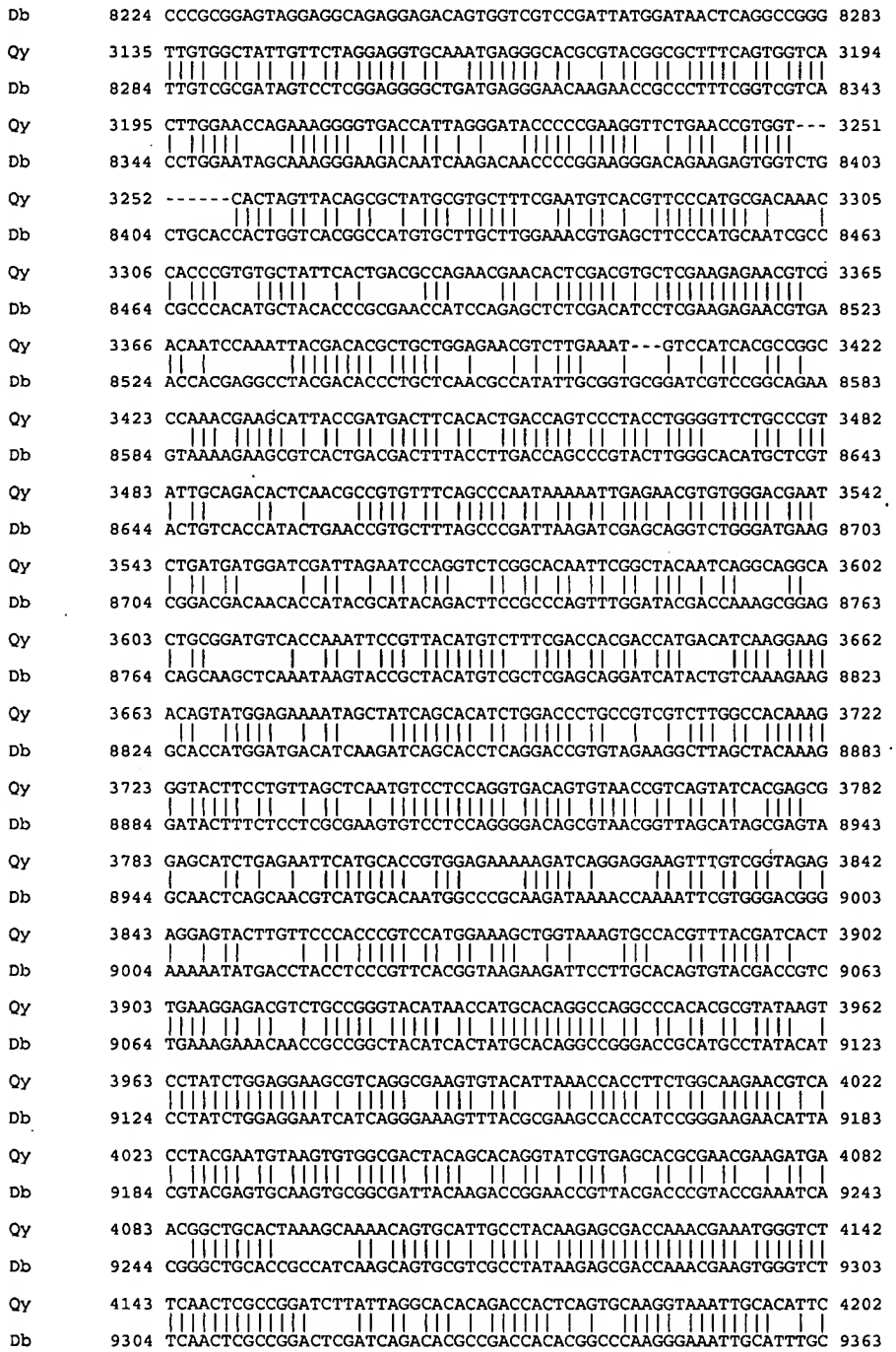
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DEFINITION  Sindbis-like virus isolate S.A.AR86, complete genome.
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VERSION     U38305.1  GI:1125069
KEYWORDS    .
SOURCE      Sindbis-like virus
  ORGANISM  Sindbis-like virus
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REFERENCE   1  (sites)
  AUTHORS   Russell,D.L., Dalrymple,J.M. and Johnston,R.E.
  TITLE     Sindbis virus mutations which coordinately affect glycoprotein
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  JOURNAL   J. Virol. 63 (4), 1619-1629 (1989)
  MEDLINE   89178848
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REFERENCE   2  (bases 1 to 11663)
  AUTHORS   Simpson,D.A., Lin,S.C. and Johnston,R.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-OCT-1995) Dennis A. Simpson, Microbiology &
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ORIGIN

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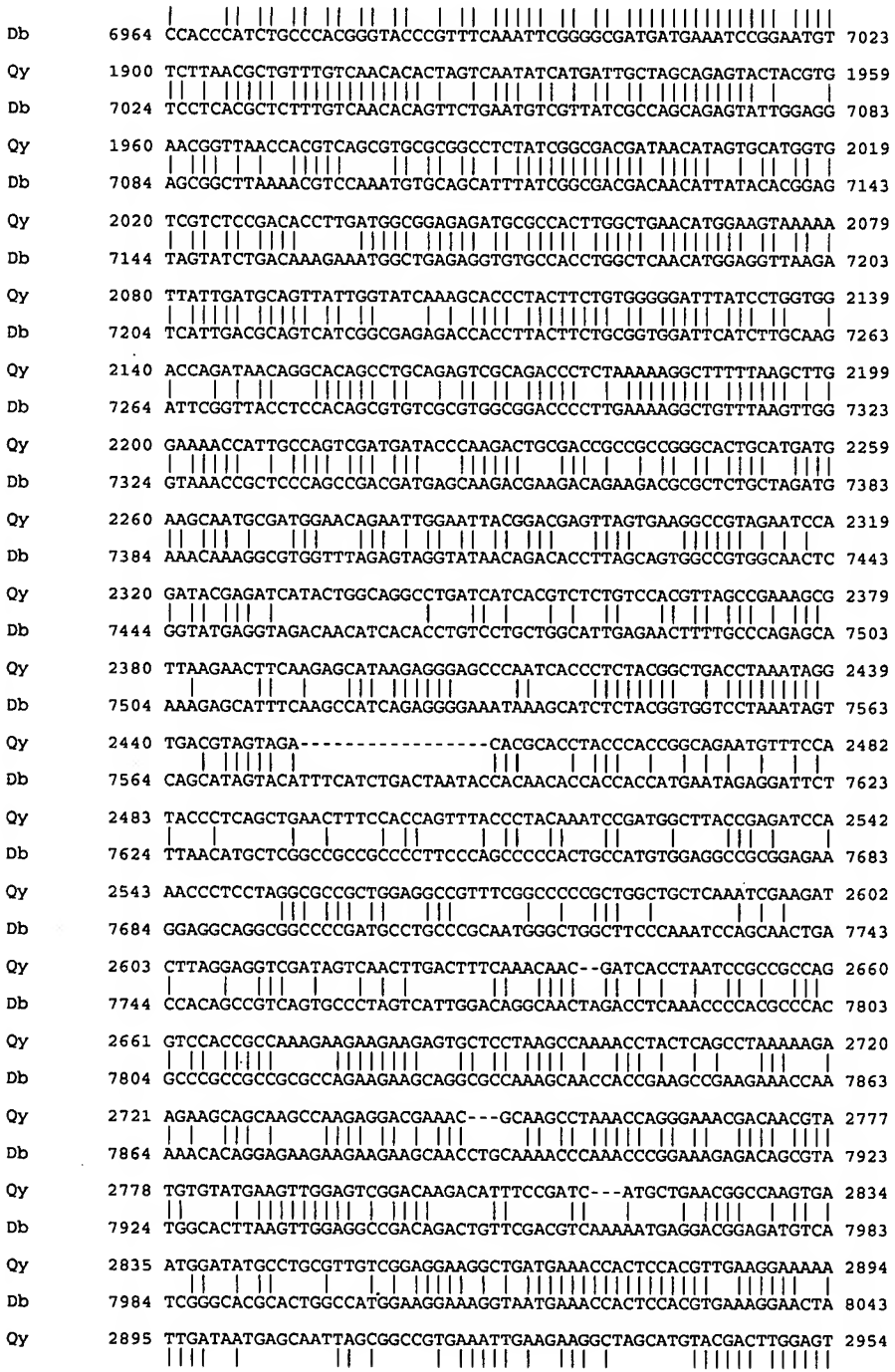

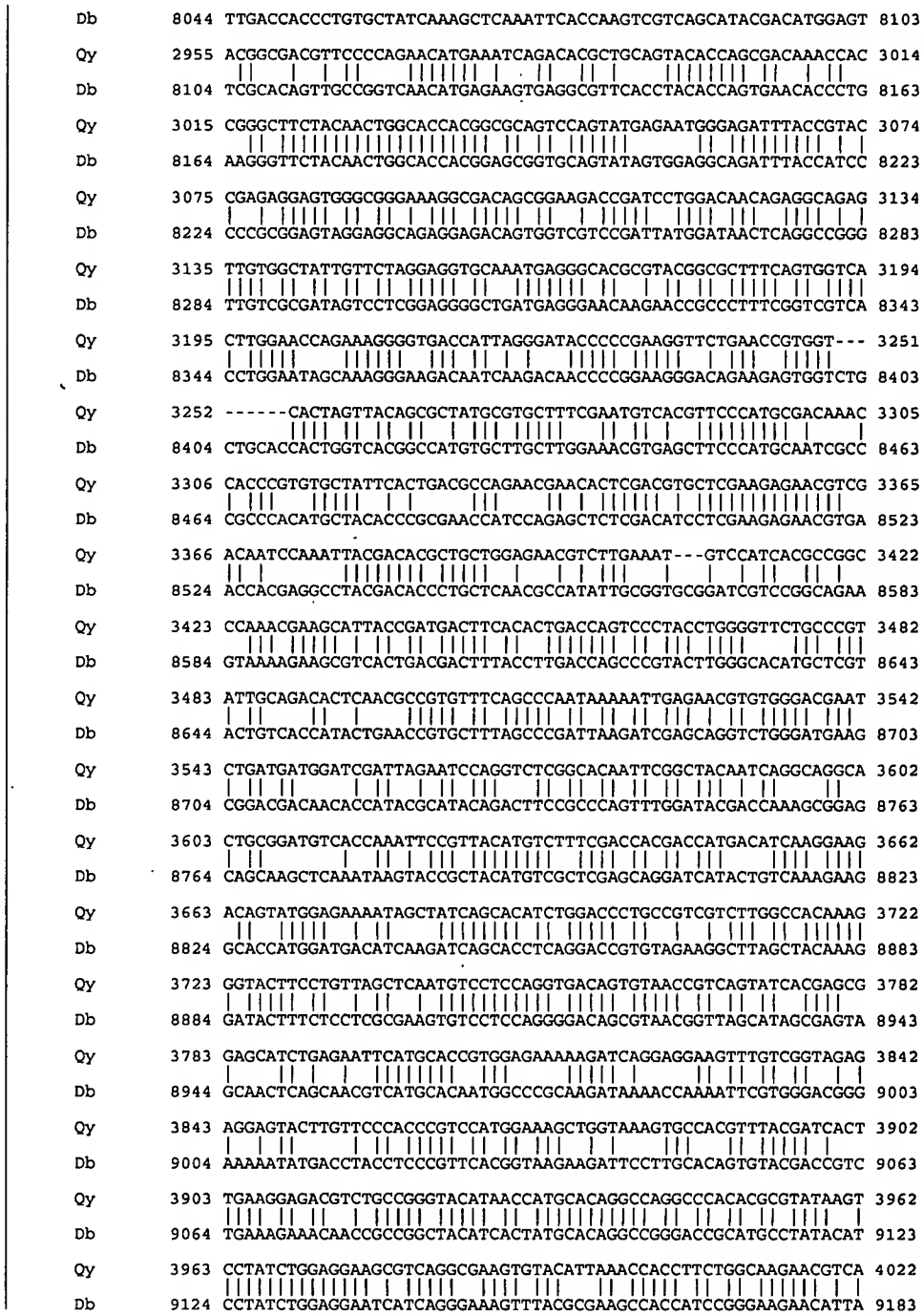

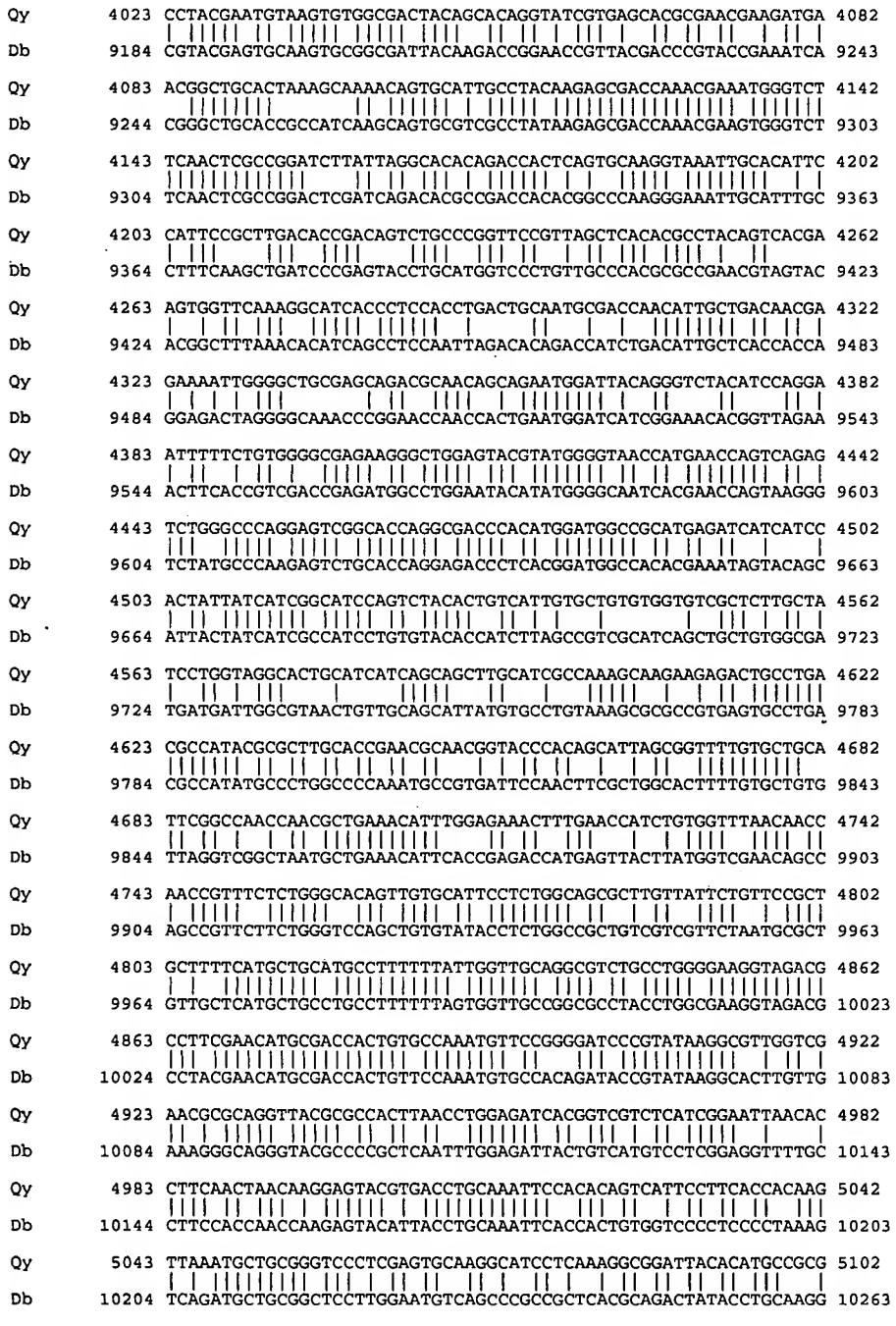
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ACCESSION   AR042412
VERSION     AR042412.1  GI:5962908
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11703)
  AUTHORS   Johnston,R.E., Davis,N.L. and Simpson,D.A.
  TITLE     System for the in vivo delivery and expression of heterologous
            genes in the bone marrow
  JOURNAL   Patent: US 5811407-A 8 22-SEP-1998;
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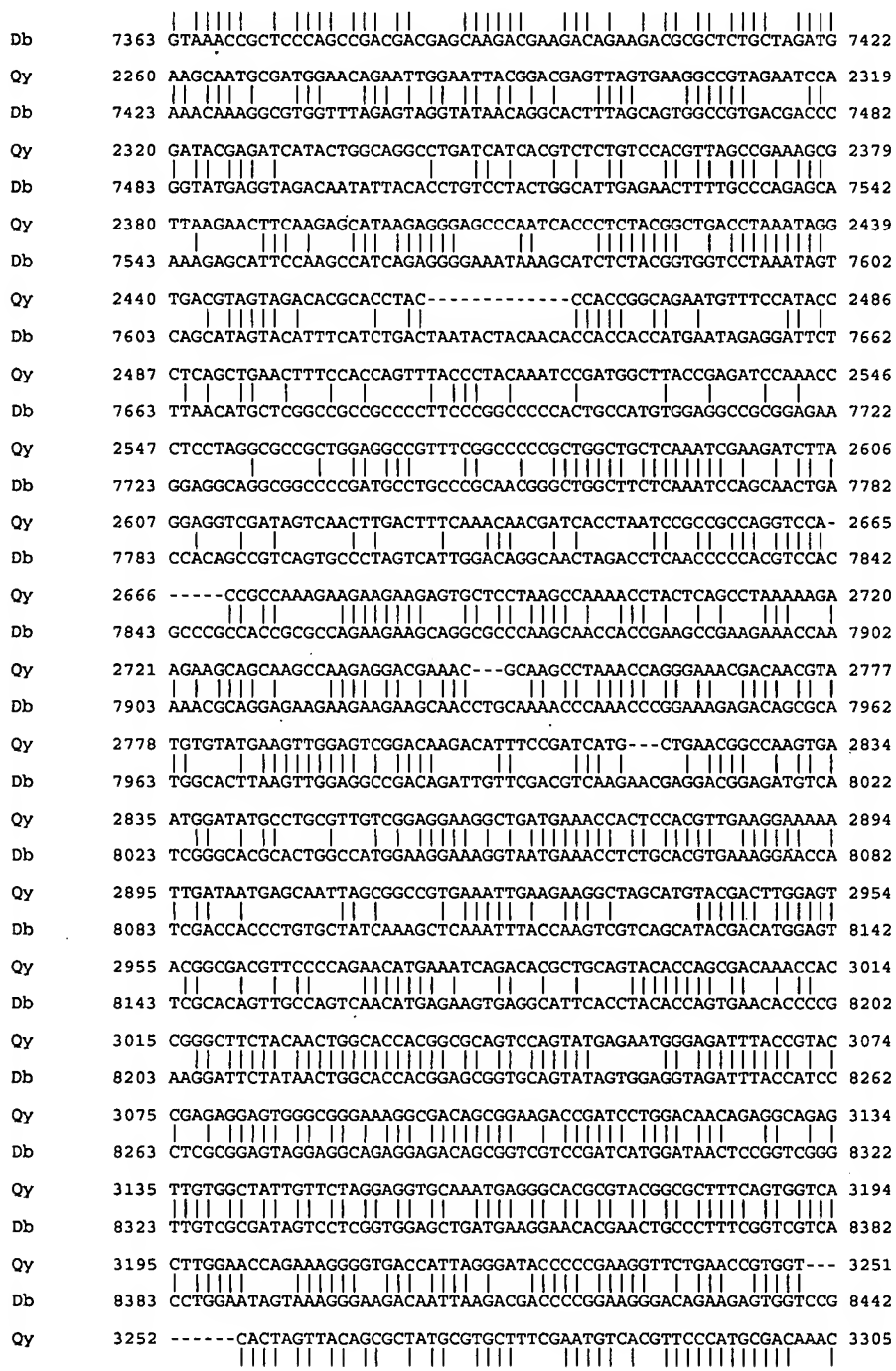
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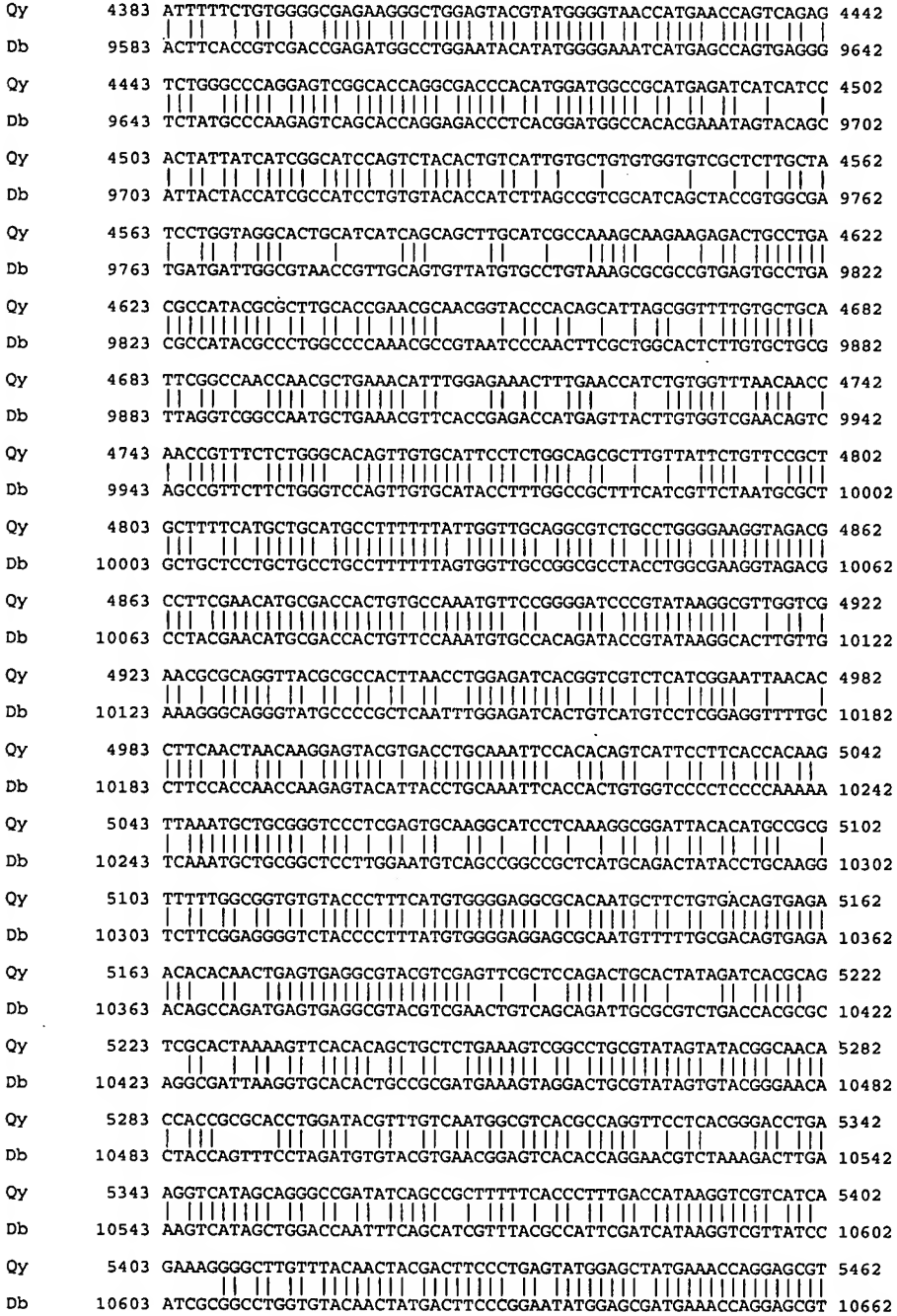

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REFERENCE 1 (bases 1 to 11703)
AUTHORS Johnston,R.E., Davis,N.L. and Simpson,D.A.
TITLE System for the in vivo delivery and expression of heterologous genes in the bone marrow
JOURNAL Patent: US 6008035-A 8 28-DEC-1999;
FEATURES Location/Qualifiers

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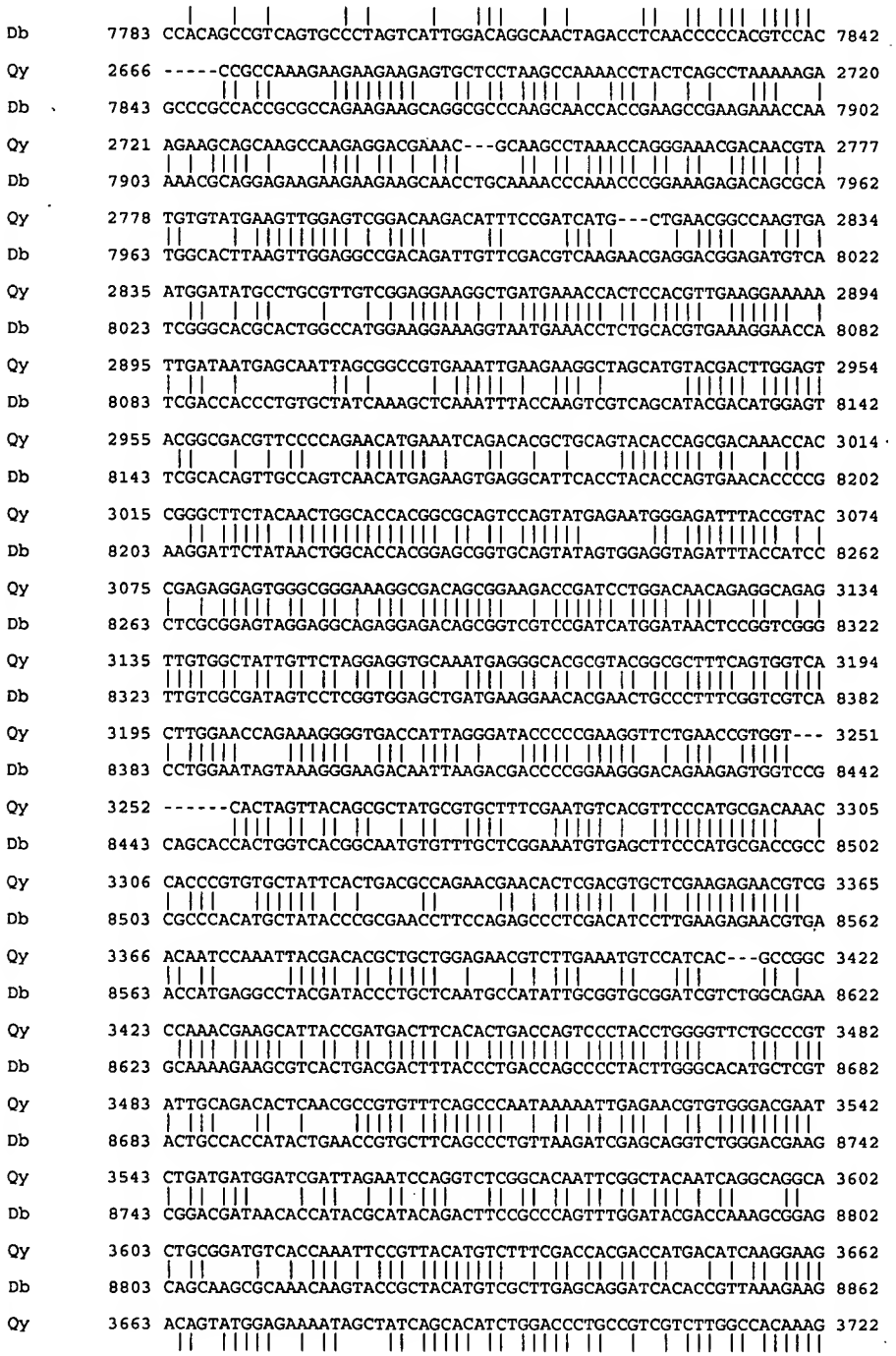

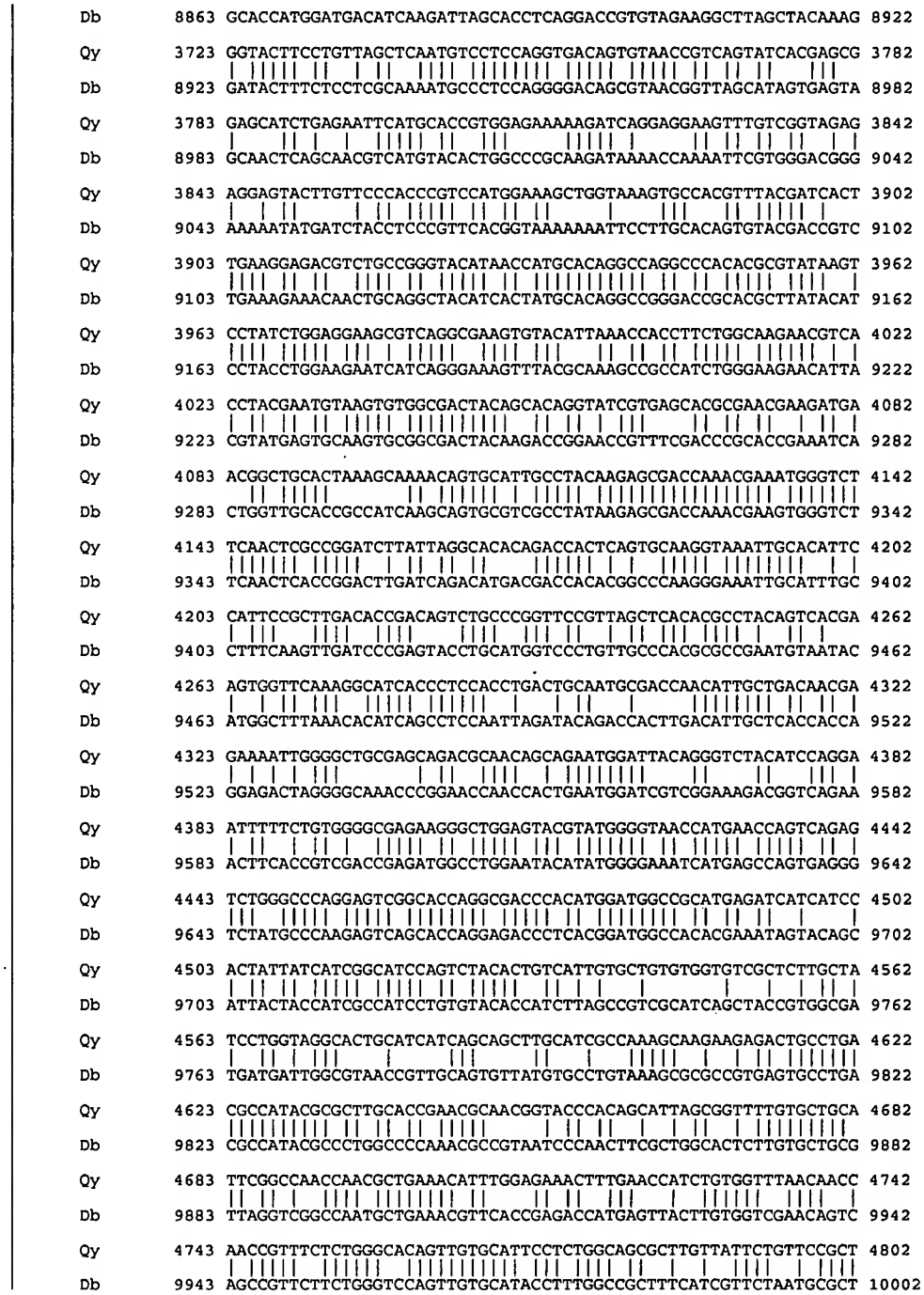

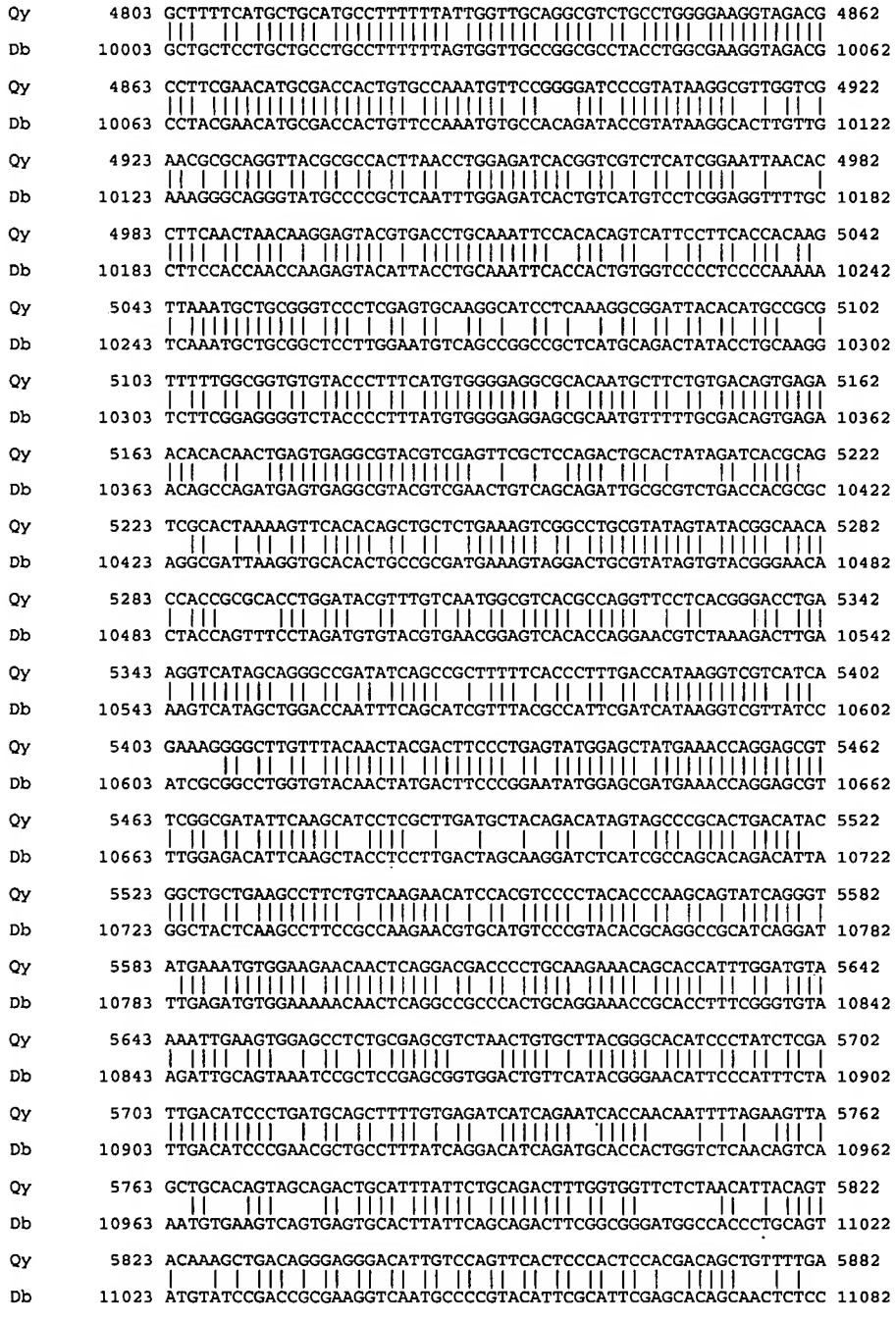

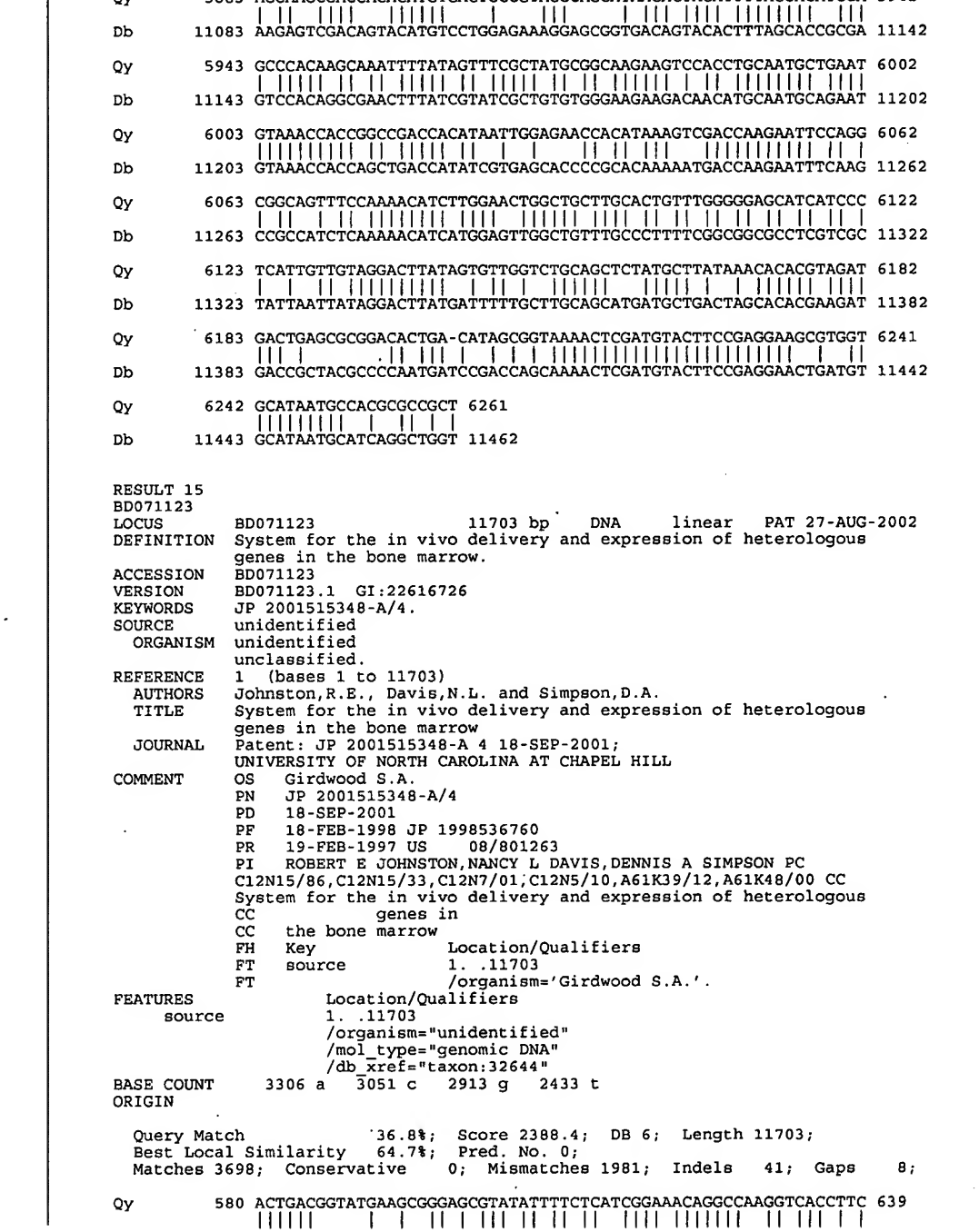

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VERSION     BD071123.1  GI:22616726
KEYWORDS    JP 2001515348-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 11703)
  AUTHORS   Johnston,R.E., Davis,N.L. and Simpson,D.A.
  TITLE     System for the in vivo delivery and expression of heterologous
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            PF   18-FEB-1998 JP 1998536760
            PR   19-FEB-1997 US    08/801263
            PI   ROBERT E JOHNSTON,NANCY L DAVIS,DENNIS A SIMPSON PC
            C12N15/86,C12N15/33,C12N7/01;C12N5/10,A61K39/12,A61K48/00 CC
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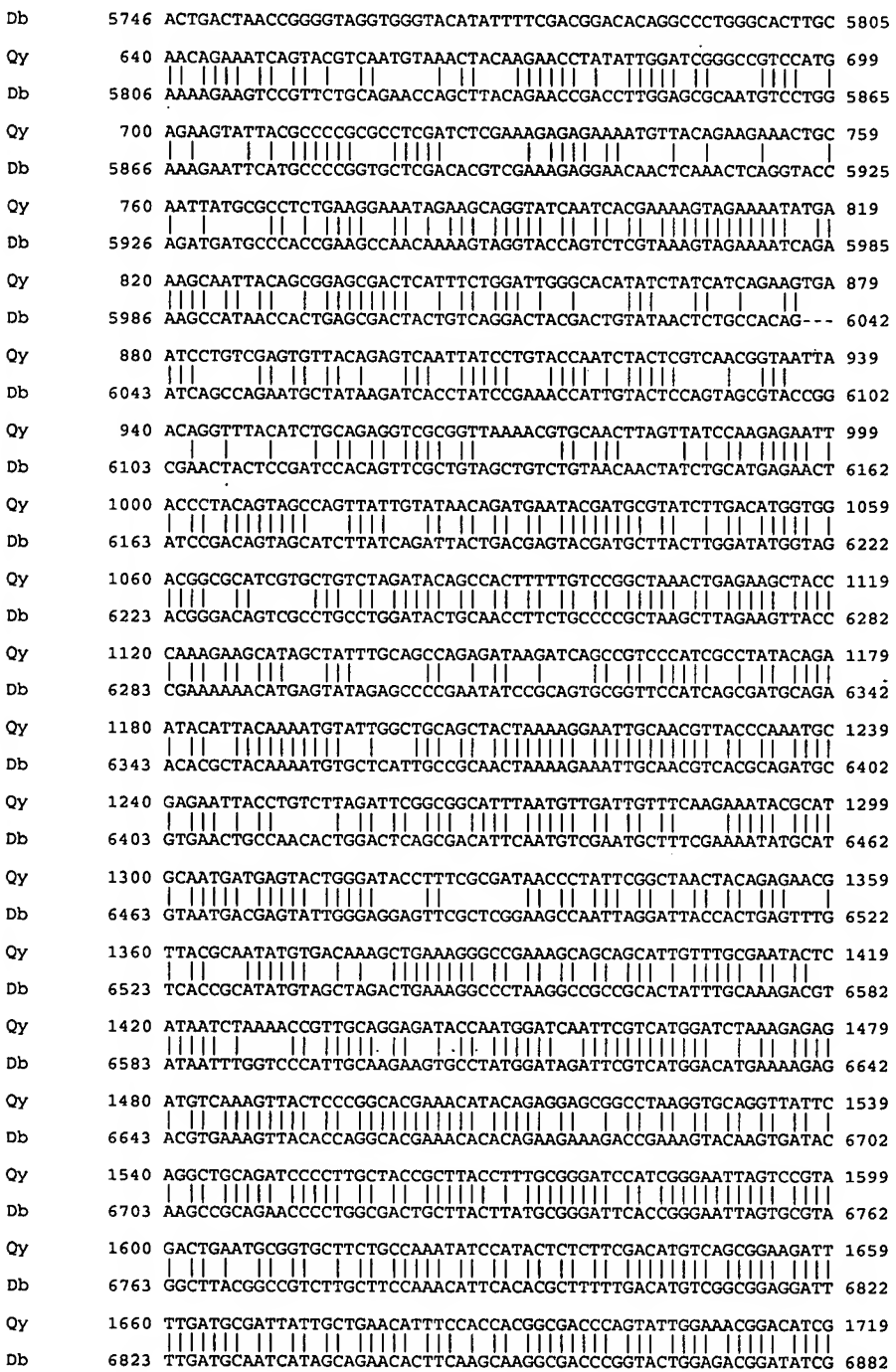
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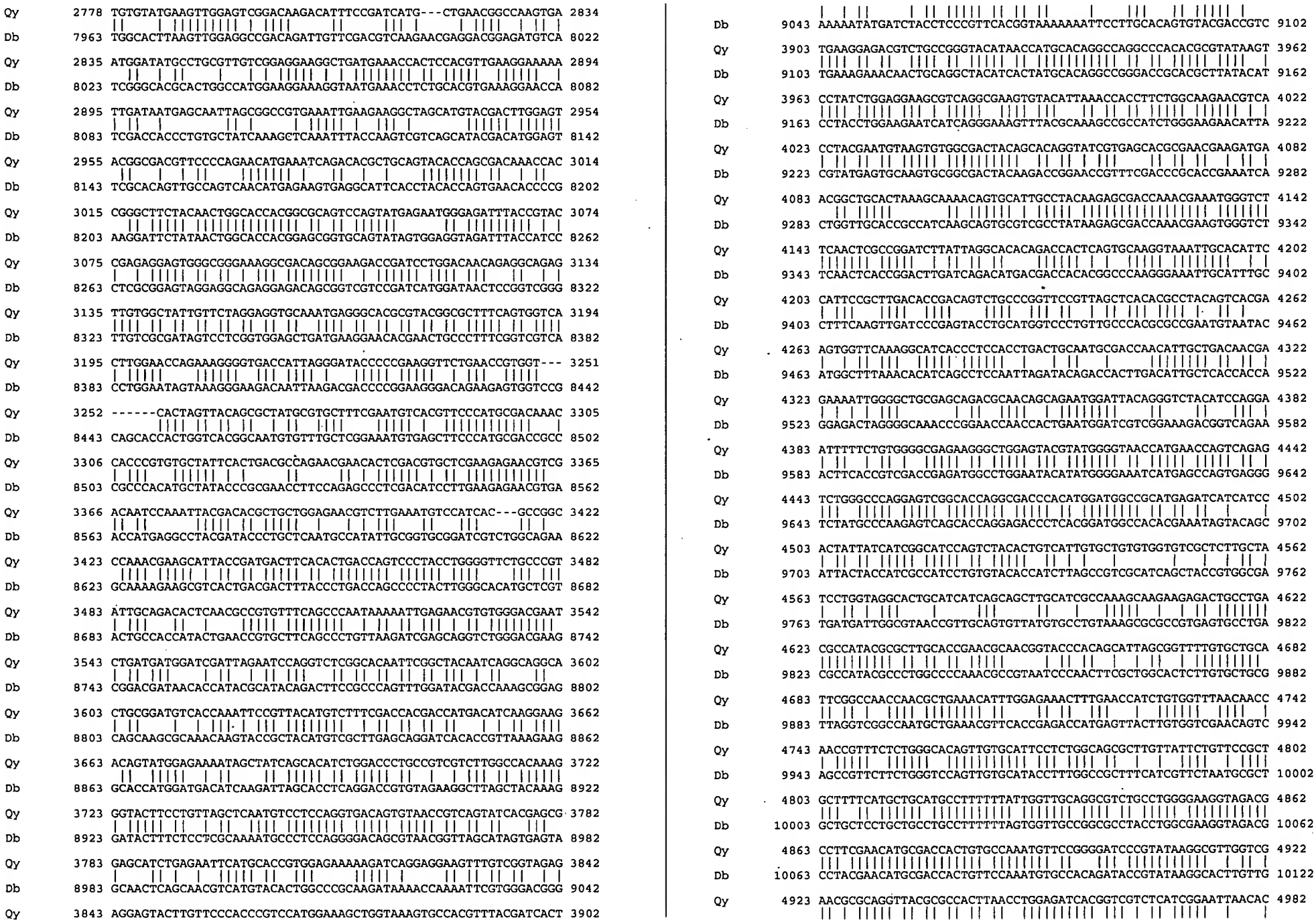

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Db      10843 AGATTGCAGTAAATCCGCTCCGAGCGGTGGACTGTTCATACGGGAACATTCCCATTTCTA 10902

Qy       5703 TTGACATCCCTGATGCAGCTTTTGTGAGATCATCAGAATCACCAACAATTTTAGAAGTTA 5762
              ||||||||||  | || || ||| | ||  |||||||  |||||    | | |  ||| |
Db      10903 TTGACATCCCGAACGCTGCCTTTATCAGGACATCAGATGCACCACTGGTCTCAACAGTCA 10962

Qy       5763 GCTGCACAGTAGCAGACTGCATTTATTCTGCAGACTTTGGTGGTTCTCTAACATTACAGT 5822
              ||   |||    || |||| |||||| |||||||| || ||        ||  | ||||
Db      10963 AATGTGAAGTCAGTGAGTGCACTTATTCAGCAGACTTCGGCGGGATGGCCACCCTGCAGT 11022

Qy       5823 ACAAAGCTGACAGGGAGGGACATTGTCCAGTTCACTCCCACTCCACGACAGCTGTTTTGA 5882
              |   | | ||| | || || || || || || || || || || | |||||   | |
Db      11023 ATGTATCCGACCGCGAAGGTCAATGCCCCGTACATTCGCATTCGAGCACAGCAACTCTCC 11082

Qy       5883 AGGAAGCGACCACACATGTGACTGCCGTAGGCAGCATAACACTACATTTTAGCACATCGA 5942
              | ||  ||||   ||||||    |    |||     | ||| |||| ||||||||  |||
Db      11083 AAGAGTCGACAGTACATGTCCTGGAGAAAGGAGCGGTGACAGTACACTTTAGCACCGCGA 11142

Qy       5943 GCCCACAAGCAAATTTTATAGTTTCGCTATGCGGCAAGAAGTCCACCTGCAATGCTGAAT 6002
              | ||||| || || ||||| || ||||| || || |||||| | || ||||||| ||||
Db      11143 GTCCACAGGCGAACTTTATCGTATCGCTGTGTGGGAAGAAGACAACATGCAATGCAGAAT 11202

Qy       6003 GTAAACCACCGGCCGACCACATAATTGGAGAACCACATAAAGTCGACCAAGAATTCCAGG 6062
              |||||||||| || ||||| ||  |  |    || || |||   |||||||||| || |
Db      11203 GTAAACCACCAGCTGACCATATCGTGAGCACCCCGCACAAAAATGACCAAGAATTTCAAG 11262

Qy       6063 CGGCAGTTTCCAAAACATCTTGGAACTGGCTGCTTGCACTGTTTGGGGGAGCATCATCCC 6122
              | ||  | || |||||||| |||| ||||| |||| || ||  || || || || | |
Db      11263 CCGCCATCTCAAAAACATCATGGAGTTGGCTGTTTGCCCTTTTCGGCGGCGCCTCGTCGC 11322

Qy       6123 TCATTGTTGTAGGACTTATAGTGTTGGTCTGCAGCTCTATGCTTATAAACACACGTAGAT 6182
              | |  || ||||||||||  | || |  ||||||   ||||| |  | |||||| ||||
Db      11323 TATTAATTATAGGACTTATGATTTTTGCTTGCAGCATGATGCTGACTAGCACACGAAGAT 11382

Qy       6183 GACTGAGCGCGGACACTGA-CATAGCGGTAAAACTCGATGTACTTCCGAGGAAGCGTGGT 6241
              |||  |          || ||| |  | | | ||||||||||||||||||||||||  |  ||
Db      11383 GACCGCTACGCCCCAATGATCCGACCAGCAAAACTCGATGTACTTCCGAGGAACTGATGT 11442

Qy       6242 GCATAATGCCACGCGCCGCT 6261
              |||||||||  |  || | |
Db      11443 GCATAATGCATCAGGCTGGT 11462
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Search completed: November 16, 2003, 05:39:13
Job time : 22826 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2003, 12:03:02 ; Search time 8996 Seconds
(without alignments)
13508.491 Million cell updates/sec

Title: US-10-023-649-1_COPY_1_5000
Perfect score: 5000
Sequence: 1 accctacaaactaatcgatc.....ataattctagaaacgccacc 5000

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	49.8	1.0	885	13	BX425603	BX425603 BX425603
2	47	0.9	1201	13	BX381961	BX381961 BX381961
c 3	43.8	0.9	1098	13	BX436460	BX436460 BX436460
c 4	42	0.8	1201	13	BX381961	BX381961 BX381961
c 5	41.2	0.8	646	14	CD393733	CD393733 Gm_ck1332
c 6	40.8	0.8	398	12	BG984025	BG984025 IL5-CN006
7	40.8	0.8	971	13	BU173419	BU173419 AGENCOURT
8	40.8	0.8	1101	29	CNS017SY	AL108460 Drosophil
9	40.6	0.8	380	12	BJ198034	BJ198034 BJ198034
10	40.6	0.8	453	12	BJ198451	BJ198451 BJ198451
11	40.6	0.8	455	12	BJ198768	BJ198768 BJ198768
12	40.6	0.8	456	12	BJ203653	BJ203653 BJ203653
13	40.4	0.8	715	12	BI195766	BI195766 602754145
c 14	40.4	0.8	1201	13	BX376097	BX376097 BX376097
15	40.2	0.8	634	10	BE017217	BE017217 fk78b02.y
16	39.8	0.8	413	14	CB384158	CB384158 TgESTzyh5
17	39.8	0.8	916	10	BG541362	BG541362 602569867
18	39.6	0.8	343	9	AW501797	AW501797 UI-HF-BR0
19	39.6	0.8	402	9	AW501918	AW501918 UI-HF-BR0
20	39.6	0.8	449	9	AW499678	AW499678 UI-HF-BR0
21	39.6	0.8	480	9	AW499647	AW499647 UI-HF-BR0
22	39.6	0.8	491	9	AW502451	AW502451 UI-HF-BR0
23	39.6	0.8	859	14	CA971504	CA971504 AGENCOURT
24	39.6	0.8	1011	10	BE563150	BE563150 601335780
25	39.4	0.8	504	13	BU926381	BU926381 sas90a08.
26	39.4	0.8	597	12	BM308456	BM308456 sak46c12.
27	39.4	0.8	619	13	BU927494	BU927494 sat13b07.
28	39.2	0.8	999	12	BM477724	BM477724 AGENCOURT
29	39	0.8	243	14	CB391641	CB391641 OSTF156A8
c 30	39	0.8	560	28	AZ738168	AZ738168 RPCI-24-1
31	39	0.8	599	13	BQ873224	BQ873224 QGI17P07.
32	39	0.8	626	13	BQ849532	BQ849532 QGB10C11.
c 33	39	0.8	997	29	CNS005TE	AL060767 Drosophil
34	39	0.8	1240	10	BG739729	BG739729 602630430
35	38.8	0.8	342	12	BI177442	BI177442 EST518387
c 36	38.8	0.8	650	28	BH900647	BH900647 Otb00189
37	38.8	0.8	687	12	BM406647	BM406647 EST580974
c 38	38.8	0.8	705	12	BI432608	BI432608 EST535369
39	38.8	0.8	718	10	BG598366	BG598366 EST503266
c 40	38.8	0.8	1101	29	CNS017GS	AL108022 Drosophil
c 41	38.8	0.8	1182	9	AL513775	AL513775 AL513775
42	38.4	0.8	413	13	BQ281915	BQ281915 WHE3026_H
43	38.4	0.8	1003	29	CNS04H1P	AL290374 Tetraodon
c 44	38.4	0.8	1076	29	CNS05HXN	AL338180 Tetraodon
c 45	38.4	0.8	1163	29	CC290181	CC290181 CH261-100

ALIGNMENTS

RESULT 1
BX425603/c
LOCUS BX425603 885 bp mRNA linear EST 15-MAY-2003
DEFINITION BX425603 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone CL0BB022ZA07 3-PRIME, mRNA sequence.
ACCESSION BX425603
VERSION BX425603.1 GI:30770486
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 885)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CL0BB022ZA07FP1.
FEATURES Location/Qualifiers
source 1. .885
/organism="Homo sapiens"

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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CL0BB022ZA07"
                     /tissue_type="NEUROBLASTOMA"
                     /clone_lib="Homo sapiens NEUROBLASTOMA"
                     /note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
BASE COUNT       15 a     23 c     69 g    154 t    624 others
ORIGIN

  Query Match             1.0%;  Score 49.8;  DB 13;  Length 885;
  Best Local Similarity   2.7%;  Pred. No. 0.012;
  Matches   15;  Conservative  169;  Mismatches  378;  Indels    0;  Gaps    0;

Qy       1058 CAACTGACGTTAGTGTGGATGACGCACAAAAACTATTGGTTGGGCTCAACCAAAGGATTG 1117
              |:    ::                                    :       ::::     : : :
Db        865 CMNNMMMMNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNKNNNNNNNMMMMNNNNNKNKNK 806

Qy       1118 TCGTCAATGGTAGGACGCAAAGAAATACTAACACAATGCAGAACTATCTATTACCAGTGG 1177
               :  ::                                 :::::  :: ::: : : :  ::::
Db        805 NMMMMMNNNNNNNNNNNMNNNNNNNNNNNNNNNNMMMMMMMMMMMMMMMMMMMMMMMMM 746

Qy       1178 TCGCCCAGGCGTTTTCCAGGTGGGCGCGTGAACATCGTGCCGACTTGGACGACGAGAAAG 1237
               : ::::       :::   : : :  :::: :   ::         ::     :
Db        745 MMMMMMMNNNNNNMMMMNNNKNKNKKNKKMMNMNNNKKNNNNNNNNNNNNNNNKMMNNNK 686

Qy       1238 AACTAGGGGTGCGGGAGCGCACTCTTACTATGGGCTGCTGCTGGGCTTTCAAGACCCAGA 1297
                  ::::: |:: :      :          :       :   ::: ::::: :
Db        685 KNKGKNKKKKKKGKKGKKNTNKNMNNNNNNNNNNNNMMNNNNNNMMMMMMMMMMMMM 626

Qy       1298 AAATCACATCCATCTACAAGAAGCCTGGTACGCAAACAATTAAGAAAGTACCTGCCGTCT 1357
               : | :: | ::: : :::: :: ::                              ::
Db        625 MNAMMMNAMMMMAMMMMMMMMMMMMMMNNNNNNNNNNNNNNNNNNNNNNNNNKKKKNKNNNN 566

Qy       1358 TTGACTCATTTGTGATTCCACGCCTTACCAGCCACGGGCTCGATATGGGCTTCCGCCGTA 1417
                  ::          :  ::  :::: ::::   : : | :    :  :: ::
Db        565 NNNNNNMMNNMNNNNNNNNMAMMMMMMMMMMMMMMMMMMMMAMMMMMMMMMMMNNN 506

Qy       1418 GGCTCAAGCTGCTGCTTGAACCAACTGTCAAACCCGCACCGGCTATTACAATGGCCGATG 1477
                     :        :::   :|::::: ::::   : :  ::::   :: : :
Db        505 NNNNNNNNNNNNNKNNNNKNNNMMMMMAMAMMMMMMMMMNCMMMMMMMMMMMMMNMNN 446

Qy       1478 TGGAGCATCTGCGTGGCTTACAGCAAGAAGCTGAAGAAGTGGCTGCAGCGGAAGAGATCA 1537
                 : :::::   : :       :::                |
Db        445 NNNMNMMKMKNNNKNKNNNNNNMMMMNNNNNNNNNTKNNTNNNNTNNNNTNNNNNNNNN 386

Qy       1538 GAGAAGCCCTGCCACCCTTGCTCCCTGAAATAGAAAAAGAGACCGTAGAGGCAGAAGTAG 1597
                     : ::::   : :::  : : | ::||| : :::   | :  :: ::  :
Db        385 TTNNNMNNNMMMNMMMMAMMMMMMMMAMCMMAMMMAAANMMMMMNNANMMMMMMMMMMM 326

Qy       1598 ACCTCATTATGCAAGAGGCAGG 1619
               :       :   |      ||
Db        325 MNNNNNNNNCSNNNGNNNKNGG 304


RESULT 2
BX381961
LOCUS       BX381961               1201 bp    mRNA    linear   EST 08-MAY-2003
DEFINITION  BX381961 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI072YF05 3-PRIME, mRNA sequence.
ACCESSION   BX381961
VERSION     BX381961.1  GI:30453007
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI072CC03NP1.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI072YF05"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT       95 a    191 c    115 g     55 t    745 others
ORIGIN

  Query Match             0.9%;  Score 47;  DB 13;  Length 1201;
  Best Local Similarity   5.5%;  Pred. No. 0.1;
  Matches   38;  Conservative  251;  Mismatches  404;  Indels    2;  Gaps    1;

Qy        743 CGGTTGGTTCAACAATCTACACAGAAGATAGATCACTGTTACGTAGCTGGCATCTTCCAA 802
              :  : :::       |   :       ::  : :       :: : :  :        ::| :
Db        454 MNNKNKKKNNKNNNNTKNNMNNNNCNKMNNKNKKNNNNNKMNKNMMNKNNNCNNNKMCKM 513

Qy        803 ACGTGTTCCACTTGAAAGGAAAGTCTAACTTCACAGGTAGATGTGGGACCATTGTCAGCT 862
              :    : ::: :        ::  :      ::: :   :  :          :     :
Db        514 MNMMNKMMMMNKMMNNNCNKMMNAMNNKKMNKMMMNKNNMMNCKTNNNNNNNNKNNNNNK 573

Qy        863 GTGAAGGGTACGTCATCAAAAAGATAACGATCAGCCCAGGACTATACGGTAAAGTTGAGA 922
                 ::::  :          :    | :          :   |  :  :::: :
Db        574 NNNNNKKKKKKKNNNNNKNNNMNNNNANKNNNNNNNNNKNNCMNKKKKKKMKMMMMNKMN 633

Qy        923 ACTTGGCGTCCACAATGCATCGCGAGGGTTTCTTGAGTTGCAAAGTCACAGATACGCTGC 982
              :  :        : ::   . :                          :    : :
Db        634 NNNNNKKNKNNNKNNNNMNKMNNNNNKNNNMNNNNNNNNNNNNNNNKKKKKKKKNNNNNNN 693

Qy        983 GCGGCGAGAGGGTTTCTTTTGCTGTGTGTACGTATGTACCAGCCACACTTTGCGATCAGA 1042
                  :::   :: ::| : ::   ::      :          ::    |  :
Db        694 NNNNNNMKMNNNNKKNKKTNKKKKNNAKKNNTNNKMMNNKNNNNNNMMNNCNCNKKKNNK 753

Qy       1043 TGACAGGGATTCTGGCAACTGACGTTAGTGTGGATGACGCACAAAAACTATTGGTTGGGC 1102
              | :          ::     :           ::   : |:   :   :| : ::::: ::
Db        754 TNMNNMMNNNNNKKNNNNNKNNNNNNNNNNNKKMKMSKCKKKKMCCKMCCMCKKKKKMBKG 813

Qy       1103 TCAACCAAAGGATTGTCGTCAATGGTAGGACGCAAAGAAATACTAACACAATGCAGAACT 1162
              ::: :| :: : ::  | ::::  :   ::| :    ::: :   ::::   : :
Db        814 KMVCMCKMMMKNKKCMCMKBMMMCKMCMKMCMBKKNMMMMMMKMKMMMMNKNKAMMKKDN 873

Qy       1163 ATCTATTACCAGTGGTCGCCCAGGCGTTTTCCAGGTGGGCGCGTGAACATCGTGCCGACT 1222
              : : :  |::    ::  ::: : |  :: ||: :::: :   : ::: :: :|: . :
Db        874 MMMMMMCAMMCMMMKKNMMMBKKNCMMKKMCCMMKKKKHKKNMMKKMMMCKKBMMCKKNK 933

Qy       1223 TGGACGACGAGAAAGAACTAGGGGTGCGGGAGCGCACTCTTACTATGGGCTGCTGCTGGG 1282
              : : : :|::   | :: : : | ::: :: :|  :: : : ::::  : :::
Db        934 MMNKMMVKKKKAMMNBKCVMKMKMKMCCKKVMMBKMCAKKKKMCMCVKKVMCMCDBKMCM 993

Qy       1283 CTTTCAAGACCCAGAAAATCACATCCATCTACAA--GAAGCCTGGTACGCAAACAATTAA 1340
              |:::::  ::||     ::: ::||  :: ::|:::   :::::     :: ::   :: :
Db        994 CKKKBMKKVCCKKMCMMMMMCAMKVMMMBAMMMMBAMVVMMMMNNMMMMCKKMVMKKK 1053

Qy       1341 GAAAGTACCTGCCGTCTTTGACTCATTTGTGATTCCACGCCTTACCAGCCACGGGCTCGA 1400
              ::  :: ::::::   :  :::::   :|  :   |:|: |   :   |:::|::  |:
Db       1054 KMCKKKBMSKKMMMNKKVCKMBBMCMSKGGCMMCGCMCKGCVGCMNSCCMMBGSKGCCKK 1113

Qy       1401 TATGGGCTTCCGCCGTAGGCTCAAGCTGCTGCTTG 1435
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Db        1114 KMBKCMMCCCMCMCBCMCBKKVCVKKKKKCKKKKKK 1148


RESULT 3
BX436460/c
LOCUS       BX436460               1098 bp    mRNA    linear   EST 15-MAY-2003
DEFINITION  BX436460 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP001YL10
            5-PRIME, mRNA sequence.
ACCESSION   BX436460
VERSION     BX436460.1  GI:30779481
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1098)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0CAP001DF05QP1.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
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                     /clone="CS0CAP001YL10"
                     /tissue_type="THYMUS"
                     /clone_lib="Homo sapiens THYMUS"
                     /note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
BASE COUNT       56 a    289 c    225 g    229 t    299 others
ORIGIN

  Query Match             0.9%;  Score 43.8;  DB 13;  Length 1098;
  Best Local Similarity   20.5%;  Pred. No. 0.87;
  Matches   83;  Conservative  130;  Mismatches  192;  Indels    0;  Gaps    0;

Qy       2667 GCCGCACAAAGATGATCTGATTCTAACCTGTTTCAGAGGATGGGTGAAACAGCTACAGAT 2726
Db        682 GGCGGACNMMGGGMMMMMAARAAAANANGKAGDAAAKKAAKAKKDAMAAMAAKAAKAAA 623

Qy       2727 TGACTACAAAAATCACGAAATCATGACTGCGGCTGCATCGCAAGGACTTACGCGGAAAGG 2786
Db        622 AAKDKAKDAAARKKGKKRAAKKKAGKAAKAAKAAKAAADAAAADAAKAKAAGKKKAAAAA 563

Qy       2787 CGTTTATGCTGTCAGGTACAAAGTCAACGAGAATCCACTCTACTCGCAGACTTCTGAGCA 2846
Db        562 RKDDKKKKNAAAAAAAAAAAAAKARKKKKAKKKAAARKKAGKKAMAAAAVKKKKKAAAAM 503

Qy       2847 CGTGAACGTGTTACTTACACGCACAGAAAAACGCATTGTCTGGAAGACGCTAGCTGGTGA 2906
Db        502 GAAAAAAAMKKKAAAAAMAKKAAMMKAAMMMAMMKAKKAAKMMMAMAKMAAKAMKKMKK 443

Qy       2907 TCCCTGGATAAAGACACTTACAGCTAAATATCCCGGGGATTTCACGGCTTCATTGGACGA 2966
Db        442 MMMMMMKAMAMMKAMMMAKAMKMMMMMMKMMMMKMMKMKKMVMCACMCMMVKMMKMMAA 383

Qy       2967 CTGGCAGCGCGAACACGACGCCATTATGGCACGCGTTCTTGATAAGCCGCAGACAGCTGA 3026
Db        382 MMAVKMVMKKCCAKKAKACCCMCAACACKAKCKCCCACAAKAKKAKCCKCAAMAAAAACA 323

Qy       3027 TGTGTTCCAGAATAAGGTGAACGTCTGCTGGGCGAAGGCTTTAGA 3071
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Db         322 AKCAAKVKAKASAAAAAKKAKKKRKGGAGGAAGAAAKGAKTAKKA 278


RESULT 4
BX381961/c
LOCUS       BX381961               1201 bp    mRNA    linear   EST 08-MAY-2003
DEFINITION  BX381961 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI072YF05 3-PRIME, mRNA sequence.
ACCESSION   BX381961
VERSION     BX381961.1  GI:30453007
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI072CC03NP1.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI072YF05"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT       95 a    191 c    115 g     55 t    745 others
ORIGIN

  Query Match             0.8%;  Score 42;  DB 13;  Length 1201;
  Best Local Similarity   4.7%;  Pred. No. 3.2;
  Matches   32;  Conservative  241;  Mismatches  398;  Indels    4;  Gaps    2;

Qy        810 CCACTTGAAAGGAAAGTCTAACTTCACAGGTAGATGTGGGACCATTGTCAG---CTGTGA 866
Db       1071 BMMNKKKMMSKVMMMGKMMMMKBKMMGKKKKKNNKKKKBBKTVKKKKTVKKKBMKTGKKK 1012

Qy        867 AGGGTACGTCATCAAAAAGATAACGATCAGCCCAGGACTATACGGTAAAGTTGAGAACTT 926
Db       1011 KKKGKMMGGBMMKVMMMGKGKMVHGKGKBMMBGKGKMMMMTGKMVKKBMMGGKMKMKMKB 952

Qy        927 GGCGTCCACAATGCATCGCGAGGGTTTCTTGAGTTGCAAAGTCACAGATACGCTGCGCGG 986
Db        951 GMVNKKTMMMMBKKMNKKMNMMGKKVMMGKKKMMKKNMMDMMMMKKGGKMMKKGNMMVKK 892

Qy        987 CGAGAGGGTTTCTTTTGCTGTGTGTACGTATGTACCAGCCACACTTTGCGATCAGATGAC 1046
Db        891 KNMMKKKGKKTGKKKKKKNHMMKKTMNMNKKKKMKMKKKKKKNMMVKGKMKGKMGKKKVM 832

Qy       1047 AGGGATTCTGGCAACTGACGTTAGTGTGGATGACG-CACAAAAACTATTGGTTGGGCTCA 1105
Db        831 KGKGMMNMKKKMGKGBKMCMVKMMMMMGKGGKMGGKMMMMGMSKMKMNNNNNNNNNNMN 772

Qy       1106 ACCAAAGGATTGTCGTCAATGGTAGGACGCAAAGAAATACTAACACAATGCAGAACTATC 1165
Db         771 NNNNMMNNNNKKNNKNAMNNMMMNGNGNNKKNNNNNNMNNKKMNNANNMMTNNMMMMNA 712

Qy       1166 TATTACCAGTGGTCGCCCAGGCGTTTTCCAGGTGGGCGCGTGAACATCGTGCCGACTTGG 1225
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```
Db        711 MMNMMNNNNKMKNNNNNNNNNNNNNMMMMMMMNNNNNNNNNNNNNNKNNNMNNNNNKMN 652

Qy       1226 ACGACGAGAAAGAACTAGGGGTGCGGGAGCGCACTCTTACTATGGGCTGCTGCTGGGCTT 1285

Db        651 KNNNNMNNNMMMNNNNNNKMNKKKKMKMMMMMNKGNNMNNNNNNNNNNMNTNNNNKNNN 592

Qy       1286 TCAAGACCCAGAAAATCACATCCATCTACAAGAAGCCTGGTACGCAAACAATTAAGAAAG 1345

Db        591 MNNNNNMMMMMMMNNNNNNMNNNNNNMNNNNNNNNAMGNKKNNMNKKKMNKMMNNKTNKKMN 532

Qy       1346 TACCTGCCGTCTTTGACTCATTTGTGATTCCACGCCTTACCAGCCACGGGCTCGATATGG 1405

Db        531 GNNNKKMNKKKKMNKKNKKMGKMNNNGNNNMNKKNMNKMNNNNNMMNMNNKMNGNNNNKN 472

Qy       1406 GCTTCCGCCGTAGGCTCAAGCTGCTGCTTGAACCAACTGTCAAACCCGCACCGGCTATTA 1465

Db        471 NMANNNNMNNMMMNMNNKKNNTNGNNNNNMMMMMMMNKNMMNKKMMMNMKGMMMMNN 412

Qy       1466 CAATGGCCGATGTGG 1480

Db        411 NKKKMGMNNNNNTNG 397
```

RESULT 5
CD393733/c
LOCUS CD393733 646 bp mRNA linear EST 01-JUN-2003
DEFINITION Gm_ck13327 Soybean induced by Salicylic Acid Glycine max cDNA 3', mRNA sequence.
ACCESSION CD393733
VERSION CD393733.1 GI:31308530
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
REFERENCE 1 (bases 1 to 646)
AUTHORS Tian,A.-G., Wang,J., Cui,P., Han,Y.-J., Xu,H., Cong,L.-J., Huang ,X.-G., Wang,X.-L., Jiao,Y.-Z., Wang,B.-J., Wang,Y.-J., Zhang,J.-S. , Chen,S.-Y. and Yu,J.
TITLE Soybean Expressed Sequence Tags Sequencing
JOURNAL Unpublished
COMMENT Contact: Chen S-Y
Plant Biotechnology Laboratory
Institute of Genetics and Developmental Biology, CAS, China
Datun road, Beijing 100101, China
Tel: 86-10-64886859
Fax: 86-10-64873428
Email: sychen@genetics.ac.cn
Email: sychen@genetics.ac.cn
Seq primer: T7 primer.
FEATURES Location/Qualifiers
source 1. .646
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Kefeng 1"
/db_xref="taxon:3847"
/tissue_type="Seedlings"
/dev_stage="two-week seedlings"
/lab_host="XL1-Blue MRF' strain"
/clone_lib="Soybean induced by Salicylic Acid"
/note="Vector: pBluescript SK+; Site_1: EcoR I; Site_2: Xho I; The cDNA library was constructed by He, C-Y from mRNA isolated from two-week seedlings (cultivar Kefeng 1) treated by spraying 2.0mM salicylic acid for 24, 36, 48 and 72 h. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI striction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XL1-Blue MRF' host cells (Stratagene)."
BASE COUNT 206 a 134 c 134 g 172 t
ORIGIN

```
  Query Match              0.8%;  Score 41.2;  DB 14;  Length 646;
  Best Local Similarity   48.9%;  Pred. No. 3.4;
  Matches  139;  Conservative    0;  Mismatches  143;  Indels    2;  Gaps    1;

Qy       2331 AGTGCTTCTAAATGGGGTTAAGCACCCCGTTAACACTCTGTACATTGATGAGGCATTTGC 2390

Db        599 AGTTCTGCCAAATCAAGAGGGGTTTTAAGATCATAGTGTGTGTTTTGCAACAATGGCTAA 540

Qy       2391 CTGCCATGCAGGGACGCTGCTGGCACTGATTGCCATCGTCAAACCTAAGAAAGTGGTATT 2450

Db        539 GTTCTTTGCTGCTATGATCTTGGCACTCTTTGCCATTTCCATACTTCAAACAGTGGTAAT 480

Qy       2451 GTGCGGGGACCCAAAACAATGCGGCTTCTTTAACATGATGTGCCTGAAAGTACATTTTAA 2510

Db        479 GGCTGCTAATGAACAAGGAGGCCACTTGTATGACAACAAGAGCAAATATGGAAGTGGAAG 420

Qy       2511 CCATGACATATGCACTGAAGTGTACCATAAAAGCATCTCTAGGAGGTGCACACAGACTGT 2570

Db        419 TGTCAAGAGTTACCGTAAAATGCCCATCACAATG--CTCGAGGAGATGTAGCCAGACCCA 362

Qy       2571 AACCGCCATCGTCTCCACGCTCTTCTACGACAAGCGAATGAAGA 2614

Db        361 ATACCACAAGCCCTGCATGTTTTTCTGTCAGAAGTGCTGCAGGA 318
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RESULT 6
BG984025/c
LOCUS BG984025 398 bp mRNA linear EST 12-JUN-2001
DEFINITION IL5-CN0065-190301-403-d07 CN0065 Homo sapiens cDNA, mRNA sequence.
ACCESSION BG984025
VERSION BG984025.1 GI:14386760
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 398)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=IL5&t2=IL5-CN0065-190301-403-d07&t3=2001-03-19&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 370.
FEATURES Location/Qualifiers
source 1. .398
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CN0065"

/note="Organ: colon_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 34 a 156 c 97 g 111 t
ORIGIN

Query Match 0.8%; Score 40.8; DB 12; Length 398;
Best Local Similarity 51.7%; Pred. No. 3.1;
Matches 93; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

Qy 1445 TCAAACCCGCACCGGCTATTACAATGGCCGATGTGGAGCATCTGCGTGGCTTACAGCAAG 1504
Db 243 TTAAAACAGCAGCGGCAACTGCAGCAGCAGCAGCAGCGAGACCCCGAGGCACACATCAAA 184

Qy 1505 AAGCTGAAGAAGTGGCTGCAGCGGAAGAGATCAGAGAAGCCCTGCCACCCTTGCTCCCTG 1564
Db 183 CACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTG 124

Qy 1565 AAATAGAAAAAGAGACCGTAGAGGCAGAAGTAGACCTCATTATGCAAGAGGCAGGAGCAG 1624
Db 123 GAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTGCAGGAGGAGGAGCAGCAGCGG 64

RESULT 7
BU173419
LOCUS BU173419 971 bp mRNA linear EST 04-SEP-2002
DEFINITION AGENCOURT_7942821 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6171839 5', mRNA sequence.
ACCESSION BU173419
VERSION BU173419.1 GI:22687403
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 971)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13540 row: m column: 24
High quality sequence start: 106
High quality sequence stop: 362.
FEATURES Location/Qualifiers
source 1. .971
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6171839"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Library constructed by Life Technologies."
BASE COUNT 269 a 276 c 308 g 118 t
ORIGIN

Query Match 0.8%; Score 40.8; DB 13; Length 971;
Best Local Similarity 51.7%; Pred. No. 6.2;
Matches 93; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

Qy 1445 TCAAACCCGCACCGGCTATTACAATGGCCGATGTGGAGCATCTGCGTGGCTTACAGCAAG 1504
Db 329 TTAAAACAGCAGCAGCAGCTGCAACAGCAGCAGCAGCGAGACCCCGAGGCACACATCAAA 388

Qy 1505 AAGCTGAAGAAGTGGCTGCAGCGGAAGAGATCAGAGAAGCCCTGCCACCCTTGCTCCCTG 1564
Db 389 CACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTG 448

Qy 1565 AAATAGAAAAAGAGACCGTAGAGGCAGAAGTAGACCTCATTATGCAAGAGGCAGGAGCAG 1624
Db 449 GAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGG 508

RESULT 8
CNS017SY
LOCUS CNS017SY 1101 bp DNA linear GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC BACN37L08 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL108460
VERSION AL108460.1 GI:5628764
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.
FEATURES Location/Qualifiers
source 1. .1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN37L08"
/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
BASE COUNT 254 a 176 c 160 g 152 t 359 others
ORIGIN

Query Match 0.8%; Score 40.8; DB 29; Length 1101;
Best Local Similarity 16.4%; Pred. No. 6.9;
Matches 65; Conservative 169; Mismatches 160; Indels 2; Gaps 1;

Qy 1269 GGGCTGCTGCTGGGCTTTCAAGACCCAGAAAATCACATCCATCTACAAGAAGCCTGGTAC 1328
Db 665 RSGSGGSSCCGGKKAKGGVRGGRVCCAGGGASCACMAADCGGCCAKMACCSSSSASSSGS 724

Qy 1329 GCAAACAATTAAGAAAGTACCTGCCGTCTTTGACTCATTTGTGATTCCACGCCTTACCAG 1388
Db 725 SCASTSSSASRGGMVSSCACSGSGSGGASACGASGAGGGSGRGGGSGCCASSGVCGAACS 784

Qy 1389 CCACGGGCTCGATATGGGCTTCCGCCGTAGGCTCAAGCTGCTGCTTGAACCAACTGTCAA 1448
Db 785 SASCSSASMCGVSSGSSCSASCGSCCGVSSCSAVSASSASSVMSKVASAVASCSAVASGM 844

Qy 1449 ACCCGCACCGGCTATTACAATGGCCGATGTGG--AGCATCTGCGTGGCTTACAGCAAGAA 1506

```
Db        845 SAGAVSSSCRSSVASSVSAAASVSSSVSSSSSSSVVSAAAVSASSSSASSASMAVAAAAA 904

Qy       1507 GCTGAAGAAGTGGCTGCAGCGGAAGAGATCAGAGAAGCCCTGCCACCCTTGCTCCCTGAA 1566
              :  : :::|: ::: :: :::: |::::   :|  |:::: ::: :::| :: ::: : |
Db        905 VAVSSVSVASVVSSSSSCSSSSSASVVVSASVAASASSVSSSSSSSVSTSSSASVSSVSA 964

Qy       1567 ATAGAAAAAGAGACCGTAGAGGCAGAAGTAGACCTCATTATGCAAGAGGCAGGAGCAGGT 1626
              : ::|::  :|: :::  : :::|:||: | |    | | :: |:|: :::  :: ::
Db        965 VSMSAVVSSSASSSSSVSVSSVVAVAASAAAAAAAAAAAAASSSSASAVAVVSASSSSSSA 1024

Qy       1627 AGCGTGGAGACACCACGAGGACACATCAGGGTGACA 1662
                ::: ::|: :::::::: :  :::: : ::: :|:|
Db       1025 SSSSSSSASSSVSSVSSSSCSVVSVVSSSSVSVAVA 1060
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RESULT 9
BJ198034
LOCUS BJ198034 380 bp mRNA linear EST 24-JAN-2002
DEFINITION BJ198034 normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata Physcomitrella patens subsp. patens cDNA clone pphn30g20 5', mRNA sequence.
ACCESSION BJ198034
VERSION BJ198034.1 GI:18365956
KEYWORDS EST.
SOURCE Physcomitrella patens subsp. patens
ORGANISM Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
REFERENCE 1 (bases 1 to 380)
AUTHORS Fujita,T., Shin-i,T., Seki,M., Kamiya,A., Uchiyama,I., Nishiyama,T., Carninci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe,M.
TITLE Comparison of the moss Physcomitrella patens genome with flowering plants genome
JOURNAL Unpublished
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
A backbone of the vector is pBluescript II, that was in vivo excised from a modified lPS phage vector (Mo bi Tec, Germany). XhoI digested-5' end of cDNA is ligated to SalI site of the vector, and the BamHI digested-3' end including poly-A tail is ligated to BamHI site of the vector. cDNA instert could be amplified with conventional T7 and T3 primers. This normarized full- length cDNA library was generated basically according to the method described in Genome Research 10, 1617-1630 (2000), Carninci, P. et al. Protonemata were blended by the POLYTRON, and then cultivated on the BCD medium containing 1uM NAA (naphthalene acetic acid) for 8 to 11 days under the continuous light.
FEATURES Location/Qualifiers
source 1. .380
/organism="Physcomitrella patens subsp. patens"
/mol_type="mRNA"
/sub_species="patens"
/db_xref="taxon:145481"
/clone="pphn30g20"
/tissue_type="mixture of chloronemata, caulonemata and rhizoid-like protonemata"
/clone_lib="normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata"
BASE COUNT 131 a 75 c 121 g 53 t
ORIGIN

Query Match 0.8%; Score 40.6; DB 12; Length 380;
Best Local Similarity 50.8%; Pred. No. 3.4;
Matches 97; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

```
Qy       1474 GATGTGGAGCATCTGCGTGGCTTACAGCAAGAAGCTGAAGAAGTGGCTGCAGCGGAAGAG 1533
              || | |||| |       |  ||||  | || || ||||||||  |  | ||  |||||
```

```
Db        103 GAGGAGGAGGAGGACGAAGATTTACGACCAGCAGTTGAAGAAGAAGAAGAAGAAGAAGAA 162

Qy       1534 ATCAGAGAAGCCCTGCCACCCTTGCTCCCTGAAATAGAAAAAGAGACCGTAGAGGCAGAA 1593
                 | || |    ||    |   |   |||  |||| ||||  | ||||  | || |
Db        163 GAAGCTGTAGTCGAAGCAGAAGTCGACGAAGAAGAAGAAGAAGAAGCTGTAGTCGAAGCA 222

Qy       1594 GTAGACCTCATTATGCAAGAGGCAGGAGCAGGTAGCGTGGAGACACCACGAGGACACATC 1653
              | || |  |       |||| | || ||||||  | |  |       |.|| ||   |
Db        223 GAAGTCGACGAAGAAGAAGAAGAAGCAGCAGGAGGAGGAGGACGCATAAGAAGAAGAAGA 282

Qy       1654 AGGGTGACAAG 1664
              ||  || |||
Db        283 AGAAGGAGAAG 293
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RESULT 10
BJ198451
LOCUS BJ198451 453 bp mRNA linear EST 24-JAN-2002
DEFINITION BJ198451 normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata Physcomitrella patens subsp. patens cDNA clone pphn31f22 5', mRNA sequence.
ACCESSION BJ198451
VERSION BJ198451.1 GI:18366372
KEYWORDS EST.
SOURCE Physcomitrella patens subsp. patens
ORGANISM Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
REFERENCE 1 (bases 1 to 453)
AUTHORS Fujita,T., Shin-i,T., Seki,M., Kamiya,A., Uchiyama,I., Nishiyama,T., Carninci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe,M.
TITLE Comparison of the moss Physcomitrella patens genome with flowering plants genome
JOURNAL Unpublished
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
A backbone of the vector is pBluescript II, that was in vivo excised from a modified lPS phage vector (Mo bi Tec, Germany). XhoI digested-5' end of cDNA is ligated to SalI site of the vector, and the BamHI digested-3' end including poly-A tail is ligated to BamHI site of the vector. cDNA instert could be amplified with conventional T7 and T3 primers. This normarized full- length cDNA library was generated basically according to the method described in Genome Research 10, 1617-1630 (2000), Carninci, P. et al. Protonemata were blended by the POLYTRON, and then cultivated on the BCD medium containing 1uM NAA (naphthalene acetic acid) for 8 to 11 days under the continuous light.
FEATURES Location/Qualifiers
source 1. .453
/organism="Physcomitrella patens subsp. patens"
/mol_type="mRNA"
/sub_species="patens"
/db_xref="taxon:145481"
/clone="pphn31f22"
/tissue_type="mixture of chloronemata, caulonemata and rhizoid-like protonemata"
/clone_lib="normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata"
BASE COUNT 138 a 110 c 134 g 71 t
ORIGIN

Query Match 0.8%; Score 40.6; DB 12; Length 453;
Best Local Similarity 50.8%; Pred. No. 3.9;
Matches 97; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

```
Qy       1474 GATGTGGAGCATCTGCGTGGCTTACAGCAAGAAGCTGAAGAAGTGGCTGCAGCGGAAGAG 1533
              || | |||| |       |  ||||  | || || ||||||||  |  | ||  |||||
```

```
Db        103 GAGGAGGAGGAGGACGAAGATTTACGACCAGCAGTTGAAGAAGAAGAAGAAGAAGAAGAA 162

Qy       1534 ATCAGAGAAGCCCTGCCACCCTTGCTCCCTGAAATAGAAAAAGAGACCGTAGAGGCAGAA 1593

Db        163 GAAGCTGTAGTCGAAGCAGAAGTCGACGAAGAAGAAGAAGAAGAAGCTGTAGTCGAAGCA 222

Qy       1594 GTAGACCTCATTATGCAAGAGGCAGGAGCAGGTAGCGTGGAGACACCACGAGGACACATC 1653

Db        223 GAAGTCGACGAAGAAGAAGAAGAAGCAGCAGGAGGAGGAGGACGCATAAGAAGAAGAAGA 282

Qy       1654 AGGGTGACAAG 1664

Db        283 AGAAGGAGAAG 293


RESULT 11
BJ198768
LOCUS       BJ198768                455 bp    mRNA    linear   EST 24-JAN-2002
DEFINITION  BJ198768 normalized full length cDNA library, chloronemata,
            caulonemata and rhizoid-like protonemata Physcomitrella patens
            subsp. patens cDNA clone pphn32c20 5', mRNA sequence.
ACCESSION   BJ198768
VERSION     BJ198768.1  GI:18366689
KEYWORDS    EST.
SOURCE      Physcomitrella patens subsp. patens
  ORGANISM  Physcomitrella patens subsp. patens
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
            Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
REFERENCE   1  (bases 1 to 455)
  AUTHORS   Fujita,T., Shin-i,T., Seki,M., Kamiya,A., Uchiyama,I., Nishiyama,T.
            , Carninci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe
            ,M.
  TITLE     Comparison of the moss Physcomitrella patens genome with flowering
            plants genome
  JOURNAL   Unpublished
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            A backbone of the vector is pBluescript II, that was in vivo
            excised from a modified lPS phage vector (Mo bi Tec, Germany). XhoI
            digested-5' end of cDNA is ligated to SalI site of the vector, and
            the BamHI digested-3' end including poly-A tail is ligated to BamHI
            site of the vector. cDNA instert could be amplified with
            conventional T7 and T3 primers. This normarized full- length cDNA
            library was generated basically according to the method described
            in Genome Research 10, 1617-1630 (2000), Carninci, P. et al.
            Protonemata were blended by the POLYTRON, and then cultivated on
            the BCD medium containing 1uM NAA (naphthalene acetic acid) for 8
            to 11 days under the continuous light.
FEATURES             Location/Qualifiers
     source          1. .455
                     /organism="Physcomitrella patens subsp. patens"
                     /mol_type="mRNA"
                     /sub_species="patens"
                     /db_xref="taxon:145481"
                     /clone="pphn32c20"
                     /tissue_type="mixture of chloronemata, caulonemata and
                     rhizoid-like protonemata"
                     /clone_lib="normalized full length cDNA library,
                     chloronemata, caulonemata and rhizoid-like protonemata"
BASE COUNT      138 a    111 c    134 g     72 t
ORIGIN

  Query Match             0.8%;  Score 40.6;  DB 12;  Length 455;
  Best Local Similarity   50.8%;  Pred. No. 3.9;
  Matches   97;  Conservative    0;  Mismatches   94;  Indels    0;  Gaps    0;

Qy       1474 GATGTGGAGCATCTGCGTGGCTTACAGCAAGAAGCTGAAGAAGTGGCTGCAGCGGAAGAG 1533

Db        103 GAGGAGGAGGAGGACGAAGATTTACGACCAGCAGTTGAAGAAGAAGAAGAAGAAGAAGAA 162

Qy       1534 ATCAGAGAAGCCCTGCCACCCTTGCTCCCTGAAATAGAAAAAGAGACCGTAGAGGCAGAA 1593

Db        163 GAAGCTGTAGTCGAAGCAGAAGTCGACGAAGAAGAAGAAGAAGAAGCTGTAGTCGAAGCA 222

Qy       1594 GTAGACCTCATTATGCAAGAGGCAGGAGCAGGTAGCGTGGAGACACCACGAGGACACATC 1653

Db        223 GAAGTCGACGAAGAAGAAGAAGAAGCAGCAGGAGGAGGAGGACGCATAAGAAGAAGAAGA 282

Qy       1654 AGGGTGACAAG 1664

Db        283 AGAAGGAGAAG 293


RESULT 12
BJ203653
LOCUS       BJ203653                456 bp    mRNA    linear   EST 25-JAN-2002
DEFINITION  BJ203653 normalized full length cDNA library, chloronemata,
            caulonemata and rhizoid-like protonemata Physcomitrella patens
            subsp. patens cDNA clone pphn49j14 5', mRNA sequence.
ACCESSION   BJ203653
VERSION     BJ203653.1  GI:18372051
KEYWORDS    EST.
SOURCE      Physcomitrella patens subsp. patens
  ORGANISM  Physcomitrella patens subsp. patens
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
            Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   Fujita,T., Shin-i,T., Seki,M., Kamiya,A., Uchiyama,I., Nishiyama,T.
            , Carninci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe
            ,M.
  TITLE     Comparison of the moss Physcomitrella patens genome with flowering
            plants genome
  JOURNAL   Unpublished
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            A backbone of the vector is pBluescript II, that was in vivo
            excised from a modified lPS phage vector (Mo bi Tec, Germany). XhoI
            digested-5' end of cDNA is ligated to SalI site of the vector, and
            the BamHI digested-3' end including poly-A tail is ligated to BamHI
            site of the vector. cDNA instert could be amplified with
            conventional T7 and T3 primers. This normarized full- length cDNA
            library was generated basically according to the method described
            in Genome Research 10, 1617-1630 (2000), Carninci, P. et al.
            Protonemata were blended by the POLYTRON, and then cultivated on
            the BCD medium containing 1uM NAA (naphthalene acetic acid) for 8
            to 11 days under the continuous light.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Physcomitrella patens subsp. patens"
                     /mol_type="mRNA"
                     /sub_species="patens"
                     /db_xref="taxon:145481"
                     /clone="pphn49j14"
                     /tissue_type="mixture of chloronemata, caulonemata and
                     rhizoid-like protonemata"
                     /clone_lib="normalized full length cDNA library,
                     chloronemata, caulonemata and rhizoid-like protonemata"
BASE COUNT      138 a    111 c    134 g     73 t
ORIGIN

  Query Match             0.8%;  Score 40.6;  DB 12;  Length 456;
  Best Local Similarity   50.8%;  Pred. No. 4;
  Matches   97;  Conservative    0;  Mismatches   94;  Indels    0;  Gaps    0;

Qy       1474 GATGTGGAGCATCTGCGTGGCTTACAGCAAGAAGCTGAAGAAGTGGCTGCAGCGGAAGAG 1533
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Db        103 GAGGAGGAGGAGGACGAAGATTTACGACCAGCAGTTGAAGAAGAAGAAGAAGAAGAAGAA 162

Qy       1534 ATCAGAGAAGCCCTGCCACCCTTGCTCCCTGAAATAGAAAAAGAGACCGTAGAGGCAGAA 1593

Db        163 GAAGCTGTAGTCGAAGCAGAAGTCGACGAAGAAGAAGAAGAAGAAGCTGTAGTCGAAGCA 222

Qy       1594 GTAGACCTCATTATGCAAGAGGCAGGAGCAGGTAGCGTGGAGACACCACGAGGACACATC 1653

Db        223 GAAGTCGACGAAGAAGAAGAAGAAGCAGCAGGAGGAGGAGGACGCATAAGAAGAAGAAGA 282

Qy       1654 AGGGTGACAAG 1664

Db        283 AGAAGGAGAAG 293


RESULT 13
BI195766
LOCUS       BI195766                715 bp    mRNA    linear   EST 10-JUL-2001
DEFINITION  602754145F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4889938 5',
            mRNA sequence.
ACCESSION   BI195766
VERSION     BI195766.1  GI:14650786
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 715)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM1766  row: i  column: 11
            High quality sequence stop: 556.
FEATURES             Location/Qualifiers
     source          1. .715
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4889938"
                     /tissue_type="neuroblastoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_19"
                     /note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Library constructed  by Ling Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and  Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      202 a    194 c    251 g     68 t
ORIGIN

  Query Match             0.8%;  Score 40.4;  DB 12;  Length 715;
  Best Local Similarity   50.5%;  Pred. No. 6.5;
  Matches   98;  Conservative    0;  Mismatches   96;  Indels    0;  Gaps    0;

Qy       1445 TCAAACCCGCACCGGCTATTACAATGGCCGATGTGGAGCATCTGCGTGGCTTACAGCAAG 1504

Db        223 TTAAAACAGCAGCAGCAGCTGCAGCAGCAGCAGCAGCGAGACCCCGAGGCACACATCAAA 282

Qy       1505 AAGCTGAAGAAGTGGCTGCAGCGGAAGAGATCAGAGAAGCCCTGCCACCCTTGCTCCCTG 1564

Db        283 CACCTGCTGCACCAGCGGCAGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTG 342
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Qy       1565 AAATAGAAAAAGAGACCGTAGAGGCAGAAGTAGACCTCATTATGCAAGAGGCAGGAGCAG 1624

Db        343 GAGGAGCAACAGCGGCGGGAGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGG 402

Qy       1625 GTAGCGTGGAGACA 1638

Db        403 CGGCCTGGAGGACA 416


RESULT 14
BX376097/c
LOCUS       BX376097                1201 bp    mRNA    linear   EST 08-MAY-2003
DEFINITION  BX376097 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DC022YM12 5-PRIME, mRNA sequence.
ACCESSION   BX376097
VERSION     BX376097.1  GI:30434756
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 2866.f
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DC022BG06QP1.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DC022YM12"
                     /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      79 a    152 c     66 g    270 t    634 others
ORIGIN

  Query Match             0.8%;  Score 40.4;  DB 13;  Length 1201;
  Best Local Similarity   13.7%;  Pred. No. 9.7;
  Matches  135;  Conservative  297;  Mismatches  551;  Indels    2;  Gaps    2;

Qy       1487 TGCGTGGCTTACAGCAAGAAGCTGAAGAAGTGGCTGCAGCGGAAGAGATCAGAGAAGCCC 1546

Db       1186 KRKGGKGDAAADAAAAAAAAAGKAAAAAARDAKGKWAGKKAAAAGARAAKRKARAGKAGK 1127

Qy       1547 TGCCACCCTTGCTCCCTGAAATAGAAAAAGAGACCGTAGAGGCAGAAGTAGACCTCATTA 1606

Db       1126 ARGAAAAAGKAGAGKAGAGGGARRKAKAGAGTARWGKTAAAGKWRKARAAKKKRKADAAD 1067

Qy       1607 TGCAAGAGGCAGGAGCAGGTAGCGTGGAGACACCACGAGGACACATCAGGGTGACAAGTT 1666

Db       1066 GGKAAKAGKWAGAAAGAGKAGGGKKGGGKAAAKKTMTMKTMMMMMNMMMMMMMMMMMM 1007

Qy       1667 ACCCAGGCGAAGAGAAGATTGGGTCTTACGCTATACTTTCACCCCAGGCGGTATTGAATA 1726

Db       1006 MMMMMMMMMMHKMHMHMKMKKHMMHKTMTNTKWMKTKTMMMMMMMMMVKKMMMKMMMM 947

Qy       1727 GTGAAAAACTGGCGTGTATCCACCCATTGGCGGAACAAGTACTGGTAATGACTCACAAAG 1786

Db        946 KMMMMMNYMMMTGMMMMMGKHMMVMVMMMMMMMGMMMKTMMMKMMMGGKGGTMGGMGG 887
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Qy       1787 GTAGGGCAGGGAGATACAAAGTCGAGCCATACCACGGTAAGGTCATTGTACCAGAAGGGA 1846
Db        886 GMMMVGMRGGGVMMMGTGKKTMGKWNMMGKMMGMMMGNTDMMKTMTMKMMMKHMTMTKGN 827

Qy       1847 CGGCGGTCCCTGTTCAAGACTTCCAGGCATTGAGTGAGAGCGCTACGATCGTTTTCAACG 1906
Db        826 GKTMHGKMMNMMVKMKTMMNVGAAAAAAADAGGGAAAAAAAAGAAAAAKAGAKAGKHMNK 767

Qy       1907 AGAGGGAGTTCGTAAACAGATACCTGCACCACATCGCAATCAACGGAGGAGCGCTAAACA 1966
Db         766 NMGKTMMGTMMMGTGKMMGKMGTMHMTMKMVMMMMMMMMMKGKMMMMKMGKMNMMAMMK 707

Qy       1967 CTGACGAAGAGTACTATAAGACTGTAAAGAC-TCAGGACACAGACTCAGAATACGTCTTC 2025
Db         706 MKMMTMTMTGTMMMTMTMMGKKKTMMTMKNBNKMMKKAGKKMNANMKKNNKNAMNNNGKM 647

Qy       2026 GATATTGACGCACGAAAGTGTGTTAAGCGAGAAGACGCAGGTCCCTTGTGCCTAACCGGT 2085
Db         646 NNMKKKTKKKNNMKKKNMKKNNNNNMMNNKMNMMKMGKMNMGKAKANNMKMKMNNNKMMMN 587

Qy       2086 GATCTGGTAGATCCACCATTTCACGAGTTTGCGTACGAGAGTCTCAAGACACGACCAGCA 2145
Db         586 NMKMKKKMKNNMKNNMKKNKKMNMNNNKKKKMMMKMNNMNGK-KMGKNNNMNAGKKMKMM 528

Qy       2146 GCACCTCACAAAGTCCCAACCATCGGAGTCTATGGAGTGCCAGGTTCAGGTAAATCTGGA 2205
Db         527 MMMMNMNMNMMMNNMMNMNMKKNNNNMNMKKMNNMMNMMMAMAMMMGNNNGKKMNMMMKM 468

Qy       2206 ATCATCAAAAGCGCTGTGACTAAGAAAGATCTGGTTGTGAGTGCGAAGAAGGAAAACTGC 2265
Db         467 GNGMMMNANMMMAKKNAAAMNAAANAAGKKGKNNAKAAAANAANANAKKAKAANAACNNC 408

Qy       2266 GCAGAAATCATCAGGGATGTAAGGAGGATGAGACGTATGGATGTTGCTGCTAGGACTGTC 2325
Db         407 MNMACMNNKAKNNKKKAKKNNNNNMMNMMKANKNAKAAKCNCNANNNKNAAAKKAAKNAN 348

Qy       2326 GATTCAGTGCTTCTAAATGGGGTTAAGCACCCCGTTAACACTCTGTACATTGATGAGGCA 2385
Db         347 NAANAAANNAAACNANANNNCKNNCACKAAAANNANCANNAAKAAAKNNAAAAKACAKCA 288

Qy       2386 TTTGCCTGCCATGCAGGGACGCTGCTGGCACTGATTGCCATCGTCAAACCTAAGAAAGTG 2445
Db         287 GKAKNNKKAAAAAKANANNNNCANCNANANAKNNKACANAKAACTAANANCCAKAATAAC 228

Qy       2446 GTATTGTGCGGGGACCCAAAACAAT 2470
Db         227 GTATAAAGAACCNCCACAAAACAKT 203
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RESULT 15
BE017217
LOCUS BE017217 634 bp mRNA linear EST 30-AUG-2000
DEFINITION fk78b02.y1 Zebrafish Research Genetics C32 fin Danio rerio cDNA 5' similar to SW:APE_BRARE O42364 APOLIPOPROTEIN E PRECURSOR ;, mRNA sequence.
ACCESSION BE017217
VERSION BE017217.1 GI:8281665
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes ; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 634)
AUTHORS Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE WashU Zebrafish EST Project 1998
JOURNAL Unpublished
COMMENT Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
cDNA Library Preparation: Ning Wu. cDNA Library Arrayed by: Research Genetics. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Research Genetics web address: http://www.researchgenetics.com/
Seq primer: T3 ET from Amersham
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .634
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/tissue_type="Fin"
/lab_host="GeneHogs (HS996, a phage-resistant isolate of DH10B)"
/clone_lib="Zebrafish Research Genetics C32 fin"
/note="Vector: pT7T3D-Pac with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was prepared from zebrafish(C32) fin, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is non-normalized. Library was constructed by Ning Wu. NOTE: This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info.llnl.gov)for further information"
BASE COUNT 190 a 170 c 142 g 132 t
ORIGIN

Query Match 0.8%; Score 40.2; DB 10; Length 634;
Best Local Similarity 50.3%; Pred. No. 6.7;
Matches 99; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

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Qy       4115 TGTACCGAAAATGGCCGGCTGCTTTTGATAGACAGCCAATAGCTGTCGGGACGGCTAGAC 4174
Db         60 TGGACCGATTATGGCCTGATGTGTCTTAACTCTACACACAAACTGTCGGCTTGGTGCAAA 119

Qy       4175 TTGTGAAGCACGAACCGCTCATCATACATGCTGTAGGACCCAATTTTTCTAAGATGCCGG 4234
Db        120 ACATCAAGGGCTCCCAACTCATCACAGAGCTTGAAACACTAATTACTGACACCATGGCTG 179

Qy       4235 AACCGGAGGGCGACCTTAAGCTCGCAGCTGCCTACATGAGCATAGCGTCCATCGTCAACG 4294
Db        180 AACTGAGCTCATACAGTGAAAATATACAAACCCACATGACCTCATACTCCTTTGATGCTG 239

Qy       4295 CTGAGCGGATTACAAAA 4311
Db        240 CTGGTCAGATCAGAAAA 256
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Search completed: November 15, 2003, 19:56:26
Job time : 9001 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2003, 22:31:43 ; Search time 12073 Seconds
(without alignments)
13055.125 Million cell updates/sec

Title: US-10-023-649-1_COPY_5000_11484
Perfect score: 6485
Sequence: 1 caccgccagcaacgacaacc.....tattttgtttttaaaatttc 6485

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	58	0.9	985	13	BX436838	BX436838 BX436838
c	2	53.6	0.8	836	29	CNS04Q18	AL302021 Tetraodon
	3	53.4	0.8	1101	29	CNS003DQ	AL064580 Drosophil
	4	52	0.8	1146	29	CNS021G2	AL176843 Tetraodon
c	5	50.8	0.8	1201	13	BX358198	BX358198 BX358198
c	6	50.4	0.8	997	29	CNS005TE	AL060767 Drosophil
c	7	50.2	0.8	1101	29	CNS0182P	AL108811 Drosophil
c	8	49.4	0.8	460	14	CB472367	CB472367 sn54_C04.
c	9	49	0.8	844	29	AG042177	AG042177 Pan trogl
	10	49	0.8	1101	29	CNS00E7Y	AL069057 Drosophil
c	11	49	0.8	1165	13	BX338369	BX338369 BX338369
c	12	48.8	0.8	1198	13	BX395612	BX395612 BX395612
c	13	48.8	0.8	1201	13	BX385348	BX385348 BX385348
	14	48.2	0.7	440	13	BU497603	BU497603 PfESToab8
	15	48.2	0.7	566	12	BM275442	BM275442 PfESToaa6
	16	48.2	0.7	569	12	BM273626	BM273626 PfESToaa5
c	17	48	0.7	887	13	BX441520	BX441520 BX441520
	18	47.8	0.7	946	13	BX459436	BX459436 BX459436
	19	47.6	0.7	993	13	BQ729165	BQ729165 AGENCOURT
	20	47.4	0.7	1065	9	AL515373	AL515373 AL515373
c	21	47.4	0.7	1101	29	CNS0021J	AL061936 Drosophil
	22	47.4	0.7	1225	29	CNS0161D	AL106171 Drosophil
c	23	47.2	0.7	240	9	AU074526	AU074526 AU074526
c	24	47.2	0.7	944	29	CNS06WVA	AL418940 T3 end of
	25	47.2	0.7	994	13	BX414650	BX414650 BX414650
	26	47.2	0.7	1005	13	BX441452	BX441452 BX441452
c	27	47.2	0.7	1201	9	AL548154	AL548154 AL548154
c	28	47	0.7	712	13	BX416727	BX416727 BX416727
c	29	47	0.7	1201	9	AL558113	AL558113 AL558113
c	30	46.8	0.7	905	29	CNS00KHX	AL077798 Drosophil
c	31	46.8	0.7	913	28	AZ546811	AZ546811 ENTEL88TR
	32	46.8	0.7	975	13	BX414927	BX414927 BX414927
c	33	46.8	0.7	994	29	CNS015XG	AL106030 Drosophil
	34	46.6	0.7	589	28	AQ541309	AQ541309 RPCI-11-3
c	35	46.6	0.7	794	28	BH498125	BH498125 BOGWF71TR
c	36	46.6	0.7	964	29	CNS017VX	AL108567 Drosophil
c	37	46.6	0.7	1101	29	CNS0183Y	AL108856 Drosophil
c	38	46.6	0.7	1161	13	BX332029	BX332029 BX332029
c	39	46.6	0.7	1201	13	BX399692	BX399692 BX399692
	40	46.4	0.7	923	28	AZ538694	AZ538694 ENTEY15TF
	41	46.4	0.7	1101	29	CNS003DX	AL064587 Drosophil
c	42	46.4	0.7	1201	13	BX336719	BX336719 BX336719
c	43	46.4	0.7	1201	29	CNS016AD	AL106495 Drosophil
c	44	46.2	0.7	1101	29	CNS003DQ	AL064580 Drosophil
	45	46.2	0.7	1167	29	CNS07360	AL427102 clone BA0

ALIGNMENTS

RESULT 1
BX436838
LOCUS BX436838 985 bp mRNA linear EST 15-MAY-2003
DEFINITION BX436838 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP003YH18 3-PRIME, mRNA sequence.
ACCESSION BX436838
VERSION BX436838.1 GI:30789527
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 985)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0CAP003DD09NP1.
FEATURES Location/Qualifiers
source 1. .985
/organism="Homo sapiens"

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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0CAP003YH18"
                     /tissue_type="THYMUS"
                     /clone_lib="Homo sapiens THYMUS"
                     /note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
BASE COUNT      337 a    120 c     95 g    277 t    156 others
ORIGIN

  Query Match             0.9%;  Score 58;  DB 13;  Length 985;
  Best Local Similarity   46.7%;  Pred. No. 5.5;
  Matches   84;  Conservative   27;  Mismatches   69;  Indels    0;  Gaps    0;

Qy       6303 TAATGCTGTGCAGTGTCACATTAATCGTATATCACACTACATATTAACAACACTATATCA 6362
              ::|:  | |  |   | | ||  ||  ||||| ::: |:  ||||   :: : |:|:|
Db        746 WWAWATTWTAAAAAWTAATATATATATTATATAWHWTTWWTTATTTTTWWTWATWTWTAT 805

Qy       6363 CTTTTATGAGACTCACTATGGGTCTCTAATATACACTACACATATTTTACTTAAAAACAC 6422
               |:|||    : : | |||   | | :|||||  |   |   ||: : ||  :|| |: |
Db        806 ATWTTAATTAWWWWATTATATATATAWAATATAAATAATTTATWAWATATAWAATAWTAT 865

Qy       6423 TATACACACTTTATAAATTCTTTTATAATTTTTCTTTTGTTTTTATTTTGTTTTTAAAAT 6482
              |: : |  ||| ||| | | :|||| ||| | ::|| |:|:|||| | |||| || ||
Db        866 ATTWTWTATATTAAAAAATATAWTATATTTTATWWHTTTWTWTATTATHTTTTAAATAT 925


RESULT 2
CNS04Q18/c
LOCUS       CNS04Q18                836 bp    DNA     linear   GSS 01-SEP-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            128L13 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL302021
VERSION     AL302021.1  GI:8179132
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
  MEDLINE   20296633
   PUBMED   10835645
REFERENCE   2
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
  MEDLINE   20359837
   PUBMED   10899143
REFERENCE   3  (bases 1 to 836)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .836
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="128L13"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0BG128CF07SP1~end :
                     PUC-Ori"
BASE COUNT      301 a     30 c    173 g    299 t     33 others
ORIGIN

  Query Match             0.8%;  Score 53.6;  DB 29;  Length 836;
  Best Local Similarity   57.8%;  Pred. No. 33;
  Matches   89;  Conservative    3;  Mismatches   62;  Indels    0;  Gaps    0;

Qy       6331 ATATCACACTACATATTAACAACACTATATCACTTTTATGAGACTCACTATGGGTCTCTA 6390
              || | |  ||| |||  || :| | || ||   |||||  | |  ||  |  |    |
Db        579 ATYTTAATCTAAATAAAAAAMAAATTAAATTTATTTTAATAAAACCAAATTTTTTTAAAA 520

Qy       6391 ATATACACTACACATATTTTACTTAAAAACACTATACACACTTTATAAATTCTTTTATAA 6450
              |||  :| |  ||||| :|  ||||| | |  || |||| |  | ||  ||||||  |
Db        519 ATACTMATTTTACATAAAWTTATTAAATAAAAMATCCACAATCAAAAATCTCTTTTTAAT 460

Qy       6451 TTTTTCTTTTGTTTTTATTTTGTTTTTAAAATTT 6484
              || ||  ||| ||| |   || ||||| ||||||
Db        459 TTATTTATTTATTTATTCATTTTTTTTCAAATTT 426


RESULT 3
CNS003DQ
LOCUS       CNS003DQ                1101 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR08I09 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL064580
VERSION     AL064580.1  GI:4941932
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .1101
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR08I09"
                     /clone_lib="RPCI-98"
                     /note="end : TET3"
BASE COUNT      291 a     51 c    117 g    404 t    238 others
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```
ORIGIN

  Query Match             0.8%;  Score 53.4;  DB 29;  Length 1101;
  Best Local Similarity   51.5%;  Pred. No. 33;
  Matches   84;  Conservative   14;  Mismatches   65;  Indels    0;  Gaps    0;

Qy       6322 ATTAATCGTATATCACACTACATATTAACAACACTATATCACTTTTATGAGACTCACTAT 6381
              ||:|:|     :: | | || |||| || || |  ||:  |  | ||| | |   |  :|
Db        274 ATWAWTWTATAWWAAWAWTAAATATAAAWAAAAAAATWAWAAATATATAAAAAATATAWT 333

Qy       6382 GGGTCTCTAATATACACTACACATATTTTACTTAAAAACACTATACACACTTTATAAATT 6441
              : |:  |||          |:|||||  |||||| | :|||   | |||  ||| |
Db        334 WWAATWTTWTAATATTTATATATTWTTTTATATAAAAAWAAWATATTTATTTTTAAAAAT 393

Qy       6442 CTTTTATAATTTTTCTTTTGTTTTTATTTTGTTTTTAAAATTT 6484
              ||||   | |||| |||| ||||||:||| || |||:  ::|
Db        394 ATTTTTATAATTTTATTTTWTTTTTAWTTTWTTATTAWTTWWT 436


RESULT 4
CNS021G2
LOCUS       CNS021G2                1146 bp    DNA     linear   GSS 01-SEP-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            225004 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL176843
VERSION     AL176843.1  GI:7814900
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
  MEDLINE   20296633
   PUBMED   10835645
REFERENCE   2
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
  MEDLINE   20359837
   PUBMED   10899143
REFERENCE   3  (bases 1 to 1146)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .1146
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="225004"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG225BH02LP1~end : T7"
BASE COUNT      393 a     60 c     73 g    274 t    346 others
ORIGIN

  Query Match             0.8%;  Score 52;  DB 29;  Length 1146;
  Best Local Similarity   31.7%;  Pred. No. 57;
  Matches  113;  Conservative   71;  Mismatches  172;  Indels    0;  Gaps    0;

Qy       6126 TTGTTGTAGGACTTATAGTGTTGGTCTGCAGCTCTATGCTTATAAACACACGTAGATGAC 6185
              ||:||  |::: ::::   |: ::  :: |:   ||:: || | |    | : |:|  |
Db        692 TTDTTTAAKKRKKKRKKWAGKGKKRAKKRAKAAKTAKRRTTTTKAKATKAARAARAAAAA 751

Qy       6186 TGAGCGCGGACACTGACATAGCGGTAAAACTCGATGTACTTCCGAGGAAGCGTGGTGCAT 6245
                |     ::  :::: ::: :: |||| : ::::|  :   : |:|:: | |  : |
Db        752 AAATTATTKRRKBKRRKKKRRKKKRAAAAKKKBRKKTGRKGRRKGGRARKKGRGAARGAA 811

Qy       6246 AATGCCACGCGCCGCTTGACACTAAAACTCGATGTATTTCCGAGGAAGCACAGTGCATAA 6305
              : :    |       ||:|   |  || | :|: | |||   ::: :   :::  |
Db        812 GRRKKNKKGDAWATTTTDATTATTTAATTTRADATTTTTADARKKKKKKKKKKKKKTTT 871

Qy       6306 TGCTGTGCAGTGTCACATTAATCGTATATCACACTACATATTAACAACACTATATCACTT 6365
              |  | |  : : |     ||  |  | | | | | |  | |||:| ||    | |  |  |
Db        872 TTTTTTTRTKTTTTTTTTTTTTTTTTTTAAATTTTAAATTWAAAATTTAAAAAAAANT 931

Qy       6366 TTATGAGACTCACTATGGGTCTCTAATATACACTACACATATTTTACTTAAAAACACTAT 6425
              |||  | | |    | :       |  :: : : |     ::|||:: | |||||  : |:|
Db        932 TTAAAAAAATTTDAAAKTAAAANTTTKRRDKRTTTTTTTDRTTTWWTTAAAAAAAWTTWT 991

Qy       6426 ACACACTTTATAAATTCTTTTATAATTTTTCTTTTGTTTTTATTTTGTTTTTAAAA 6481
                :  ||  || |      | |:|||     |||| ||||| |::| |||| || :
Db        992 TAWTTTTTATTATAAAWAATAAWAATAAAAATTTTTTTTTTTTTWWTTTTTTAAANR 1047


RESULT 5
BX358198/c
LOCUS       BX358198                1201 bp    mRNA    linear   EST 05-MAY-2003
DEFINITION  BX358198 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI035YE19 5-PRIME, mRNA sequence.
ACCESSION   BX358198
VERSION     BX358198.1  GI:30368196
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 1590.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI035AC10QP1&cluster=1590.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI035AC10QP1.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI035YE19"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      373 a    144 c    192 g    367 t    125 others
ORIGIN

  Query Match             0.8%;  Score 50.8;  DB 13;  Length 1201;
```

```
  Best Local Similarity   39.6%;  Pred. No. 90;
  Matches   89;  Conservative   36;  Mismatches  100;  Indels    0;  Gaps    0;

Qy       6260 CTTGACACTAAAACTCGATGTATTTCCGAGGAAGCACAGTGCATAATGCTGTGCAGTGTC 6319
              | |:::  |||  :|   : | || |   |  |: |::|    | ||| :: |  |   :|
Db       1016 CCTRRSSTTAAYYYTTTTWWTTTTCCAAAAWAMCCMMAAAAAAAAAATTYYTTWAAAAAWC 957

Qy       6320 ACATTAATCGTATATCACACTACATATTAACAACACTATATCACTTTTATGAGACTCACT 6379
              :|    |  | |  |: :| |: | | || |:: |  | |   ||||  | : ::::  |
Db        956 CMAAATTTATTTTTCCMWMCMAMTTTTAAAAAMMCCCCTTTTTTTTTTTTTTWMMYYYYTT 897

Qy       6380 ATGGGTCTCTAATATACACTACACATATTTTACTTAAAAACACTATACACACTTTATAAA 6439
               |:|: |: |  |: | |  |    || :|:  |    :| || ::   : |||  ||:
Db        896 TTKGSMCHTTTTTWAAAAAAATKKKTACCKTWAATTTTNMCCCTTWRGGTWWTTTTAAAR 837

Qy       6440 TTCTTTTATAATTTTTCTTTTGTTTTTATTTTGTTTTTAAAATTT 6484
                :     |  ||||| |||| ||||| |||| ||||| |:|: |
Db        836 GSMCCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAWAWAT 792


RESULT 6
CNS005TE/c
LOCUS       CNS005TE                997 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR12K22 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL060767
VERSION     AL060767.1  GI:4943573
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 997)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .997
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR12K22"
                     /clone_lib="RPCI-98"
                     /note="end : TET3"
BASE COUNT       89 a     99 c     13 g    258 t    538 others
ORIGIN

  Query Match             0.8%;  Score 50.4;  DB 29;  Length 997;
  Best Local Similarity   17.6%;  Pred. No. 1.1e+02;
  Matches   91;  Conservative  169;  Mismatches  258;  Indels    0;  Gaps    0;

Qy       2672 AAGAAGAAGAAGAGTGCTCCTAAGCCAAAACCTACTCAGCCTAAAAAGAAGAAGCAGCAA 2731
              |:  |:||:|  :: |     :|   ::|:   |   ||   : : ||  : :| :: ||
Db        953 ARAGARAARAGARRAGAGARARAAARRRARRRRAGRRAGRAGRGRSAGGGRGRGGRRAAA 894
```

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Qy       2732 GCCAAGAGGACGAAACGCAAGCCTAAACCAGGGAAACGACAACGTATGTGTATGAAGTTG 2791
              |::|: : :|:|   ::   :||:    ::::  :: :    : : : | |:|| |
Db        893 ARAARDARARARARARRRARRAKAARARGARRRRGRRRRRGRAGRRRARGAGGRAGRRG 834

Qy       2792 GAGTCGGACAAGACATTTCCGATCATGCTGAACGGCCAAGTGAATGGATATGCCTGCGTT 2851
              : :  ::| |:::        :  : :  :|: ::  | : ::: :||   :   | :
Db        833 RGRGRRRARARRRAGAARARARGRRARAARARARRRRAGRRRRRARGARGRRRRGGRRRG 774

Qy       2852 GTCGGAGGAAGGCTGATGAAACCACTCCACGTTGAAGGAAAAATTGATAATGAGCAATTA 2911
              :  :::|::::   :|  :|:  |    : :  ::|| ||::|  :: :: ::|  | :
Db        773 RGGRRRGRRRRAARRARARARAGARAAARRRRARRAGAAARRARRRRRRRRRGAGARAR 714

Qy       2912 GCGGCCGTGAAATTGAAGAAGGCTAGCATGTACGACTTGGAGTACGGCGACGTTCCCCAG 2971
              : ::  :  |:|  |||::::|   : |   : |:   :::|   :: :: :      |:
Db        713 RARRRARRAARAGAGAARRRRGRRGRGAGARRRGRGRGRRRGAGARRRRRGRRMRTRRAR 654

Qy       2972 AACATGAAATCAGACACGCTGCAGTACACCAGCGACAAACCACCGGGCTTCTACAACTGG 3031
              :: : :: |  |:: | |  : :: :    :: :|  ::  |  |::     : |:  ::
Db        653 RRRRARRGAGAARRRARGARRRRRGRRGRRRRGRARGRRRRAGRGRRRGRRARGARRGRR 594

Qy       3032 CACCACGGCGCAGTCCAGTATGAGAATGGGAGATTTACCGTACCGAGAGGAGTGGGCGGG 3091
              |  : ::   ||   :: : ::|:| :  :||   :  : | ::::  |: | |  |
Db        593 RAGRRRRRARAGAGARRGRRRRGRARRAARGAARRRRARRARRRRRRAAARRGAGRAGA 534

Qy       3092 AAAGGCGACAGCGGAAGACCGATCCTGGACAACAGAGGCAGAGTTGTGGCTATTGTTCTA 3151
              :|:|: |: :: ::|:::  ::    :::  :  |::: |||:  :  :  |  :   |
Db        533 RARGRAGRARRARRARRRRRRRGGARRRGGRRGGRRRAAGARRRRAARAAARARRRARA 474

Qy       3152 GGAGGTGCAAATGAGGGCACGCGTACGGCGCTTTCAGT 3189
              |:||  : :  |                       |   |
Db        473 GRAGARRRRTNTNNNNNNNNNNNNNNNNAGCNTNNNT 436


RESULT 7
CNS0182P/c
LOCUS       CNS0182P                1101 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN37D10 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL108811
VERSION     AL108811.1  GI:5629115
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .1101
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACN37D10"
                     /clone_lib="DrosBAC"
                     /plasmid="pBeloBAC11"
                     /note="end : SP6"
BASE COUNT      274 a    268 c    128 g     73 t    358 others
ORIGIN
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```
  Query Match             0.8%;  Score 50.2;  DB 29;  Length 1101;
  Best Local Similarity   17.6%;  Pred. No. 1.2e+02;
  Matches   39;  Conservative  114;  Mismatches   68;  Indels    0;  Gaps    0;

Qy       6265 CACTAAAACTCGATGTATTTCCGAGGAAGCACAGTGCATAATGCTGTGCAGTGTCACATT 6324
              |:::::::: : :: :::: :  :: ::||  :::::: |  :  : :::|:::
Db       1019 CHHWWWHWMAYAWWWWWHYAWAMHWHHHHMMCAMCMHWYMMHMCCYMCYCCWMHMWCHHH 960

Qy       6325 AATCGTATATCACACTACATATTAACAACACTATATCACTTTTATGAGACTCACTATGGG 6384
              :   ::: |:::::: |:|:||:::: : :::::::| :   |: : | : ::::
Db        959 MTATTWHHYTYHYWMWTCHTMTTWWYHYMTMHWHHHHAAWAMAAHMHAATHTWYHMAHAH 900

Qy       6385 TCTCTAATATACACTACACATATTTTACTTAAAAACACTATACACACTTTATAAATTCTT 6444
              : |::  : | : :: : : : |:|: ::::  ||:::  : ::::::::::||:| ||
Db        899 HTTYYTTYYTYYYYYYYYYYYYTYTYTHHWWTTAAHHHWYAHWHHWHWWYHYWAAWTTTT 840

Qy       6445 TTATAATTTTTCTTTGTTTTTATTTTGTTTTTAAAATTTC 6485
              || |  |||:|::::: ||::| :|::  |:|::   |:|:
Db        839 TTTTTTTTTWTHWHYHHTTYYTTYTYYTCTYTYMCCTTWTY 799


RESULT 8
CB472367/c
LOCUS       CB472367                460 bp    mRNA    linear   EST 26-MAR-2003
DEFINITION  sn54_C04.f sn Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   CB472367
VERSION     CB472367.1  GI:29278753
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 460)
  AUTHORS   Neilan,J.G., Kutish,G.F., Lu,Z., Zsak,A. and Rock,D.L.
  TITLE     Sequence analysis of African swine fever virus infected and
            non-infected porcine macrophage cDNA libraries
  JOURNAL   Unpublished
COMMENT     Contact: Neilan JG
            Plum Island Animal Disease Center
            US Department of Agriculture, Agricultural Research Service
            PO Box 848, Greenport, NY 11944-848, USA
            Tel: 631 323 3133
            Fax: 631 323 3044
            Email: jneilan@piadc.ars.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified by
            cross_match v0.990329 and lucy v1.17p.
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .460
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /tissue_type="lymphoid"
                     /cell_type="macrophage"
                     /lab_host="DH10B"
                     /clone_lib="sn"
                     /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI;
                     Library made from pools of polyA selected RNA, isolated at
                     different times post-infection (0 to 16 hrs) from African
                     swine fever virus (isolate Pretorisuskop/96/4) infected
                     swine macrophages. Macrophages were derived from
                     peripheral blood mononuclear cells cultured for 48 hrs on
                     plastic in the presence of 30% L929 supernatant."
BASE COUNT      264 a     22 c     91 g     83 t
ORIGIN

  Query Match             0.8%;  Score 49.4;  DB 14;  Length 460;
  Best Local Similarity   55.6%;  Pred. No. 2e+02;
  Matches   95;  Conservative    0;  Mismatches   76;  Indels    0;  Gaps    0;

Qy       6314 AGTGTCACATTAATCGTATATCACACTACATATTAACAACACTATATCACTTTTATGAGA 6373
              | | |  | |||||  || ||     |   | ||   || | | | | || ||| |  ||
Db        196 ATTTTTTCTTTAATTTTAAATTTTTTTTTTCTTTTTAAAAGTTTTTTACCTTTTTTGGA 137

Qy       6374 CTCACTATGGGTCTCTAATATACACTACACATATTTTACTTAAAAACACTATACACACTT 6433
              | |   | | |  |  |     |     | ||||  ||||||||  | |       ||
Db        136 TATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAAACTTTTTTTTGTTT 77

Qy       6434 TATAAATTCTTTTATAATTTTTCTTTTGTTTTTATTTTGTTTTTAAAATTT 6484
              | |    || |||||   ||||| |||| ||||| |||| ||||||||||||
Db         76 TTTTTTTTTTTTTACCTTTTTTTTTTTTTTTTTTTTTTTTTTAAAATTT 26


RESULT 9
AG042177/c
LOCUS       AG042177                844 bp    DNA     linear   GSS 01-NOV-2001
DEFINITION  Pan troglodytes DNA, clone: PTB-020B19.F, genomic survey sequence.
ACCESSION   AG042177
VERSION     AG042177.1  GI:16570902
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library PTB
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 844)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the R&D process and may have higher chance of
            clone tracking errors.
             PRIMERS
                 Sequencing: -21M13
             LIBRARY
                 Vector    : pKS145
                 R.Site 1  : SacI
                 R.Site 2  : SacI.
FEATURES             Location/Qualifiers
     source          1. .844
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="PTB-020B19.F"
                     /sex="male"
                     /cell_type="lymphoblast"
                     /clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT      243 a     43 c     66 g    487 t      5 others
ORIGIN

  Query Match             0.8%;  Score 49;  DB 29;  Length 844;
  Best Local Similarity   51.4%;  Pred. No. 2e+02;
  Matches  112;  Conservative    0;  Mismatches  106;  Indels    0;  Gaps    0;

Qy       6264 ACACTAAAACTCGATGTATTTCCGAGGAAGCACAGTGCATAATGCTGTGCAGTGTCACAT 6323
              | |  |||| |       || |   |  ||| |   | || ||        |  ||    |
Db        601 ATAAGAAAATTAATATAATATATAATAAAGAATTATACAAAAAATAAAAAAAAGTNTATT 542

Qy       6324 TAATCGTATATCACACTACATATTAACAACACTATATCACTTTTATGAGACTCACTATGG 6383
              |||  || |  | | ||     ||| || |  |||| |  ||||| | |   | |||
Db        541 AAATAATAAAAAATAATAATATATAAAAAAATAATATAATATTTATTAAAAAAAATATAA 482

Qy       6384 GTCTCTAATATACACTACACATATTTTACTTAAAAACACTATACACACTTTATAAATTCT 6443
              | |  || | | |  | |||| |    || ||  | |||| | | |  ||||||
Db        481 ATATAAAAAAGATAAAAATAATATATACAATAGAATAAATATATAAAATAAATAAATATA 422
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Qy       6444 TTTATAATTTTTCTTTTGTTTTTATTTTGTTTTTAAAA 6481
              || | ||||     ||| |||| ||||| |||  | ||
Db        421 TTAAAAATTAGGTATTTTTTTTAATTTTTTTTAAATAA 384


RESULT 10
CNS00E7Y
LOCUS       CNS00E7Y                1101 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR28A16 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL069057
VERSION     AL069057.1  GI:4949017
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .1101
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR28A16"
                     /clone_lib="RPCI-98"
                     /note="end : TET3"
BASE COUNT      248 a    175 c    173 g    341 t    164 others
ORIGIN

  Query Match             0.8%;  Score 49;  DB 29;  Length 1101;
  Best Local Similarity   38.1%;  Pred. No. 1.9e+02;
  Matches   61;  Conservative   44;  Mismatches   55;  Indels    0;  Gaps    0;

Qy       6318 TCACATTAATCGTATATCACACTACATATTAACAACACTATATCACTTTTATGAGACTCA 6377
              ||:::::| :| :|: :|: : ::   :||  ::|   | |:|:: |||| | |   | |
Db        910 TCMMMHHAYHCMHAHTHCHTMWYWWTAWTTTTMMAWTTTTTWTMHWTTTTTTTATTTTWA 969

Qy       6378 CTATGGGTCTCTAATATACACTACACATATTTTACTTAAAAACACTATACACACTTTATA 6437
                :|   ::|: || |||   |   :|:| | |: || ::|: | |: ::: : | :
Db        970 AMHTTHYWMTMMAAAATAWTTTTATHAWAATMTMTTTTWWAWWAWTWAWHWWHTTCWYNY 1029

Qy       6438 AATTCTTTTATAATTTTTCTTTTGTTTTTATTTTGTTTTT 6477
              :|| ||||:| ::| :|:|| : ||||: |||| ||:||
Db       1030 CMTTTTTTTWTTMHTMHTHTTMWTTTTTWTTTTTTTTYTT 1069


RESULT 11
BX338369/c
LOCUS       BX338369                1165 bp    mRNA    linear   EST 02-MAY-2003
DEFINITION  BX338369 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI058YF14 5-PRIME, mRNA sequence.
ACCESSION   BX338369
VERSION     BX338369.1  GI:30343682
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1165)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI058DC07QP1.
FEATURES             Location/Qualifiers
     source          1. .1165
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI058YF14"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      567 a    109 c    140 g    251 t     98 others
ORIGIN

  Query Match             0.8%;  Score 49;  DB 13;  Length 1165;
  Best Local Similarity   41.1%;  Pred. No. 1.8e+02;
  Matches   67;  Conservative   33;  Mismatches   63;  Indels    0;  Gaps    0;

Qy       6322 ATTAATCGTATATCACACTACATATTAACAACACTATATCACTTTTATGAGACTCACTAT 6381
              ::: :|   : |  | : :| ::| ||: |: | | :|| |    |   : |   | :||
Db        977 WWWTWTWWAWAAAWATWAWATWWAATAWWAWTAWTTWATWAAAAATTAAWTATAAAAWAT 918

Qy       6382 GGGTCTCTAATATACACTACACATATTTTACTTAAAAACACTATACACACTTTATAAATT 6441
                |   || |:|:    | : :|:||||| :|||| | | |:|| | |    : |:|||
Db        917 WTTTTATTATTWTWTTTAATWTWTWTTTTATWTAAATATATTWTAWAAAAAAAWAAWATT 858

Qy       6442 CTTTTATAATTTTTCTTTTGTTTTTATTTTGTTTTTAAAATTT 6484
              :::||: :|| ::|: ||  |:||| |||: |||||    |||.
Db        857 YYWTTWAWATAWYTMATTAATWTTTTTTTTWWTTTTTTTTTTTT 815


RESULT 12
BX395612/c
LOCUS       BX395612                1198 bp    mRNA    linear   EST 13-MAY-2003
DEFINITION  BX395612 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI002YP22 3-PRIME, mRNA sequence.
ACCESSION   BX395612
VERSION     BX395612.1  GI:30616740
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1198)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
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            Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI002DH11NP1.
FEATURES              Location/Qualifiers
     source           1. .1198
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="CS0DI002YP22"
                      /tissue_type="PLACENTA COT 25-NORMALIZED"
                      /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                      /note="1st strand cDNA was primed with a NotI-oligo(dT)
                      primer. Five prime end enriched, double-strand cDNA was
                      digested with Not I and cloned into the Not I and EcoR V
                      sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      242 a    122 c    196 g    372 t    266 others
ORIGIN

  Query Match             0.8%;  Score 48.8;  DB 13;  Length 1198;
  Best Local Similarity   35.6%;  Pred. No. 2e+02;
  Matches   74;  Conservative   47;  Mismatches   87;  Indels    0;  Gaps    0;

Qy       6278 TGTATTTCCGAGGAAGCACAGTGCATAATGCTGTGCAGTGTCACATTAATCGTATATCAC 6337
             |:: ::|: ::  ||  | | :  |:  |: | |  :     :::  ||   |:|:|| :
Db        952 TDKTKKTMDKWAAAAAKAAAAYAAAKTKTKTTTTMAMCATCTMMMAMAAATTTWTWTCCM 893

Qy       6338 ACTACATATTAACAACACTATATCACTTTTATGAGACTCACTATGGGTCTCTAATATACA 6397
             | ||    : | |: :  |: | :: ||:||: |   |:::| |   : | ::| | : :
Db        892 AWTAWKMTWAACCMCMTTTMMAAMMATTWTAYMAATTTMMMTTTTTAHTTAKMACAAMAM 833

Qy       6398 CTACACATATTTTACTTAAAAACACTATACACACTTTATAAATTCTTTTATAATTTTTCT 6457
             : |:  :|||| |  |||| ||   :|:: |  :||:: |||        | |||:|
Db        832 MAAMTTWTATTATTTTTAAKAATTTKAKMAATKYTTKMMAAAAMWMMMATTKATTWTMAA 773

Qy       6458 TTTGTTTTTATTTTGTTTTTAAAATTTC 6485
             ||  |||   |:||  |||| :|:||:|
Db        772 TTCMTTTCATTWTTTCTTTTCHAWTTKC 745


RESULT 13
BX385348/c
LOCUS       BX385348               1201 bp    mRNA    linear   EST 08-MAY-2003
DEFINITION  BX385348 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
            Homo sapiens cDNA clone CS0DL010YM11 5-PRIME, mRNA sequence.
ACCESSION   BX385348
VERSION     BX385348.1  GI:30451334
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 727.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DL010AG06QP1&cluster=727.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DL010AG06QP1.
FEATURES              Location/Qualifiers
     source           1. .1201
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="CS0DL010YM11"
                      /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
                      /cell_line="RAMOS CELL LINE"
                      /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
                      25-NORMALIZED"
                      /note="1st strand cDNA was primed with a NotI-oligo(dT)
                      primer. Five prime end enriched, double-strand cDNA was
                      digested with Not I and cloned into the Not I and EcoR V
                      sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      473 a     50 c    184 g    338 t    156 others
ORIGIN

  Query Match             0.8%;  Score 48.8;  DB 13;  Length 1201;
  Best Local Similarity   56.6%;  Pred. No. 2e+02;
  Matches   86;  Conservative    2;  Mismatches   64;  Indels    0;  Gaps    0;

Qy       6328 CGTATATCACACTACATATTAACAACACTATATCACTTTTATGAGACTCACTATGGGTCT 6387
             |: | | || | || | ||  | || |  ||||| | || |   |       |       |
Db        255 CKAAAAACATATTAAAAATACAAAAAAACATATCATTATTCTCTTAAATCACAACCAAAT 196

Qy       6388 CTAATATACACTACACATATTTTACTTAAAAACACTATACACACTTTATAAATTCTTTTA 6447
             | || ||| | |  |||| ||| || ||||    ||:||   | ||| |   |  ||||
Db        195 CCAAAATAAAATKTACATTTTTCACCTAAACTACCTWTATTTATTTTTTTTTTATTTTTT 136

Qy       6448 TAATTTTTCTTTTGTTTTTATTTTGTTTTTAA 6479
             |  ||||  |||| |||| |||||   |||||
Db        135 TCTTTTTCTTTTTTTTTTCATTTTCCATTTAA 104


RESULT 14
BU497603
LOCUS       BU497603               440 bp    mRNA    linear   EST 11-SEP-2002
DEFINITION  PfESToab81g06.y1 Plasmodium falciparum 3D7 asexual cDNA Plasmodium
            falciparum 3D7 cDNA 5', mRNA sequence.
ACCESSION   BU497603
VERSION     BU497603.1  GI:22793797
KEYWORDS    EST.
SOURCE      Plasmodium falciparum 3D7
  ORGANISM  Plasmodium falciparum 3D7
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1  (bases 1 to 440)
  AUTHORS   Tang,K., Cole,R., Chakrabarti,D., Haywood,R., Clifton,S., Pape,D.,
            Marra,M., Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B.,
            Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Jentes,E., Ronko,I.,
            Tsagareishvili,R., Belaygorod,L., Franklin,C., Carr,L.; Grow,A.,
            Maguire,L., Richey,J., Wadkins,J., Kennedy,S., Levinso,D.,
            Waterston,R., Wilson,R. and Sibley,D.
  TITLE     WashU Plasmodium EST Project
  JOURNAL   Unpublished
COMMENT     Contact: L. David Sibley
            WashU Plasmodium EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Library was constructed by Debopam Chakrabarti DNA sequencing by:
            Washington University Genome Sequencing Center For information on
            obtaining a clone please contact: L. David Sibley
            (sibley@borcim.wustl.edu)., Washington University
            Seq primer: -40UP from Gibco.
FEATURES              Location/Qualifiers
     source           1. .440
                      /organism="Plasmodium falciparum 3D7"
                      /mol_type="mRNA"
                      /db_xref="taxon:36329"
                      /lab_host="DH10B (GeneHog, Invitrogen, Inc.)"
                      /clone_lib="Plasmodium falciparum 3D7 asexual cDNA"
                      /note="Vector: pBluescript SK plus; Site_1: EcoRI; Site_2:
                      XhoI; Library was constructed by Debopam Chakrabarti.
                      Total RNA samples were isolated from mixed stage
                      saponin(0.1%)-lysed P. falciparum 3D7 infected
                      erythrocytes by the acidic guanidinium-phenol chloroform
                      method. The poly A+ RNA was isolated by the polyAT-Tract
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mRNA isolation system (Promega, WI) using streptavidin Magnesphere particles. Directional cDNA libraries were constructed by oligo d(T) priming of poly(A)+ RNA (5mg) into EcoRI and XhoI sites of l ZapII vector using the Zap cDNA synthesis kit (Stragene, CA). The average size of the cDNA inserts in the library was between 1.0 and 1.5kb. Clones were mass excised using the ExAssist helper phage (Stratagene), the phagemids were precitptated with PEG 8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DH10B cells."

BASE COUNT 195 a 22 c 14 g 208 t 1 others
ORIGIN

Query Match 0.7%; Score 48.2; DB 13; Length 440;
Best Local Similarity 55.8%; Pred. No. 3.3e+02;
Matches 92; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

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Qy       6320 ACATTAATCGTATATCACACTACATATTAACAACACTATATCACTTTTATGAGACTCACT 6379
              | || |    |||||     || ||||| | || |  | |     |   |  |    |
Db        215 ATATAATATATATATTTTTATATATATTTAAAAAAAAAAAAAATATAAAAATATTTTATAT 274

Qy       6380 ATGGGTCTCTAATATACACTACACATATTTTACTTAAAAACACTATACACACTTTATAAA 6439
              ||   | | |||||||   || | |||| |   |  |||| |  ||| | |  | ||||
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RESULT 15
BM275442
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ACCESSION BM275442
VERSION BM275442.1 GI:17968772
KEYWORDS EST.
SOURCE Plasmodium falciparum 3D7
ORGANISM Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 566)
AUTHORS Tang,K., Cole,R., Chakrabarti,D., Haywood,R., Clifton,S., Pape,D., Marra,M., Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Jentes,E., Ronko,I., Tsagareishvili,R., Belaygorod,L., Franklin,C., Carr,L., Grow,A., Maguire,L., Richey,J., Wadkins,J., Kennedy,S., Levinso,D., Waterston,R., Wilson,R. and Sibley,D.
TITLE WashU Plasmodium EST Project
JOURNAL Unpublished
COMMENT Contact: L. David Sibley
WashU Plasmodium EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library was constructed by R. Haywood. DNA sequencing by:
Washington University Genome Sequencing Center For information on obtaining a clone please contact: L. David Sibley (sibley@borcim.wustl.edu), Washington University
Seq primer: -40UP from Gibco
High quality sequence stop: 423.
FEATURES Location/Qualifiers
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/organism="Plasmodium falciparum 3D7"
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/dev_stage="gametocyte (stage III-V)"
/lab_host="DH10B (GeneHog, Invitrogen, Inc.)"
/clone_lib="Plasmodium falciparum 3D7 gametocyte cDNA library"
/note="Vector: pBluescript SK plus; Site_1: EcoRI; Site_2: XhoI; The library was constructed by R Haywood. cDNAs were synthesized from ganetocyte poly(A)+ RNA by oligo d(T) priming, size-selected and directionally cloned into the EcoRi (5' end) to XhoI (3' end) sites of the Uni-ZAP XR lambda vector (Stratagene). The primary library was mass excised as phagemid using the ExAssist helper phage (Stratagene), the phagemids were precitptated with PEG 8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DH10B cells. Clone Availability: David Sibley, Washington University."

BASE COUNT 256 a 63 c 53 g 194 t
ORIGIN

Query Match 0.7%; Score 48.2; DB 12; Length 566;
Best Local Similarity 57.7%; Pred. No. 3.1e+02;
Matches 86; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

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Search completed: November 16, 2003, 08:59:44
Job time : 12079 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2003, 17:26:43 ; Search time 1496 Seconds
(without alignments)
10923.143 Million cell updates/sec

Title: US-10-023-649-1_COPY_1_5000
Perfect score: 5000
Sequence: 1 accctacaaactaatcgatc.....ataattctagaaacgccacc 5000

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2169961 seqs, 1634102185 residues

Total number of hits satisfying chosen parameters: 4339922

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	2116.4	42.3	12523	10	US-09-991-258-1	Sequence 1, Appli
3	2113.2	42.3	12379	10	US-09-991-258-14	Sequence 14, Appl
4	2113.2	42.3	13584	10	US-09-991-258-17	Sequence 17, Appl
5	2111	42.2	7479	10	US-09-991-258-2	Sequence 2, Appli
6	1567.2	31.3	10610	11	US-09-994-412-3	Sequence 3, Appli
7	1564	31.3	11517	10	US-09-901-106-1	Sequence 1, Appli
8	1564	31.3	15538	12	US-09-190-246-1	Sequence 1, Appli
9	1473.8	29.5	8100	12	US-09-190-246-4	Sequence 4, Appli
10	1300.4	26.0	8000	11	US-09-507-362-102	Sequence 102, App
11	1300.4	26.0	11740	11	US-09-507-362-103	Sequence 103, App
12	1295.6	25.9	8000	11	US-09-507-362-101	Sequence 101, App
13	1295.6	25.9	11282	10	US-09-733-042-1	Sequence 1, Appli
14	1295.6	25.9	11282	11	US-09-275-883-1	Sequence 1, Appli
15	330.8	6.6	705	12	US-10-123-101-51	Sequence 51, Appl
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17	211.4	4.2	6989	10	US-09-991-258-11	Sequence 11, Appl
18	90.8	1.8	282	12	US-09-190-246-7	Sequence 7, Appli
19	50.6	1.0	170	12	US-10-123-101-90	Sequence 90, Appl
20	49	1.0	327	12	US-10-123-101-65	Sequence 65, Appl
21	49	1.0	346	12	US-10-123-101-67	Sequence 67, Appl
22	48.6	1.0	132	12	US-10-123-101-68	Sequence 68, Appl
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32	39.6	0.8	6479	13	US-10-098-841-101	Sequence 101, App
33	39.2	0.8	775	12	US-10-140-472-120	Sequence 120, App
34	39.2	0.8	775	12	US-10-141-761-120	Sequence 120, App
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ALIGNMENTS

RESULT 1
US-10-023-649-1
; Sequence 1, Application US/10023649
; Publication No. US20030143201A1
; GENERAL INFORMATION:
; APPLICANT: The Minister of National Defence, Government of Canada
; APPLICANT: Nagata, Leslie P
; APPLICANT: Wong, Jonathon P
; TITLE OF INVENTION: No. US20030143201A1el DNA-Based Vaccine Against the Encephalitis
; FILE REFERENCE: NEL-001
; CURRENT APPLICATION NUMBER: US/10/023,649
; CURRENT FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: 60/256,948
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 11484
; TYPE: DNA
; ORGANISM: Western equine encephalomyelitis virus - strain 71V-1658
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(7428)
; OTHER INFORMATION: 5' UTR <1 .. 24
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7473)..(11183)
; OTHER INFORMATION: encodes nucleocapsid, E3, E2, 6K and E1 proteins
US-10-023-649-1

Query Match 100.0%; Score 5000; DB 12; Length 11484;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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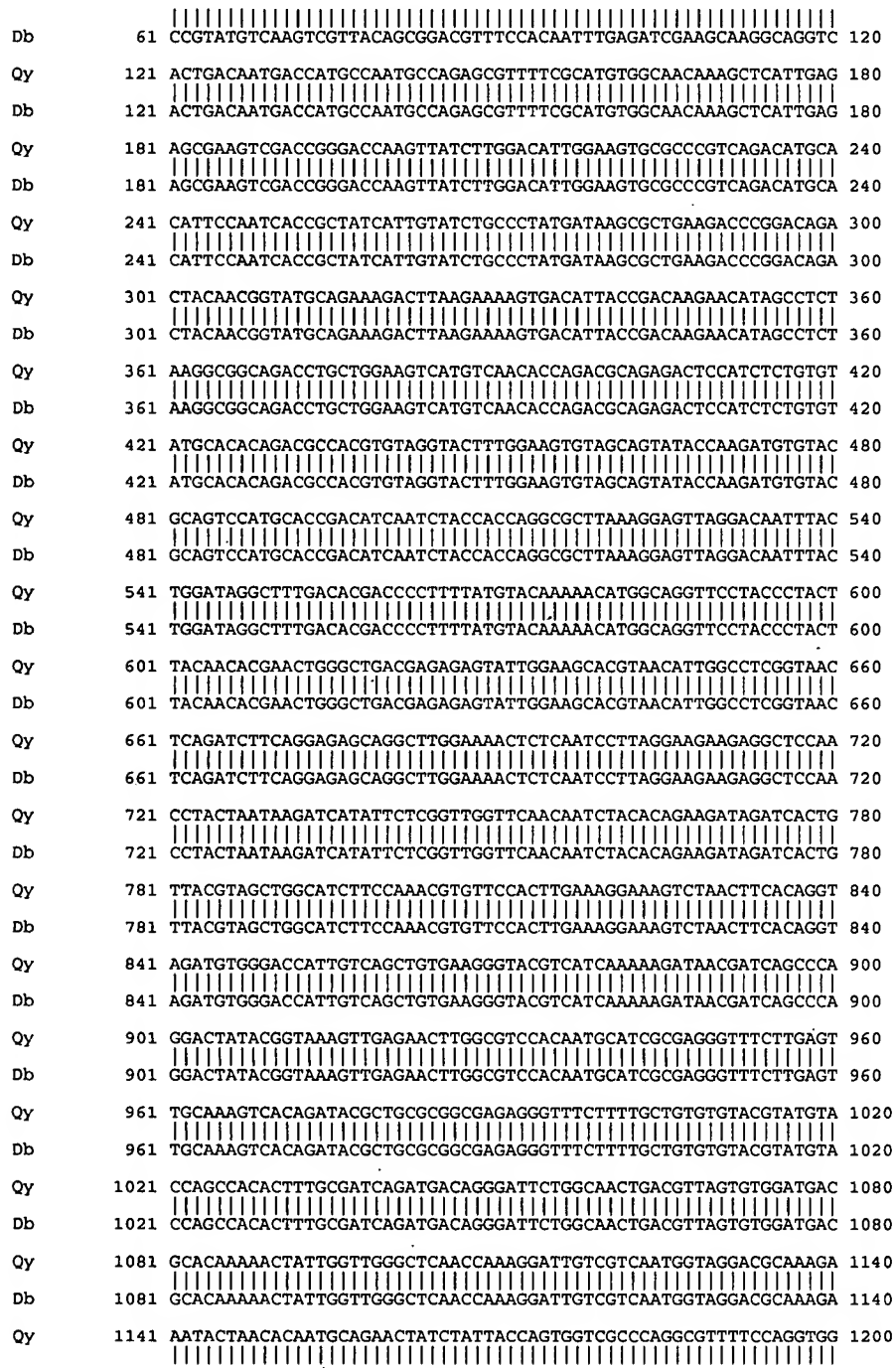
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Qy      3061 AAGGCTTTAGAGCCAGTCTTGGCCACGGCCAACATTGTGCTGACGAGACAGCAGTGGGAG 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3061 AAGGCTTTAGAGCCAGTCTTGGCCACGGCCAACATTGTGCTGACGAGACAGCAGTGGGAG 3120

Qy      3121 ACGTTGCACCCATTCAAGCATGACAGAGCGTACTCACCTGAAATGGCACTGAACTTCTTT 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3121 ACGTTGCACCCATTCAAGCATGACAGAGCGTACTCACCTGAAATGGCACTGAACTTCTTT 3180

Qy      3181 TGCACCAGGTTCTTTGGAGTAGACCTGGACAGTGGGTTATTTTCCGCTCCTACCGTCGCA 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3181 TGCACCAGGTTCTTTGGAGTAGACCTGGACAGTGGGTTATTTTCCGCTCCTACCGTCGCA 3240

Qy      3241 CTTACTTACAGGGATCAGCACTGGGATAACTCGCCAGGGAAGAACATGTATGGGCTTAAT 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3241 CTTACTTACAGGGATCAGCACTGGGATAACTCGCCAGGGAAGAACATGTATGGGCTTAAT 3300

Qy      3301 AGAGAGGTAGCAAAGGAGTTGTCACGGCGATATCCGTGCATCACAAAAGCGGTTGACACA 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3301 AGAGAGGTAGCAAAGGAGTTGTCACGGCGATATCCGTGCATCACAAAAGCGGTTGACACA 3360

Qy      3361 GGCAGGGTAGCTGATATAAGGAATAATACCATCAAGGACTACTCTCCAACAATTAATGTG 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3361 GGCAGGGTAGCTGATATAAGGAATAATACCATCAAGGACTACTCTCCAACAATTAATGTG 3420

Qy      3421 GTTCCATTAAATCGCCGGTTGCCCCACTCGTTGATCGTTGACCACAAAGGACAGGGTACA 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3421 GTTCCATTAAATCGCCGGTTGCCCCACTCGTTGATCGTTGACCACAAAGGACAGGGTACA 3480

Qy      3481 ACTGATCACAGCGGATTCCTATCTAAGATGAAGGGCAAATCTGTGTTGGTGATCGGCGAT 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3481 ACTGATCACAGCGGATTCCTATCTAAGATGAAGGGCAAATCTGTGTTGGTGATCGGCGAT 3540

Qy      3541 CCTATCAGCATTCCAGGGAAGAAAGTAGAGTCCATGGGTCCATTGCCCACTAATACCATC 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3541 CCTATCAGCATTCCAGGGAAGAAAGTAGAGTCCATGGGTCCATTGCCCACTAATACCATC 3600

Qy      3601 AGGTGTGATCTCGATTTGGGAATACCTAGCCATGTCGGTAAATATGACATTATCTTTGTC 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3601 AGGTGTGATCTCGATTTGGGAATACCTAGCCATGTCGGTAAATATGACATTATCTTTGTC 3660

Qy      3661 AATGTTAGGACCCCGTACAGGAACCATCACTACCAACAGTGCGAGGATCACGCTATCCAC 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3661 AATGTTAGGACCCCGTACAGGAACCATCACTACCAACAGTGCGAGGATCACGCTATCCAC 3720

Qy      3721 CACAGCATGCTAACGTGTAAGGCTGTCCACCACCTGAACACTGGCGGAACATGTGTGGCT 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3721 CACAGCATGCTAACGTGTAAGGCTGTCCACCACCTGAACACTGGCGGAACATGTGTGGCT 3780

Qy      3781 ATAGGGTATGGGCTTGCTGATCGCGCAACCGAGAATATCATCACTGCGGTGGCACGCTCA 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3781 ATAGGGTATGGGCTTGCTGATCGCGCAACCGAGAATATCATCACTGCGGTGGCACGCTCA 3840

Qy      3841 TTTAGGTTTACCCGTGTCTGTCAGCCTAAGAACACTGCCGAAAATACTGAGGTTCTCTTC 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3841 TTTAGGTTTACCCGTGTCTGTCAGCCTAAGAACACTGCCGAAAATACTGAGGTTCTCTTC 3900

Qy      3901 GTGTTCTTCGGCAAGGACAACGGCAACCACACACATGACCAGGACAGACTCGGTGTAGTG 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      3961 CTTGACAACATCTATCAAGGGTCAACCAGGTACGAGGCAGGGAGAGCTCCAGCGTACAGA 4020
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Qy      4021 GTGATCAGAGGTGACATTAGCAAGAGCGCTGACCAAGCTATCGTTAATGCTGCTAATAGC 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4021 GTGATCAGAGGTGACATTAGCAAGAGCGCTGACCAAGCTATCGTTAATGCTGCTAATAGC 4080

Qy      4081 AAAGGTCAACCAGGTTCCGGAGTGTGCGGTGCACTGTACCGAAAATGGCCGGCTGCTTTT 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4081 AAAGGTCAACCAGGTTCCGGAGTGTGCGGTGCACTGTACCGAAAATGGCCGGCTGCTTTT 4140

Qy      4141 GATAGACAGCCAATAGCTGTCGGGACGGCTAGACTTGTGAAGCACGAACCGCTCATCATA 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4141 GATAGACAGCCAATAGCTGTCGGGACGGCTAGACTTGTGAAGCACGAACCGCTCATCATA 4200

Qy      4201 CATGCTGTAGGACCCAATTTTTCTAAGATGCCGGAACCGGAGGGCGACCTTAAGCTCGCA 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4201 CATGCTGTAGGACCCAATTTTTCTAAGATGCCGGAACCGGAGGGCGACCTTAAGCTCGCA 4260

Qy      4261 GCTGCCTACATGAGCATAGCGTCCATCGTCAACGCTGAGCGGATTACAAAAATATCAGTA 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4261 GCTGCCTACATGAGCATAGCGTCCATCGTCAACGCTGAGCGGATTACAAAAATATCAGTA 4320

Qy      4321 CCGCTACTGTCAACCGGCATCTATTCTGGTGGCAAAGATCGAGTGATGCAATCATTGCAT 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4321 CCGCTACTGTCAACCGGCATCTATTCTGGTGGCAAAGATCGAGTGATGCAATCATTGCAT 4380

Qy      4381 CACCTGTTCACTGCTTTCGACACTACGGATGCCGATGTCACCATATATTGCTTGGATAAA 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4381 CACCTGTTCACTGCTTTCGACACTACGGATGCCGATGTCACCATATATTGCTTGGATAAA 4440

Qy      4441 CAATGGGAGACCAGGATAATCGAGGCCATTCACCGCAAAGAAAGCGTCGAAATTCTGGAT 4500
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Db       4441 CAATGGGAGACCAGGATAATCGAGGCCATTCACCGCAAAGAAAGCGTCGAAATTCTGGAT 4500

Qy       4501 GATGACAAGCCAGTAGACATTGACTTGGTCAGGGTCCACCCAAACAGCTCTTTGGCAGGC 4560
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 GATGACAAGCCAGTAGACATTGACTTGGTCAGGGTCCACCCAAACAGCTCTTTGGCAGGC 4560

Qy       4561 AGACCAGGTTACTCCGTCAATGAGGGCAAGTTGTATTCATACCTGGAAGGTACACGATTC 4620
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 AGACCAGGTTACTCCGTCAATGAGGGCAAGTTGTATTCATACCTGGAAGGTACACGATTC 4620

Qy       4621 CATCAGACCGCCAAGGACATTGCCGAAATCCATGCAATGTGGCCCAACAAATCTGAGGCT 4680
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 CATCAGACCGCCAAGGACATTGCCGAAATCCATGCAATGTGGCCCAACAAATCTGAGGCT 4680

Qy       4681 AATGAGCAGATTTGCTTGTACATCCTGGGGGAGAGTATGTCCAGCATCCGCTCCAAATGC 4740
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 AATGAGCAGATTTGCTTGTACATCCTGGGGGAGAGTATGTCCAGCATCCGCTCCAAATGC 4740

Qy       4741 CCAGTAGAGGAGTCAGAGGCGTCTGCTCCACCTCACACACTTCCATGCCTGTGTAATTAC 4800
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 CCAGTAGAGGAGTCAGAGGCGTCTGCTCCACCTCACACACTTCCATGCCTGTGTAATTAC 4800

Qy       4801 GCTATGACGGCTGAGCGCGTATACAGGTTGCGCTCTGCGAAGAAAGAACAGTTCGCCGTA 4860
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Db       4801 GCTATGACGGCTGAGCGCGTATACAGGTTGCGCTCTGCGAAGAAAGAACAGTTCGCCGTA 4860

Qy       4861 TGCTCATCATTCCTGTTGCCGAAGTACAGGATCACAGGCGTGCAGAAGCTACAGTGCAGC 4920
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 TGCTCATCATTCCTGTTGCCGAAGTACAGGATCACAGGCGTGCAGAAGCTACAGTGCAGC 4920

Qy       4921 AAACCAGTCCTGTTTTCAGGCGTCGTACCACCGGCTGTACACCCCAGGAAGTACGCGGAA 4980
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Db       4921 AAACCAGTCCTGTTTTCAGGCGTCGTACCACCGGCTGTACACCCCAGGAAGTACGCGGAA 4980

Qy       4981 ATAATTCTAGAAACGCCACC 5000
                ||||||||||||||||||||
Db       4981 ATAATTCTAGAAACGCCACC 5000


RESULT 2
US-09-991-258-1
; Sequence 1, Application US/09991258
; Patent No. US20020141975A1
; GENERAL INFORMATION:
;  APPLICANT: Olmsted, Robert
;  APPLICANT:  Keith, Paula
;  APPLICANT:  Dryga, Sergey
;  APPLICANT:  Caley, Ian
;  APPLICANT:  Maughan, Maureen
;  APPLICANT:  Johnston, Robert
;  APPLICANT:  Davis, Nancy
;  APPLICANT:  Swanstrom, Ronald
;  TITLE OF INVENTION: ALPHAVIRUS VECTORS AND VIROSOMES WITH MODIFIED HIV GENES FOR USE
;  TITLE OF INVENTION:  VACCINES
;  FILE REFERENCE: 01113.0001U3
;  CURRENT APPLICATION NUMBER: US/09/991,258
;  CURRENT FILING DATE:  2001-11-16
;  PRIOR APPLICATION NUMBER: 09/902,537
;  PRIOR FILING DATE: 2001-07-09
;  PRIOR APPLICATION NUMBER: 60/216,995
;  PRIOR FILING DATE: 2000-07-07
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 12523
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence; No. US20020141975A1e =
;   OTHER INFORMATION: synthetic construct
US-09-991-258-1
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  Best Local Similarity   64.5%;  Pred. No. 0;
  Matches 3218;  Conservative    0;  Mismatches 1746;  Indels   24;  Gaps    3;

Qy         10 ACTAATCGATCCAATATGGAAAGAATTCACGTTGACTTAGATGCTGACAGCCCGTATGTC 69
              | | | | | |||| ||||| | | ||||||||||| | || |  |||||||| |    ||
Db         30 AATTACCTACCCAAAATGGAGAAAGTTCACGTTGACATCGAGGAAGACAGCCCATTCCTC 89

Qy         70 AAGTCGTTACAGCGGACGTTTCCACAATTTGAGATCGAAGCAAGGCAGGTCACTGACAAT 129
              |   | || |||||||  || || || |||||| | ||||| | ||||||||||| |||
Db         90 AGAGCTTTGCAGCGGAGCTTCCCGCAGTTTGAGGTAGAAGCCAAGCAGGTCACTGATAAT 149

Qy        130 GACCATGCCAATGCCAGAGCGTTTTCGCATGTGGCAACAAAGCTCATTGAGAGCGAAGTC 189
              |||||||| |||||||||||||||||||| ||||  |||| || || || |  || ||
Db        150 GACCATGCTAATGCCAGAGCGTTTTCGCATCTGGCTTCAAAACTGATCGAAACGGAGGTG 209

Qy        190 GACCGGGACCAAGTTATCTTGGACATTGGAAGTGCGCCCGTCAGACATGCACATTCCAAT 249
              ||||    | |    ||| | ||||||||||||||||||| | |        |||| ||
Db        210 GACCCATCCGACACGATCCTTGACATTGGAAGTGCGCCCGCCCGCAGAATGTATTCTAAG 269

Qy        250 CACCGCTATCATTGTATCTGCCCTATGATAAGCGCTGAAGACCCGGACAGACTACAACGG 309
              |||   |||||||||||||| || |||| | | || ||||| |||||||| | |  |
Db        270 CACAAGTATCATTGTATCTGTCCGATGAGATGTGCGGAAGATCCGGACAGATTGTATAAG 329

Qy        310 TATGCAGAAAGACTTAAGAAAAGT------GACATTACCGACAAGAACATAGCCTCTAAG 363
              ||||||    |  || |||||||          || || || ||| |  | | |  ||
Db        330 TATGCAACTAAGCTGAAGAAAAACTGTAAGGAAATAACTGATAAGGAATTGGACAAGAAA 389

Qy        364 GCGGCAGACCTGCTGGAAGTCATGTCAACACCAGACGCAGAGACTCCATCTCTGTGTATG 423
                 |  || ||    | ||||||       || |||  || |||    || ||||  |
Db        390 ATGAAGGAGCTCGCCGCCGTCATGAGCGACCCTGACCTGGAAACTGAGACTATGTGCCTC 449

Qy        424 CACACAGACGCCACGTGTAGGTACTTTGGAAGTGTAGCAGTATACCAAGATGTGTACGCA 483
              |||  ||||  |||||| | |||   ||  || || || ||||| ||||| |||||
Db        450 CACGACGACGAGTCGTGTCGCTACGAAGGGCAAGTCGCTGTTTACCAGGATGTATACGCG 509

Qy        484 GTCCATGCACCGACATCAATCTACCACCAGGCGCTTAAAGGAGTTAGGACAATTTACTGG 543
              ||  | | |||||||    |||| |||||  ||   ||| ||||||||       ||||||
Db        510 GTTGACGGACCGACAAGTCTCTATCACCAAGCCAATAAGGGAGTTAGAGTCGCCTACTGG 569

Qy        544 ATAGGCTTTGACACGACCCCTTTTATGTACAAAAACATGGCAGGTTCCTACCCTACTTAC 603
              |||||||||||||| ||||||||||||   || ||| |||| ||  | || ||  | |||
Db        570 ATAGGCTTTGACACCACCCCTTTTATGTTTAAGAACTTGGCTGGAGCATATCCATCATAC 629

Qy        604 AACACGAACTGGGCTGACGAGAGAGTATTGGAAGCACGTAACATTGGCCTCGGTAACTCA 663
                 || |||||||| ||||| |  || ||    || |||||||| |||||  | | |||
Db        630 TCTACCAACTGGGCCGACGAAACCGTGTTAACGGCTCGTAACATAGGCCTATGCAGCTCT 689

Qy        664 GATCTTCAGGAGAGCAGGCTTGGAAAACTCTCAATCCTTAGGAAGAAGAGGCTCCAACCT 723
              ||  ||  |||| |     | | ||     | || || ||||| ||||||     |  ||||
Db        690 GACGTTATGGAGCGGTCACGTAGAGGGATGTCCATTCTTAGAAAGAAGTATTTGAAACCA 749

Qy        724 ACTAATAAGATCATATTCTCGGTTGGTTCAACAATCTACACAGAAGATAGATCACTGTTA 783
              | || ||  |  |||||||  ||||| || || ||||||   ||  | ||      | |
Db        750 TCCAACAATGTTCTATTCTCTGTTGGCTCGACCATCTACCACGAGAAGAGGGACTTACTG 809

Qy        784 CGTAGCTGGCATCTTCCAAACGTGTTCCACTTGAAAGGAAAGTCTAACTTCACAGGTAGA 843
              | |||||||| || ||    || || |||||    || |||   || | |||| || |
Db        810 AGGAGCTGGCACCTGCCGTCTGTATTTCACTTACGTGGCAAGCAAAATTACACATGTCGG 869

Qy        844 TGTGGGACCATTGTCAGCTGTGAAGGGTACGTCATCAAAAAGATAACGATCAGCCCAGGA 903
              |||| ||| || || || || || |||||||||  | ||||  ||| | ||||| |||||
Db        870 TGTGAGACTATAGTTAGTTGCGACGGGTACGTCGTTAAAAGAATAGCTATCAGTCCAGGC 929

Qy        904 CTATACGGTAAAGTTGAGAACTTGGCGTCCACAATGCATCGCGAGGGTTTCTTGAGTTGC 963
              || || || ||    |     ||  ||  | || ||||| |||||||| |||||| | |||
Db        930 CTGTATGGGAAGCCTTCAGGCTATGCTGCTACGATGCACCGCGAGGGATTCTTGTGCTGC 989

Qy        964 AAAGTCACAGATACGCTGCGCGGCGAGAGGGTTTCTTTTGCTGTGTGTACGTATGTACCA 1023
              ||||| ||||| ||  |   ||| |||||||| |||||| | ||||| |||||||| |||
Db        990 AAAGTGACAGACACATTAAACGGGGAGAGGGTCTCTTTTCCCGTGTGCACGTATGTGCCA 1049

Qy       1024 GCCACACTTTGCGATCAGATGACAGGGATTCTGGCAACTGACGTTAGTGTGGATGACGCA 1083
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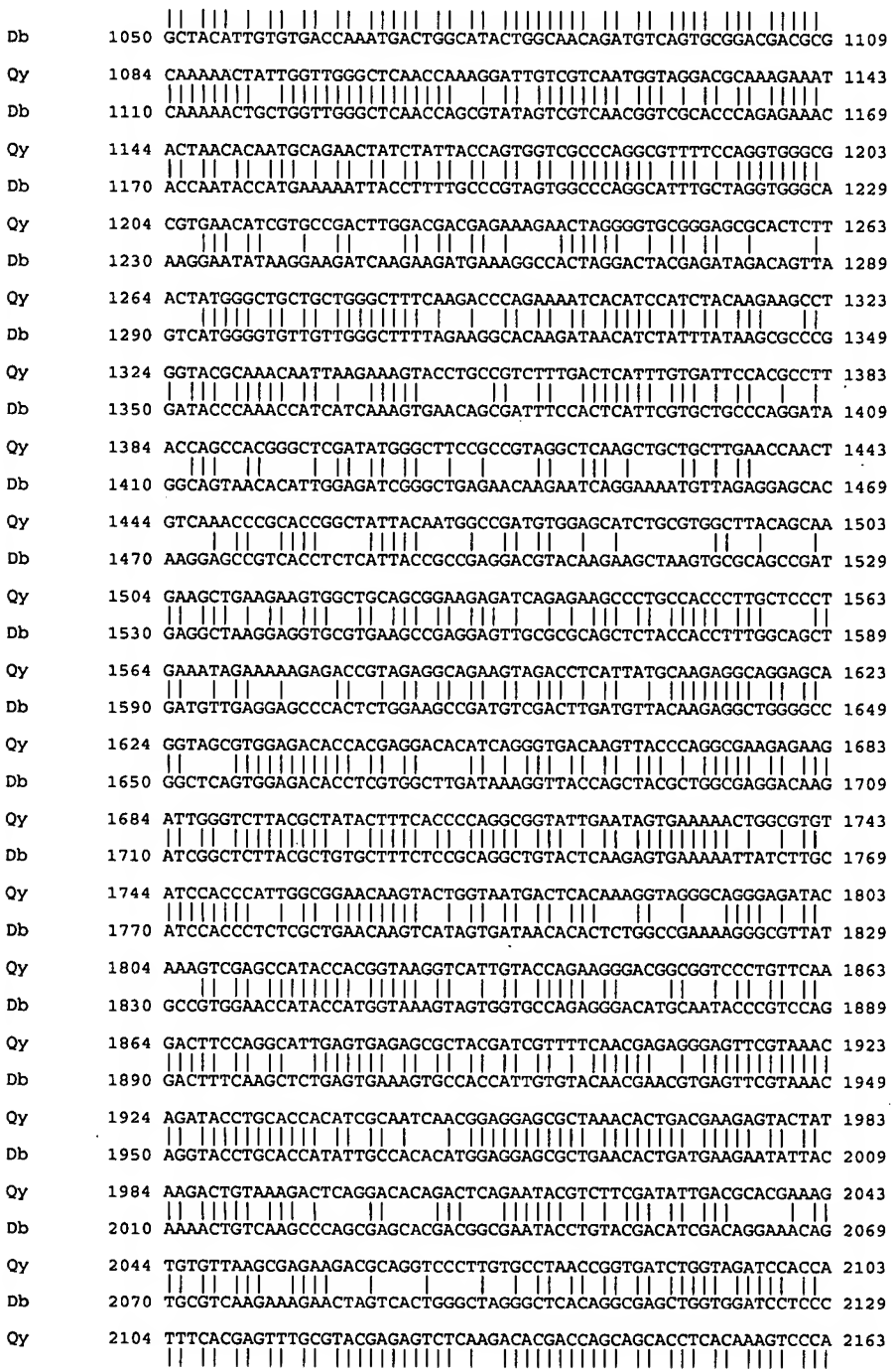
Db 1050 GCTACATTGTGTGACCAAATGACTGGCATACTGGCAACAGATGTCAGTGCGGACGACGCG 1109
Qy 1084 CAAAAACTATTGGTTGGGCTCAACCAAAGGATTGTCGTCAATGGTAGGACGCAAAGAAAT 1143
Db 1110 CAAAAACTGCTGGTTGGGCTCAACCAGCGTATAGTCGTCAACGGTCGCACCCAGAGAAAC 1169
Qy 1144 ACTAACACAATGCAGAACTATCTATTACCAGTGGTCGCCCAGGCGTTTTCCAGGTGGGCG 1203
Db 1170 ACCAATACCATGAAAAATTACCTTTTGCCCGTAGTGGCCCAGGCATTTGCTAGGTGGGCA 1229
Qy 1204 CGTGAACATCGTGCCGACTTGGACGACGAGAAAGAACTAGGGGTGCGGGAGCGCACTCTT 1263
Db 1230 AAGGAATATAAGGAAGATCAAGAAGATGAAAGGCCACTAGGACTACGAGATAGACAGTTA 1289
Qy 1264 ACTATGGGCTGCTGCTGGGCTTTCAAGACCCAGAAAATCACATCCATCTACAAGAAGCCT 1323
Db 1290 GTCATGGGGTGTTGTTGGGCTTTTAGAAGGCACAAGATAACATCTATTTATAAGCGCCCG 1349
Qy 1324 GGTACGCAAACAATTAAGAAAGTACCTGCCGTCTTTGACTCATTTGTGATTCCACGCCTT 1383
Db 1350 GATACCCAAACCATCATCAAAGTGAACAGCGATTTCCACTCATTCGTGCTGCCCAGGATA 1409
Qy 1384 ACCAGCCACGGGCTCGATATGGGCTTCCGCCGTAGGCTCAAGCTGCTGCTTGAACCAACT 1443
Db 1410 GGCAGTAACACATTGGAGATCGGGCTGAGAACAAGAATCAGGAAAATGTTAGAGGAGCAC 1469
Qy 1444 GTCAAACCCGCACCGGCTATTACAATGGCCGATGTGGAGCATCTGCGTGGCTTACAGCAA 1503
Db 1470 AAGGAGCCGTCACCTCTCATTACCGCCGAGGACGTACAAGAAGCTAAGTGCGCAGCCGAT 1529
Qy 1504 GAAGCTGAAGAAGTGGCTGCAGCGGAAGAGATCAGAGAAGCCCTGCCACCCTTGCTCCCT 1563
Db 1530 GAGGCTAAGGAGGTGCGTGAAGCCGAGGAGTTGCGCGCAGCTCTACCACCTTTGGCAGCT 1589
Qy 1564 GAAATAGAAAAAGAGACCGTAGAGGCAGAAGTAGACCTCATTATGCAAGAGGCAGGAGCA 1623
Db 1590 GATGTTGAGGAGCCCACTCTGGAAGCCGATGTCGACTTGATGTTACAAGAGGCTGGGGCC 1649
Qy 1624 GGTAGCGTGGAGACACCACGAGGACACATCAGGGTGACAAGTTACCCAGGCGAAGAGAAG 1683
Db 1650 GGCTCAGTGGAGACACCTCGTGGCTTGATAAAGGTTACCAGCTACGCTGGCGAGGACAAG 1709
Qy 1684 ATTGGGTCTTACGCTATACTTTCACCCCAGGCGGTATTGAATAGTGAAAAACTGGCGTGT 1743
Db 1710 ATCGGCTCTTACGCTGTGCTTTCTCCGCAGGCTGTACTCAAGAGTGAAAAATTATCTTGC 1769
Qy 1744 ATCCACCCATTGGCGGAACAAGTACTGGTAATGACTCACAAAGGTAGGGCAGGGAGATAC 1803
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Qy 1804 AAAGTCGAGCCATACCACGGTAAGGTCATTGTACCAGAAGGGACGGCGGTCCCTGTTCAA 1863
Db 1830 GCCGTGGAACCATACCATGGTAAAGTAGTGGTGCCAGAGGGACATGCAATACCCGTCCAG 1889
Qy 1864 GACTTCCAGGCATTGAGTGAGAGCGCTACGATCGTTTTCAACGAGAGGGAGTTCGTAAAC 1923
Db 1890 GACTTTCAAGCTCTGAGTGAAAGTGCCACCATTGTGTACAACGAACGTGAGTTCGTAAAC 1949
Qy 1924 AGATACCTGCACCACATCGCAATCAACGGAGGAGCGCTAAACACTGACGAAGAGTACTAT 1983
Db 1950 AGGTACCTGCACCATATTGCCACACATGGAGGAGCGCTGAACACTGATGAAGAATATTAC 2009
Qy 1984 AAGACTGTAAAGACTCAGGACACAGACTCAGAATACGTCTTCGATATTGACGCACGAAAG 2043
Db 2010 AAAACTGTCAAGCCCAGCGAGCACGACGGCGAATACCTGTACGACATCGACAGGAAACAG 2069
Qy 2044 TGTGTTAAGCGAGAAGACGCAGGTCCCTTGTGCCTAACCGGTGATCTGGTAGATCCACCA 2103
Db 2070 TGCGTCAAGAAAGAACTAGTCACTGGGCTAGGGCTCACAGGCGAGCTGGTGGATCCTCCC 2129
Qy 2104 TTTCACGAGTTTGCGTACGAGAGTCTCAAGACACGACCAGCAGCACCTCACAAAGTCCCA 2163
Db 2130 TTCCATGAATTCGCCTACGAGAGTCTGAGAACACGACCAGCCGCTCCTTACCAAGTACCA 2189
Qy 2164 ACCATCGGAGTCTATGGAGTGCCAGGTTCAGGTAAATCTGGAATCATCAAAAGCGCTGTG 2223
Db 2190 ACCATAGGGGTGTATGGCGTGCCAGGATCAGGCAAGTCTGGCATCATTAAAAGCGCAGTC 2249
Qy 2224 ACTAAGAAAGATCTGGTTGTGAGTGCGAAGAAGGAAAACTGCGCAGAAATCATCAGGGAT 2283
Db 2250 ACCAAAAAAGATCTAGTGGTGAGCGCCAAGAAAGAAAACTGTGCAGAAATTATAAGGGAC 2309
Qy 2284 GTAAGGAGGATGAGACGTATGGATGTTGCTGCTAGGACTGTCGATTCAGTGCTTCTAAAT 2343
Db 2310 GTCAAGAAAATGAAAGGGCTGGACGTCAATGCCAGAACTGTGGACTCAGTGCTCTTGAAT 2369
Qy 2344 GGGGTTAAGCACCCCGTTAACACTCTGTACATTGATGAGGCATTTGCCTGCCATGCAGGG 2403
Db 2370 GGATGCAAACACCCCGTAGAGACCCTGTATATTGACGAAGCTTTTGCTTGTCATGCAGGT 2429
Qy 2404 ACGCTGCTGGCACTGATTGCCATCGTCAAACCTAAGAAAGTGGTATTGTGCGGGGACCCA 2463
Db 2430 ACTCTCAGAGCGCTCATAGCCATTATAAGACCTAAAAAGGCAGTGCTCTGCGGGGATCCC 2489
Qy 2464 AAACAATGCGGCTTCTTTAACATGATGTGCCTGAAAGTACATTTTAACCATGACATATGC 2523
Db 2490 AAACAGTGCGGTTTTTTTAACATGATGTGCCTGAAAGTGCATTTTAACCACGAGATTTGC 2549
Qy 2524 ACTGAAGTGTACCATAAAAGCATCTCTAGGAGGTGCACACAGACTGTAACCGCCATCGTC 2583
Db 2550 ACACAAGTCTTCCACAAAAGCATCTCTCGCCGTTGCACTAAATCTGTGACTTCGGTCGTC 2609
Qy 2584 TCCACGCTCTTCTACGACAAGCGAATGAAGACGGTTAACCCATGTGCTGATAAAATCATC 2643
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Qy 2644 ATAGATACCACAGGGACCACAAAGCCGCACAAAGATGATCTGATTCTAACCTGTTTCAGA 2703
Db 2670 ATTGACACTACCGGCAGTACCAAACCTAAGCAGGACGATCTCATTCTCACTTGTTTCAGA 2729
Qy 2704 GGATGGGTGAAACAGCTACAGATTGACTACAAAAATCACGAAATCATGACTGCGGCTGCA 2763
Db 2730 GGGTGGGTGAAGCAGTTGCAAATAGATTACAAAGGCAACGAAATAATGACGGCAGCTGCC 2789
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Db 2790 TCTCAAGGGCTGACCCGTAAAGGTGTGTATGCCGTTCGGTACAAGGTGAATGAAAATCCT 2849
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Qy 2884 GTCTGGAAGACGCTAGCTGGTGATCCCTGGATAAAGACACTTACAGCTAAATATCCCGGG 2943
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Qy 2944 GATTTCACGGCTTCATTGGACGACTGGCAGCGCGAACACGACGCCATTATGGCACGCGTT 3003
Db 2970 AATTTCACTGCCACGATAGAGGAGTGGCAAGCAGAGCATGATGCCATCATGAGGCACATC 3029
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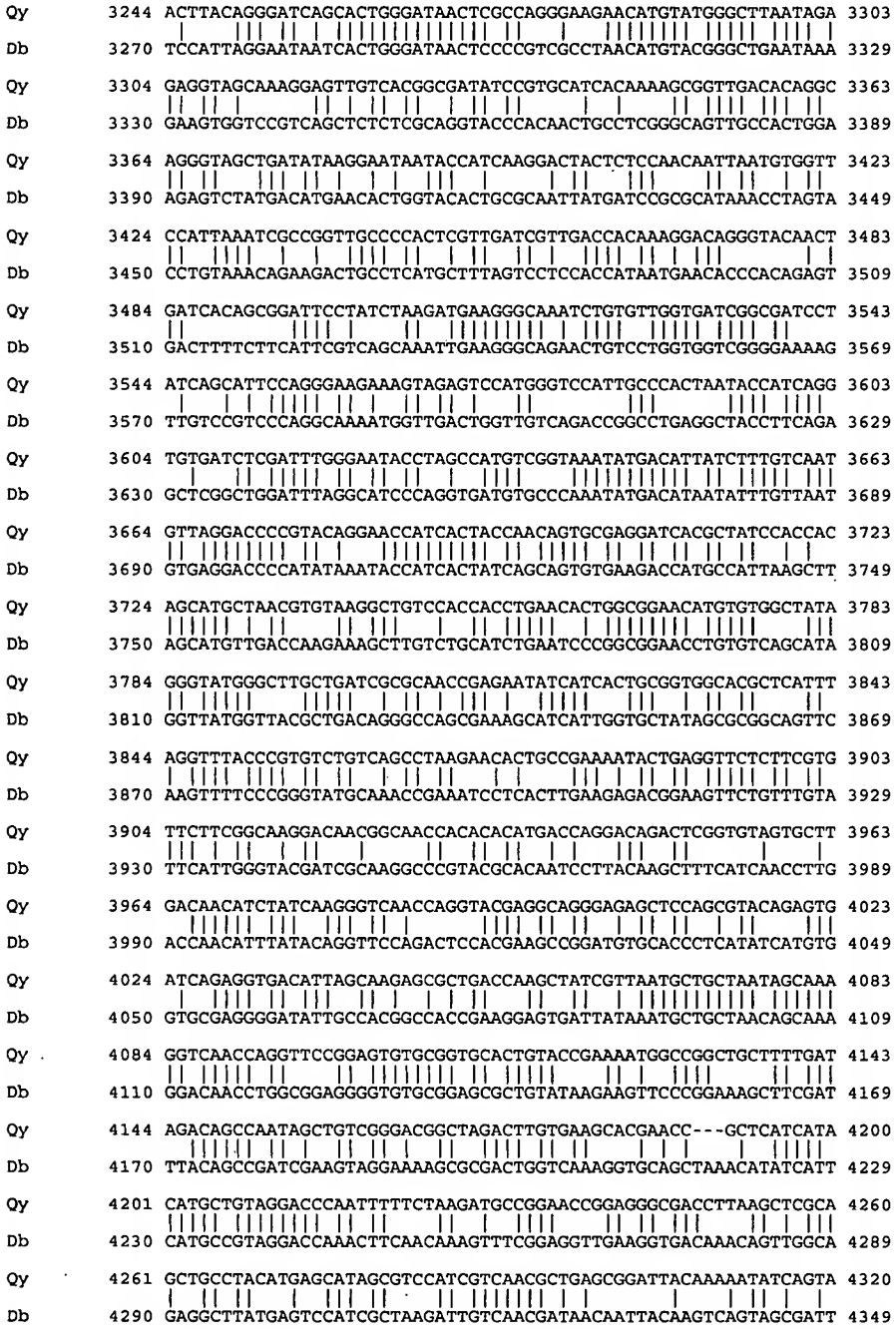

RESULT 3
US-09-991-258-14
; Sequence 14, Application US/09991258
; Patent No. US20020141975A1
; GENERAL INFORMATION:
; APPLICANT: Olmsted, Robert
; APPLICANT: Keith, Paula
; APPLICANT: Dryga, Sergey
; APPLICANT: Caley, Ian
; APPLICANT: Maughan, Maureen
; APPLICANT: Johnston, Robert
; APPLICANT: Davis, Nancy
; APPLICANT: Swanstrom, Ronald
; TITLE OF INVENTION: ALPHAVIRUS VECTORS AND VIROSOMES WITH MODIFIED HIV GENES FOR USE I
; TITLE OF INVENTION: VACCINES
; FILE REFERENCE: 01113.0001U3
; CURRENT APPLICATION NUMBER: US/09/991,258
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 09/902,537
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/216,995
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 14
; LENGTH: 12379
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; No. US20020141975A1e =
; OTHER INFORMATION: synthetic construct
US-09-991-258-14

Query Match 42.3%; Score 2113.2; DB 10; Length 12379;
Best Local Similarity 64.5%; Pred. No. 0;
Matches 3216; Conservative 0; Mismatches 1748; Indels 24; Gaps 3;

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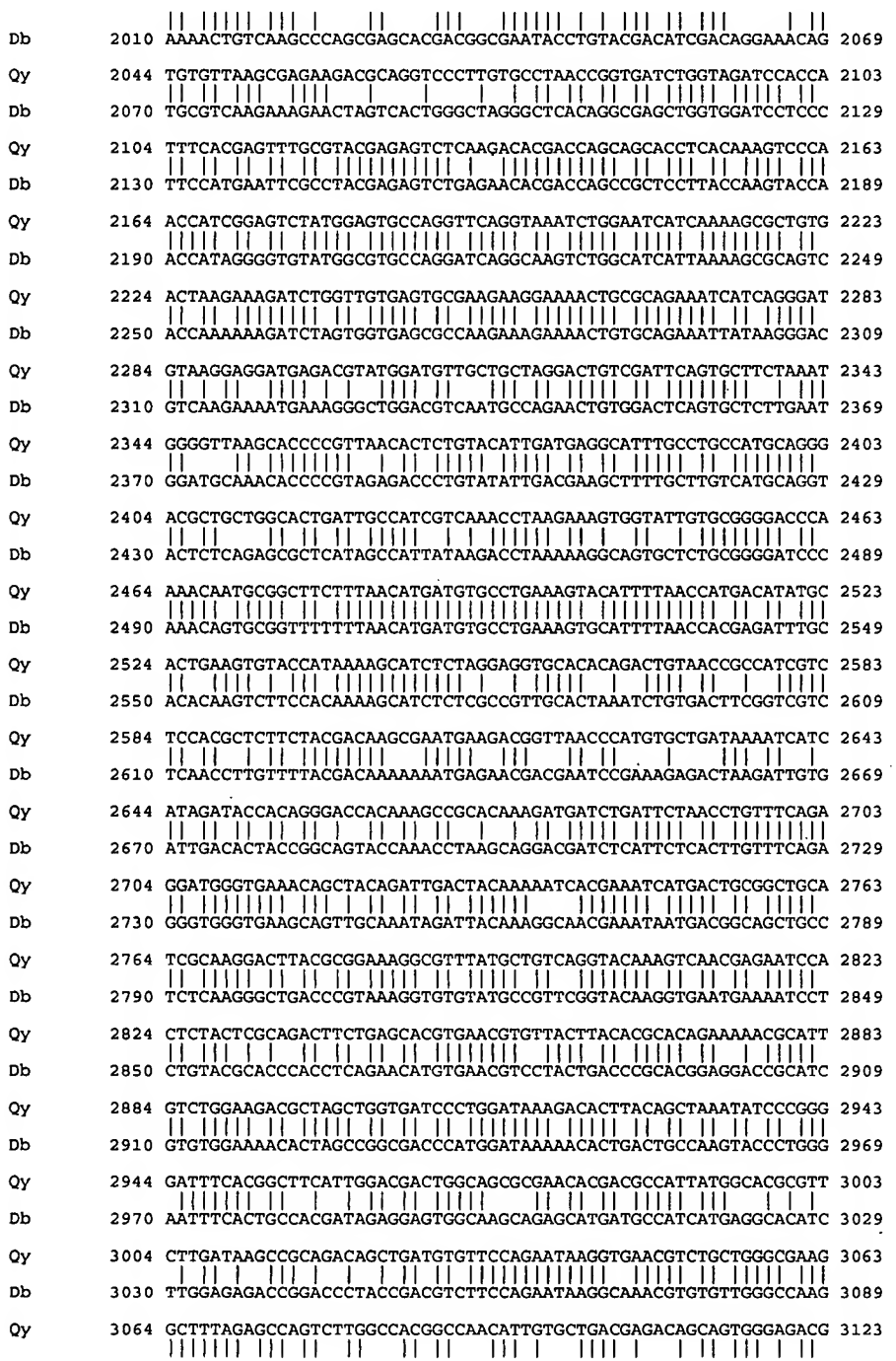
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             |||  | || |||  |  |  ||  |  ||| |||      || ||  ||  | | || ||
Db       4950 AAGATCCAATGCTCCCAGCCTATATTGTTCTCACCGAAAGTGCCTGCGTATATTCATCCA 5009

Qy       4966 AGGAAGTA 4973
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Db       5010 AGGAAGTA 5017


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US-09-991-258-17
; Sequence 17, Application US/09991258
; Patent No. US20020141975A1
; GENERAL INFORMATION:
;  APPLICANT: Olmsted, Robert
;  APPLICANT:  Keith, Paula
;  APPLICANT:  Dryga, Sergey
;  APPLICANT:  Caley, Ian
;  APPLICANT:  Maughan, Maureen
;  APPLICANT:  Johnston, Robert
;  APPLICANT:  Davis, Nancy
;  APPLICANT:  Swanstrom, Ronald
;  TITLE OF INVENTION: ALPHAVIRUS VECTORS AND VIROSOMES WITH MODIFIED HIV GENES FOR USE
;  TITLE OF INVENTION:  VACCINES
;  FILE REFERENCE: 01113.0001U3
;  CURRENT APPLICATION NUMBER: US/09/991,258
;  CURRENT FILING DATE:  2001-11-16
;  PRIOR APPLICATION NUMBER: 09/902,537
;  PRIOR FILING DATE: 2001-07-09
;  PRIOR APPLICATION NUMBER: 60/216,995
;  PRIOR FILING DATE: 2000-07-07
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 13584
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence; No. US20020141975A1e =
;   OTHER INFORMATION: synthetic construct
US-09-991-258-17

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  Best Local Similarity  64.5%;  Pred. No. 0;
  Matches 3216;  Conservative    0;  Mismatches 1748;  Indels   24;  Gaps    3;

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Qy         70 AAGTCGTTACAGCGGACGTTTCCACAATTTGAGATCGAAGCAAGGCAGGTCACTGACAAT 129
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Db         90 AGAGCTTTGCAGCGGAGCTTCCCGCAGTTTGAGGTAGAAGCCAAGCAGGTCACTGATAAT 149

Qy        130 GACCATGCCAATGCCAGAGCGTTTTCGCATGTGGCAACAAAGCTCATTGAGAGCGAAGTC 189
              |||||||| |||||||||||||||||||||||| ||||  |||| || || || |  || ||
Db        150 GACCATGCTAATGCCAGAGCGTTTTCGCATCTGGCTTCAAAACTGATCGAAACGGAGGTG 209

Qy        190 GACCGGGACCAAGTTATCTTGGACATTGGAAGTGCGCCCGTCAGACATGCACATTCCAAT 249
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Db        210 GACCCATCCGACACGATCCTTGACATTGGAAGTGCGCCCGCCCGCAGAATGTATTCTAAG 269

Qy        250 CACCGCTATCATTGTATCTGCCCTATGATAAGCGCTGAAGACCCGGACAGACTACAACGG 309
              |||   |||||||||||||| || |||| | | || ||||| |||||||||  |  |   |
Db        270 CACAAGTATCATTGTATCTGTCCGATGAGATGTGCGGAAGATCCGGACAGATTGTATAAG 329

Qy        310 TATGCAGAAAGACTTAAGAAAAGT------GACATTACCGACAAGAACATAGCCTCTAAG 363
              ||||||    |  || |||||||          || || || || ||| |  | | |   ||
Db        330 TATGCAACTAAGCTGAAGAAAAACTGTAAGGAAATAACTGATAAGGAATTGGACAAGAAA 389

Qy        364 GCGGCAGACCTGCTGGAAGTCATGTCAACACCAGACGCAGAGACTCCATCTCTGTGTATG 423
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Db        390 ATGAAGGAGCTCGCCGCCGTCATGAGCGACCCTGACCTGGAAACTGAGACTATGTGCCTC 449

Qy        424 CACACAGACGCCACGTGTAGGTACTTTGGAAGTGTAGCAGTATACCAAGATGTGTACGCA 483
              |||   ||||   ||||| | |||   ||    || || || ||||| ||||| ||||||
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Qy        484 GTCCATGCACCGACATCAATCTACCACCAGGCGCTTAAAGGAGTTAGGACAATTTACTGG 543
              ||  | | |||||||    |||| ||||| ||   ||| ||||||||       ||||||
Db        510 GTTGACGGACCGACAAGTCTCTATCACCAAGCCAATAAGGGAGTTAGAGTCGCCTACTGG 569

Qy        544 ATAGGCTTTGACACGACCCCTTTTATGTACAAAAACATGGCAGGTTCCTACCCTACTTAC 603
              |||||||||||||| ||||||||||||||  || ||| |||| ||  | || ||  | |||
Db        570 ATAGGCTTTGACACCACCCCTTTTATGTTTAAGAACTTGGCTGGAGCATATCCATCATAC 629

Qy        604 AACACGAACTGGGCTGACGAGAGAGTATTGGAAGCACGTAACATTGGCCTCGGTAACTCA 663
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Db        630 TCTACCAACTGGGCCGACGAAACCGTGTTAACGGCTCGTAACATAGGCCTATGCAGCTCT 689

Qy        664 GATCTTCAGGAGAGCAGGCTTGGAAAACTCTCAATCCTTAGGAAGAAGAGGCTCCAACCT 723
              ||  ||  |||| |    | | ||    | || || |||| ||||||   ·|  ||||
Db        690 GACGTTATGGAGCGGTCACGTAGAGGGATGTCCATTCTTAGAAAGAAGTATTTGAAACCA 749

Qy        724 ACTAATAAGATCATATTCTCGGTTGGTTCAACAATCTACACAGAAGATAGATCACTGTTA 783
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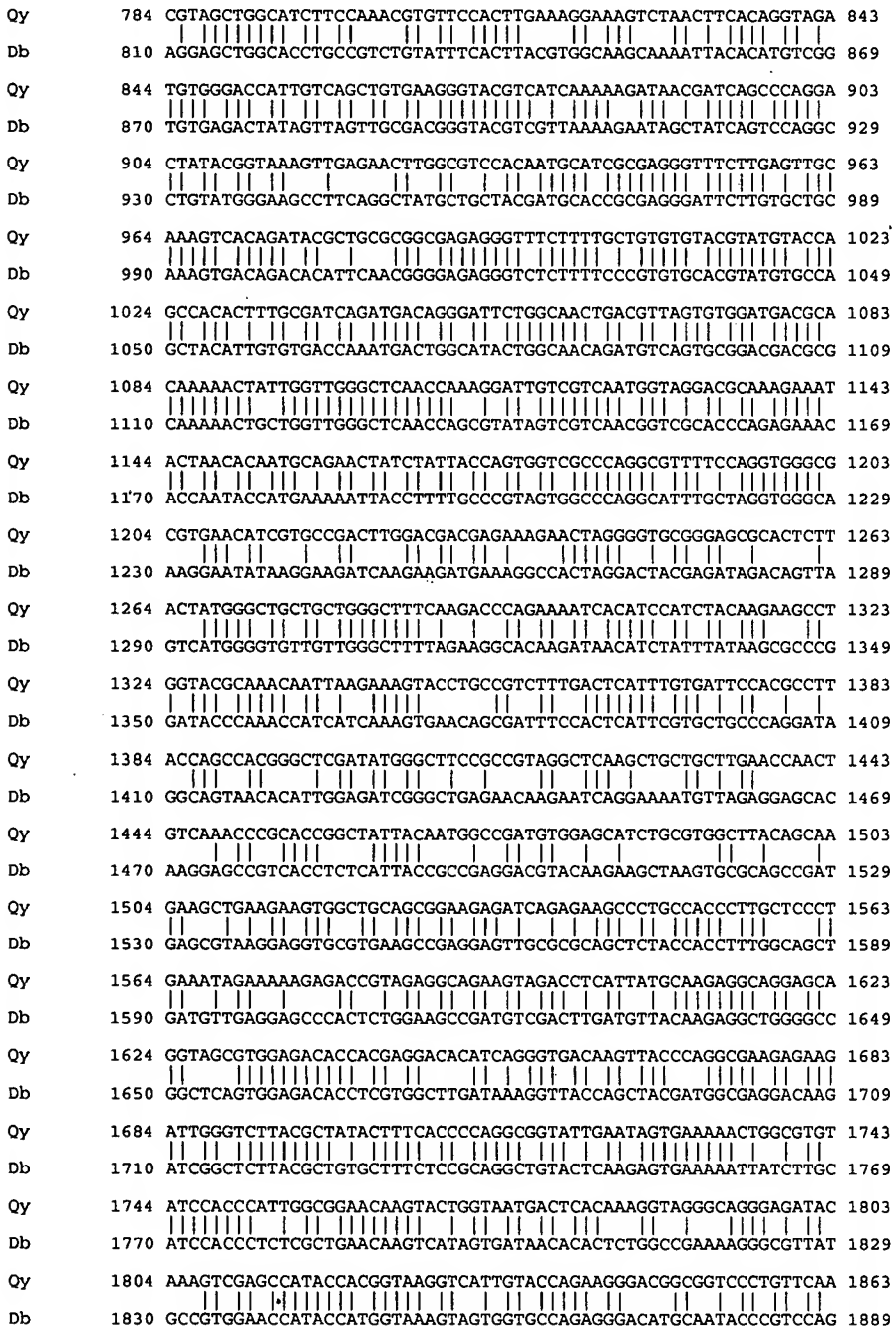

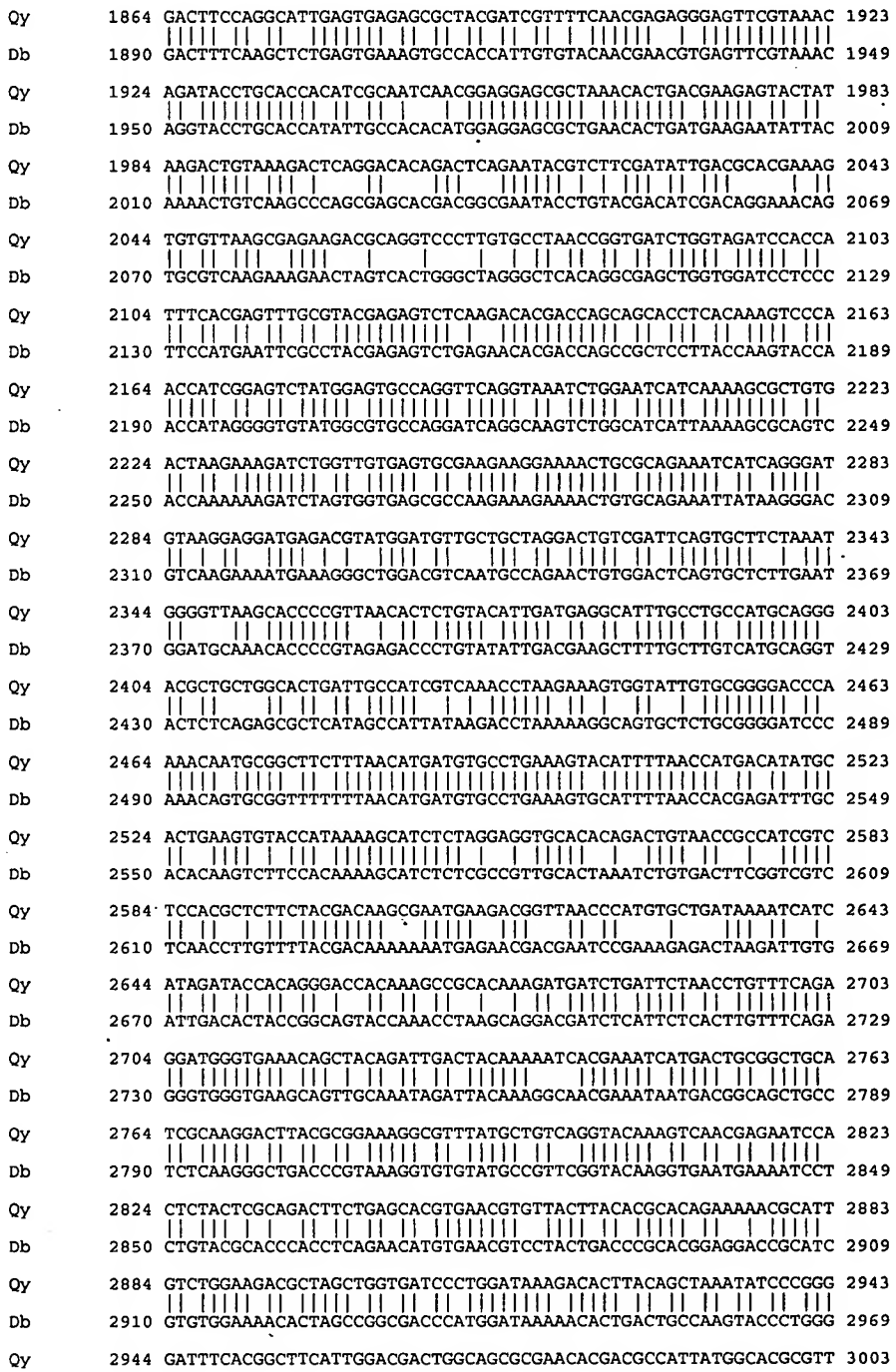

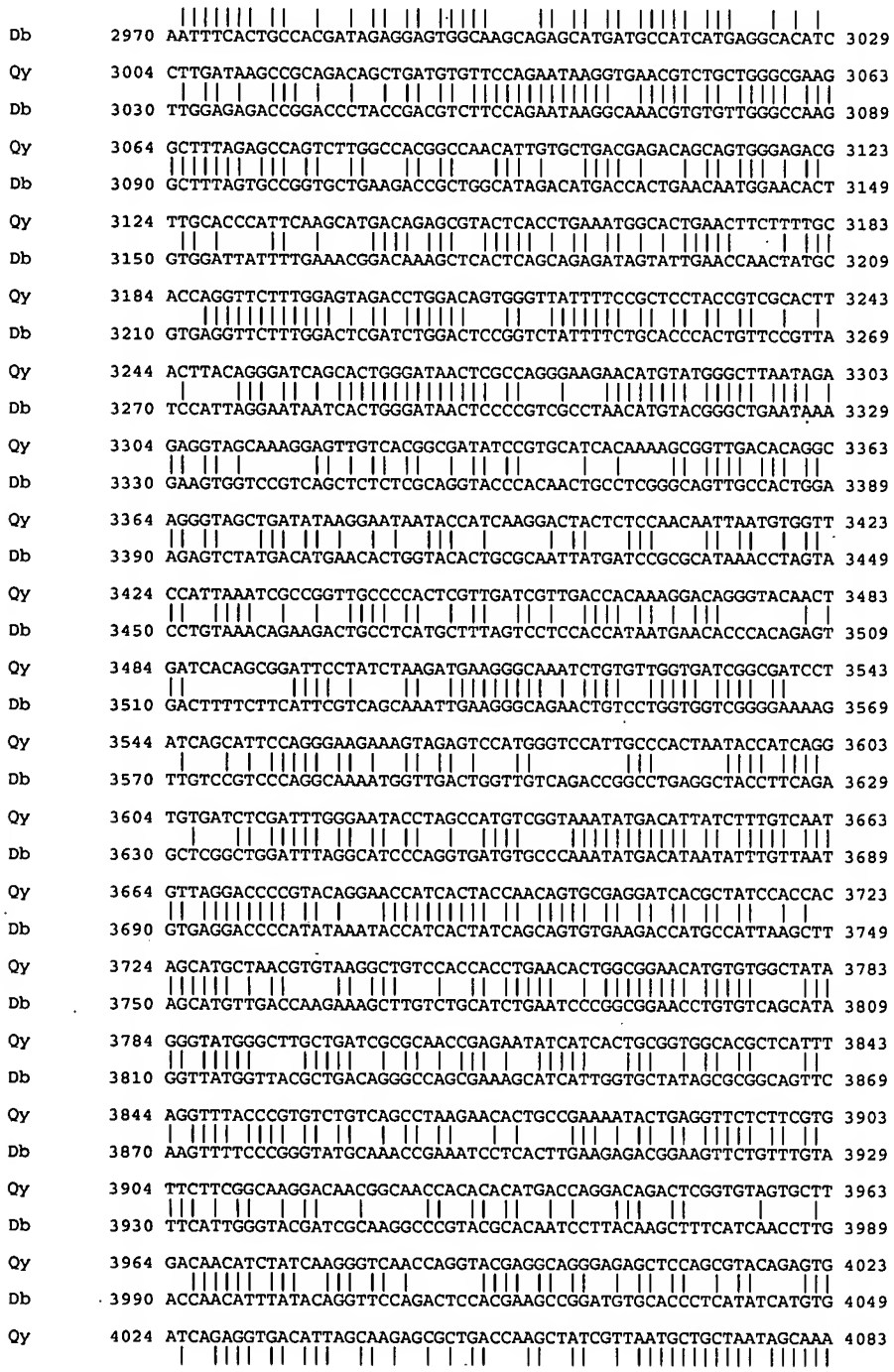

RESULT 5
US-09-991-258-2
; Sequence 2, Application US/09991258
; Patent No. US20020141975A1
; GENERAL INFORMATION:
; APPLICANT: Olmsted, Robert

```
;  APPLICANT:  Keith, Paula
;  APPLICANT:  Dryga, Sergey
;  APPLICANT:  Caley, Ian
;  APPLICANT:  Maughan, Maureen
;  APPLICANT:  Johnston, Robert
;  APPLICANT:  Davis, Nancy
;  APPLICANT:  Swanstrom, Ronald
;  TITLE OF INVENTION: ALPHAVIRUS VECTORS AND VIROSOMES WITH MODIFIED HIV GENES FOR USE
;  TITLE OF INVENTION:  VACCINES
;  FILE REFERENCE: 01113.0001U3
;  CURRENT APPLICATION NUMBER: US/09/991,258
;  CURRENT FILING DATE:  2001-11-16
;  PRIOR APPLICATION NUMBER: 09/902,537
;  PRIOR FILING DATE: 2001-07-09
;  PRIOR APPLICATION NUMBER: 60/216,995
;  PRIOR FILING DATE: 2000-07-07
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 7479
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence; No. US20020141975A1e =
;   OTHER INFORMATION: synthetic construct
;   NAME/KEY: CDS
;   LOCATION: (1)...(7479)
US-09-991-258-2

  Query Match             42.2%;  Score 2111;  DB 10;  Length 7479;
  Best Local Similarity   64.5%;  Pred. No. 0;
  Matches 3209;  Conservative    0;  Mismatches 1740;  Indels   24;  Gaps    3;

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Db          1 ATGGAGAAAGTTCACGTTGACATCGAGGAAGACAGCCCATTCCTCAGAGCTTTGCAGCGG 60

Qy         85 ACGTTTCCACAATTTGAGATCGAAGCAAGGCAGGTCACTGACAATGACCATGCCAATGCC 144
              |  || || || |||||| | ||||| | |||||||||||| |||||||||| ||||||
Db         61 AGCTTCCCGCAGTTTGAGGTAGAAGCCAAGCAGGTCACTGATAATGACCATGCTAATGCC 120

Qy        145 AGAGCGTTTTCGCATGTGGCAACAAAGCTCATTGAGAGCGAAGTCGACCGGGACCAAGTT 204
              ||||||||||||||| ||||  |||| || || || |  || || ||||    | |
Db        121 AGAGCGTTTTCGCATCTGGCTTCAAAACTGATCGAAACGGAGGTGGACCCATCCGACACG 180

Qy        205 ATCTTGGACATTGGAAGTGCGCCCGTCAGACATGCACATTCCAATCACCGCTATCATTGT 264
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Db        181 ATCCTTGACATTGGAAGTGCGCCCGCCCGCAGAATGTATTCTAAGCACAAGTATCATTGT 240

Qy        265 ATCTGCCCTATGATAAGCGCTGAAGACCCGGACAGACTACAACGGTATGCAGAAAGACTT 324
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Qy        325 AAGAAA------AGTGACATTACCGACAAGAACATAGCCTCTAAGGCGGCAGACCTGCTG 378
              ||||||      |  || || || || ||| |  | | |   ||   |  || ||
Db        301 AAGAAAAAACTGTAAGGAAATAACTGATAAGGAATTGGACAAGAAAATGAAGGAGCTCGCC 360

Qy        379 GAAGTCATGTCAACACCAGACGCAGAGACTCCATCTCTGTGTATGCACACAGACGCCACG 438
              |  ||||||       || |||   || |||    || ||||  | |||    ||
Db        361 GCCGTCATGAGCGACCCTGACCTGGAAACTGAGACTATGTGCCTCCACGACGACGAGTCG 420

Qy        439 TGTAGGTACTTTGGAAGTGTAGCAGTATACCAAGATGTGTACGCAGTCCATGCACCGACA 498
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Qy        499 TCAATCTACCACCAGGCGCTTAAAGGAGTTAGGACAATTTACTGGATAGGCTTTGACACG 558
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Db        481 AGTCTCTATCACCAAGCCAATAAGGGAGTTAGAGTCGCCTACTGGATAGGCTTTGACACC 540

Qy        559 ACCCCTTTTATGTACAAAAACATGGCAGGTTCCTACCCTACTTACAACACGAACTGGGCT 618
              ||||||||||||  || ||| |||| ||  | || ||  | |||   || ||||||||
Db        541 ACCCCTTTTATGTTTAAGAACTTGGCTGGAGCATATCCATCATACTCTACCAACTGGGCC 600

Qy        619 GACGAGAGAGTATTGGAAGCACGTAACATTGGCCTCGGTAACTCAGATCTTCAGGAGAGC 678
              ||||| |  || ||     || |||||||| |||||  | | ||| ||  ||  |||| |
Db        601 GACGAAACCGTGTTAACGGCTCGTAACATAGGCCTATGCAGCTCTGACGTTATGGAGCGG 660

Qy        679 AGGCTTGGAAAACTCTCAATCCTTAGGAAGAAGAGGCTCCAACCTACTAATAAGATCATA 738
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Db        661 TCACGTAGAGGGATGTCCATTCTTAGAAAGAAGTATTTGAAACCATCCAACAATGTTCTA 720

Qy        739 TTCTCGGTTGGTTCAACAATCTACACAGAAGATAGATCACTGTTACGTAGCTGGCATCTT 798
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Db        721 TTCTCTGTTGGCTCGACCATCTACCACGAGAAGAGGGACTTACTGAGGAGCTGGCACCTG 780

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Db        781 CCGTCTGTATTTCACTTACGTGGCAAGCAAAATTACACATGTCGGTGTGAGACTATAGTT 840

Qy        859 AGCTGTGAAGGGTACGTCATCAAAAAGATAACGATCAGCCCAGGACTATACGGTAAAGTT 918
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Db        841 AGTTGCGACGGGTACGTCGTTAAAAGAATAGCTATCAGTCCAGGCCTGTATGGGAAGCCT 900

Qy        919 GAGAACTTGGCGTCCACAATGCATCGCGAGGGTTTCTTGAGTTGCAAAGTCACAGATACG 978
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Db        901 TCAGGCTATGCTGCTACGATGCACCGCGAGGGATTCTTGTGCTGCAAAGTGACAGACACA 960

Qy        979 CTGCGCGGCGAGAGGGTTTCTTTTGCTGTGTGTACGTATGTACCAGCCACACTTTGCGAT 1038
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Db        961 TTAAACGGGGAGAGGGTCTCTTTTCCCGTGTGCACGTATGTGCCAGCTACATTGTGTGAC 1020

Qy       1039 CAGATGACAGGGATTCTGGCAACTGACGTTAGTGTGGATGACGCACAAAAACTATTGGTT 1098
              || ||||| || || |||||||| || || |||| ||| ||||| |||||||| |||||
Db       1021 CAAATGACTGGCATACTGGCAACAGATGTCAGTGCGGACGACGCGCAAAAACTGCTGGTT 1080

Qy       1099 GGGCTCAACCAAAGGATTGTCGTCAATGGTAGGACGCAAAGAAATACTAACACAATGCAG 1158
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Db       1141 AATTACCTTTTGCCCGTAGTGGCCCAGGCATTTGCTAGGTGGGCAAAGGAATATAAGGAA 1200

Qy       1219 GACTTGGACGACGAGAAAGAACTAGGGGTGCGGGAGCGCACTCTTACTATGGGCTGCTGC 1278
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Db       1261 TGGGCTTTTAGAAGGCACAAGATAACATCTATTTATAAGCGCCCGGATACCCAAACCATC 1320

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Db       1621 CCTCGTGGCTTGATAAAGGTTACCAGCTACGCTGGCGAGGACAAGATCGGCTCTTACGCT 1680

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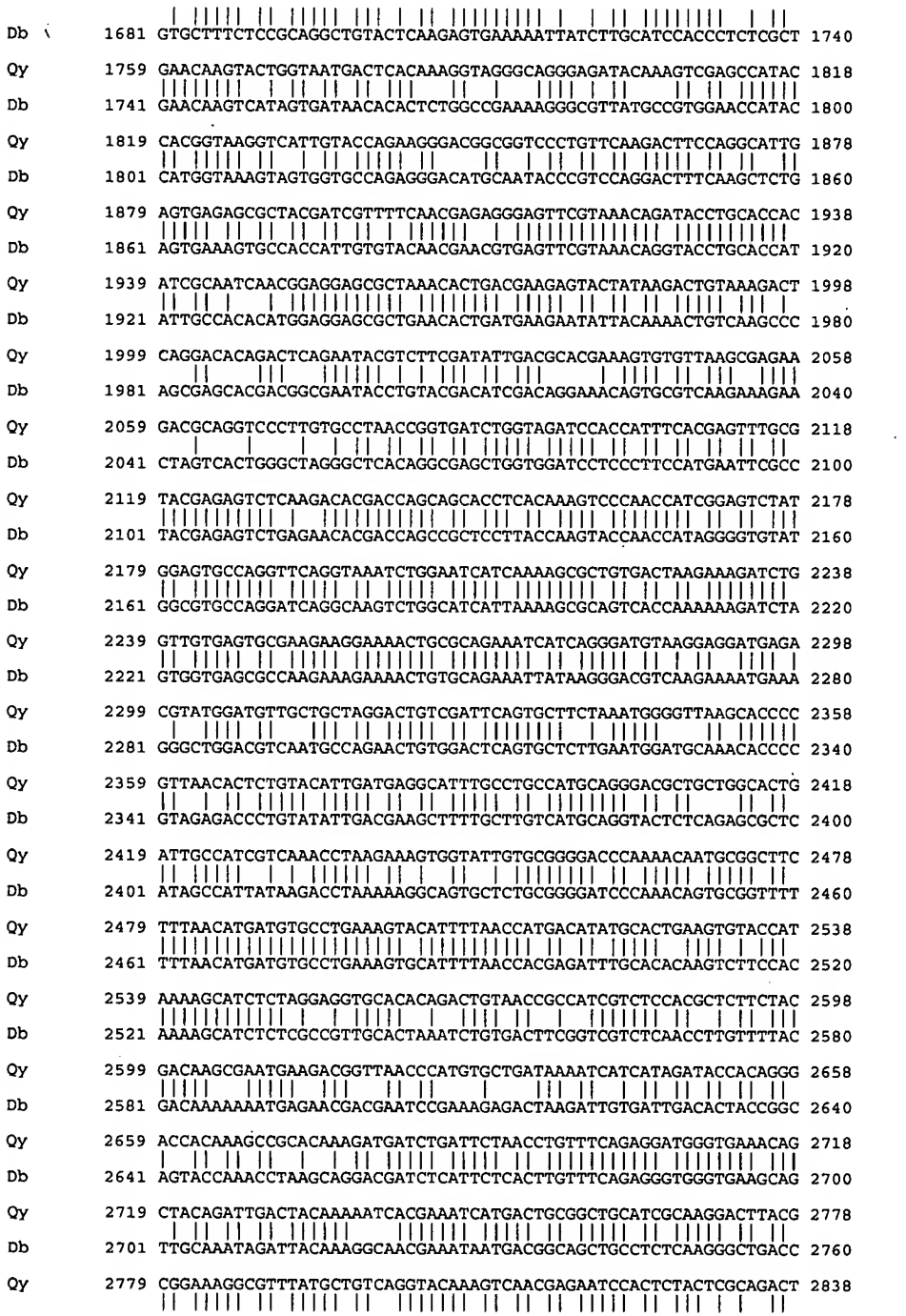
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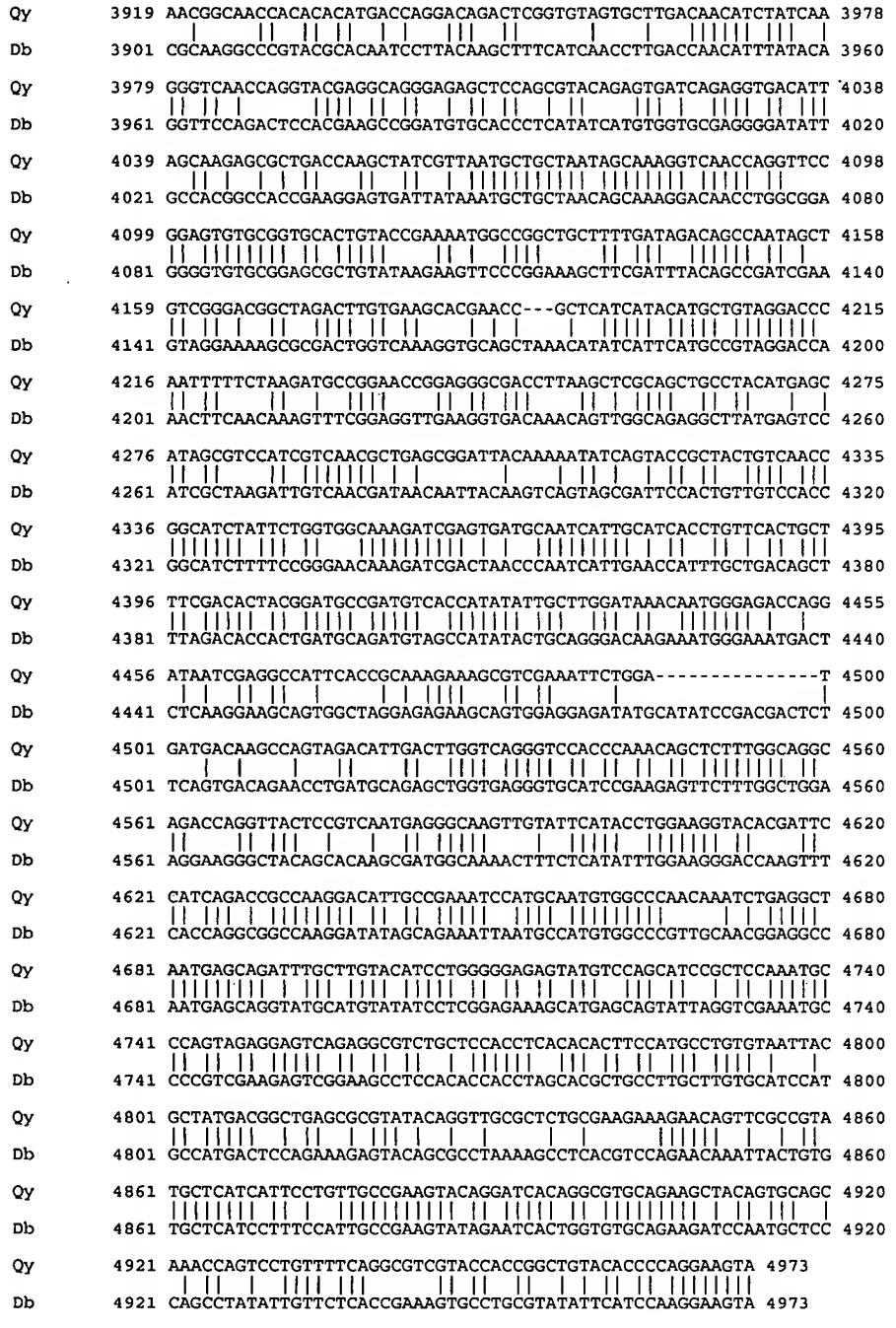
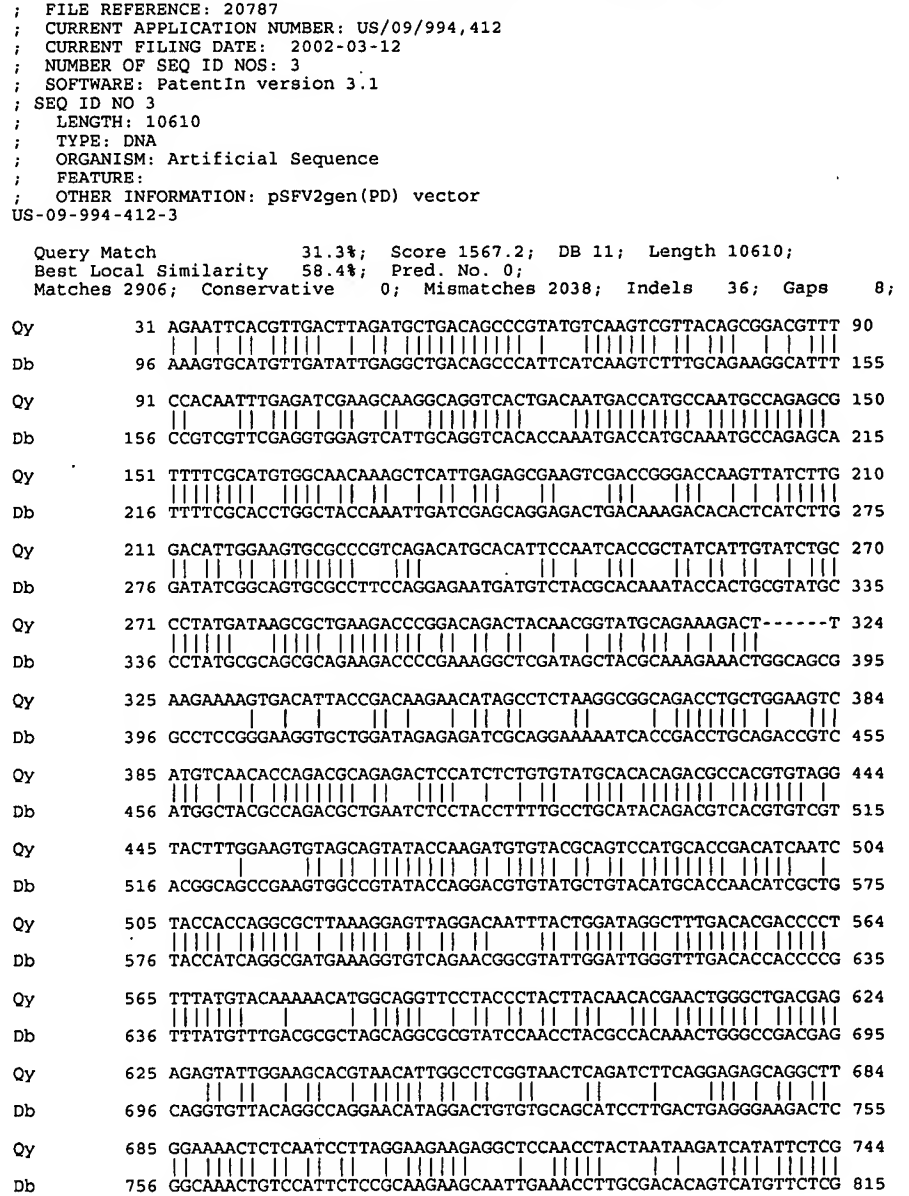
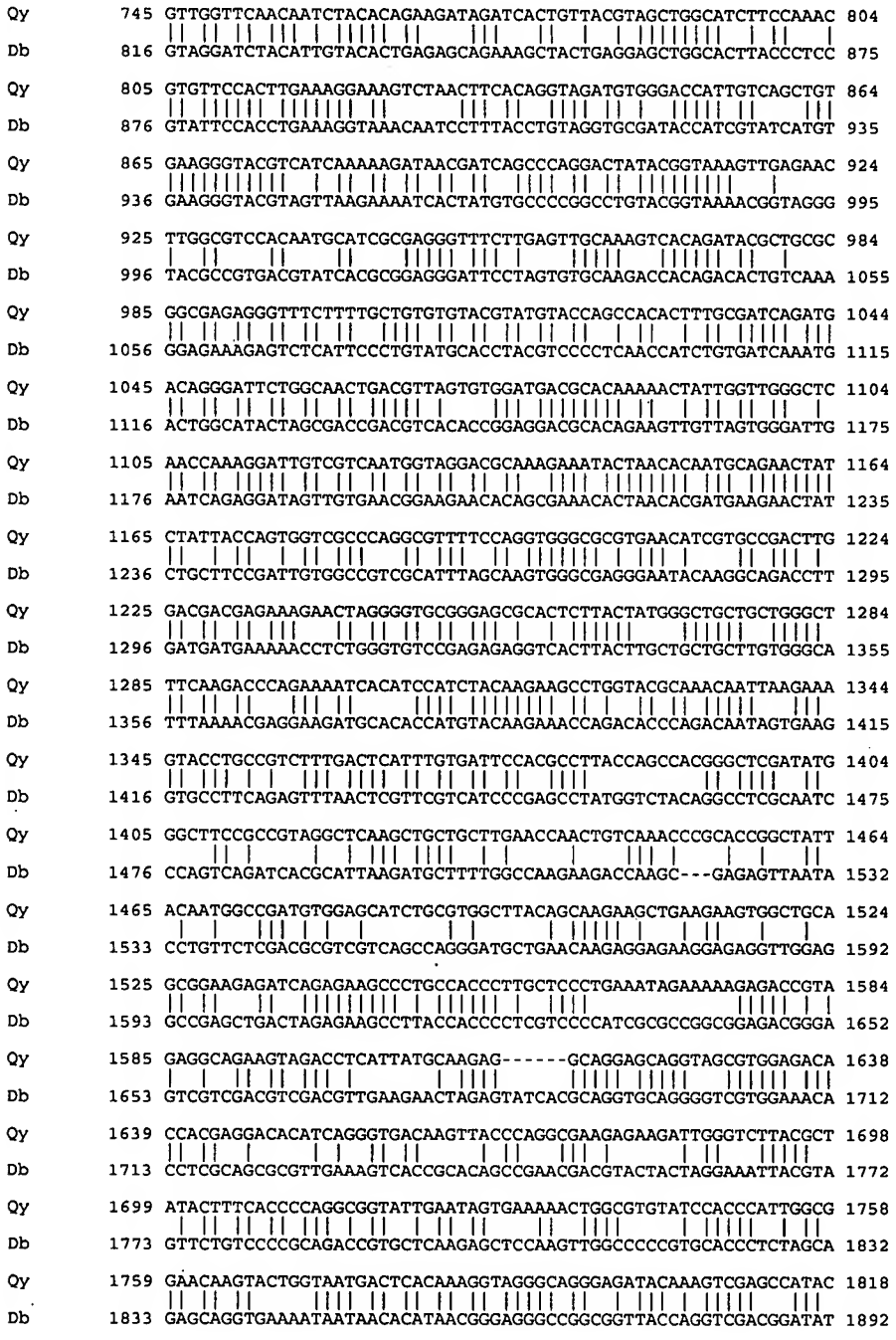
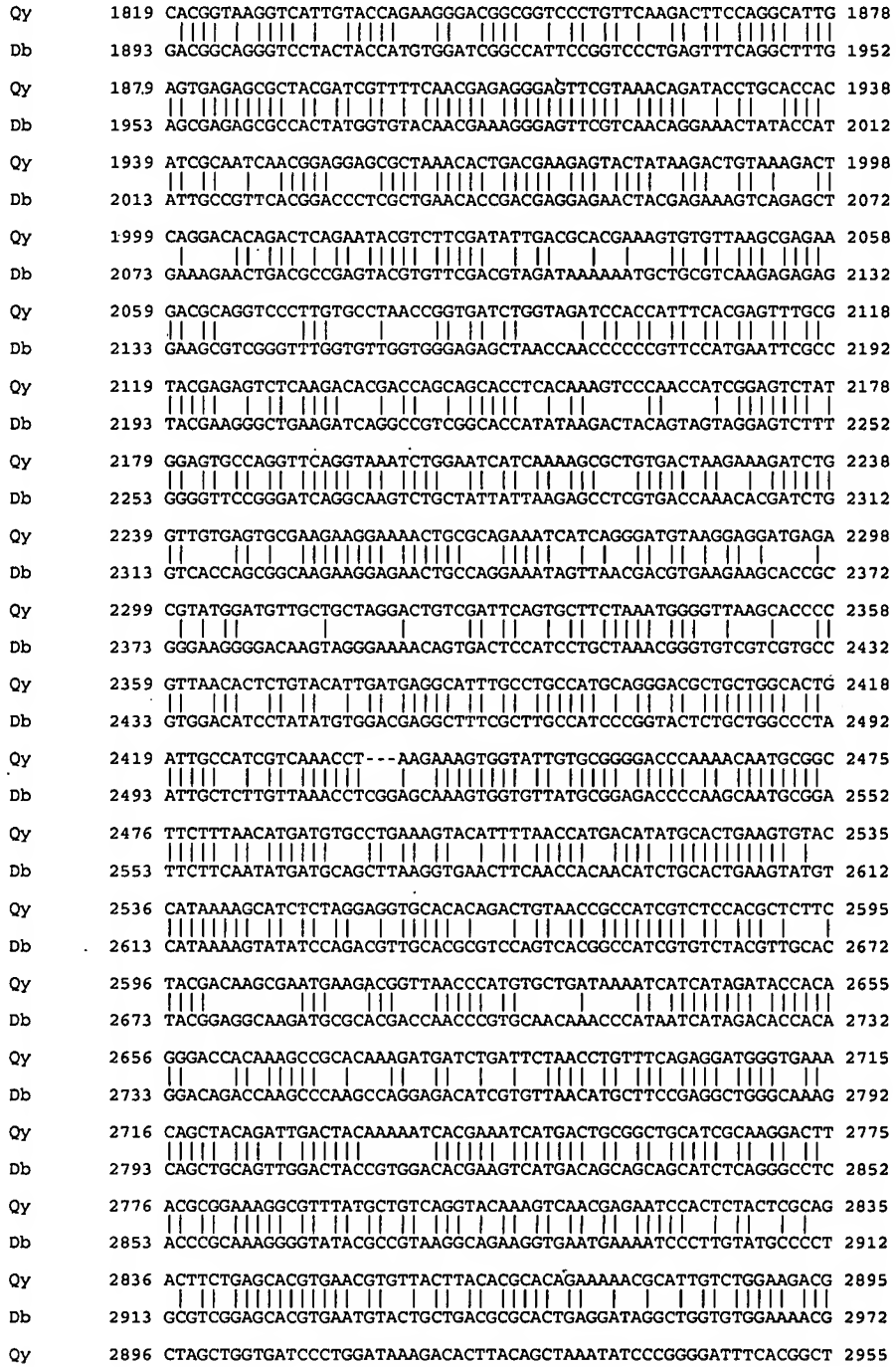


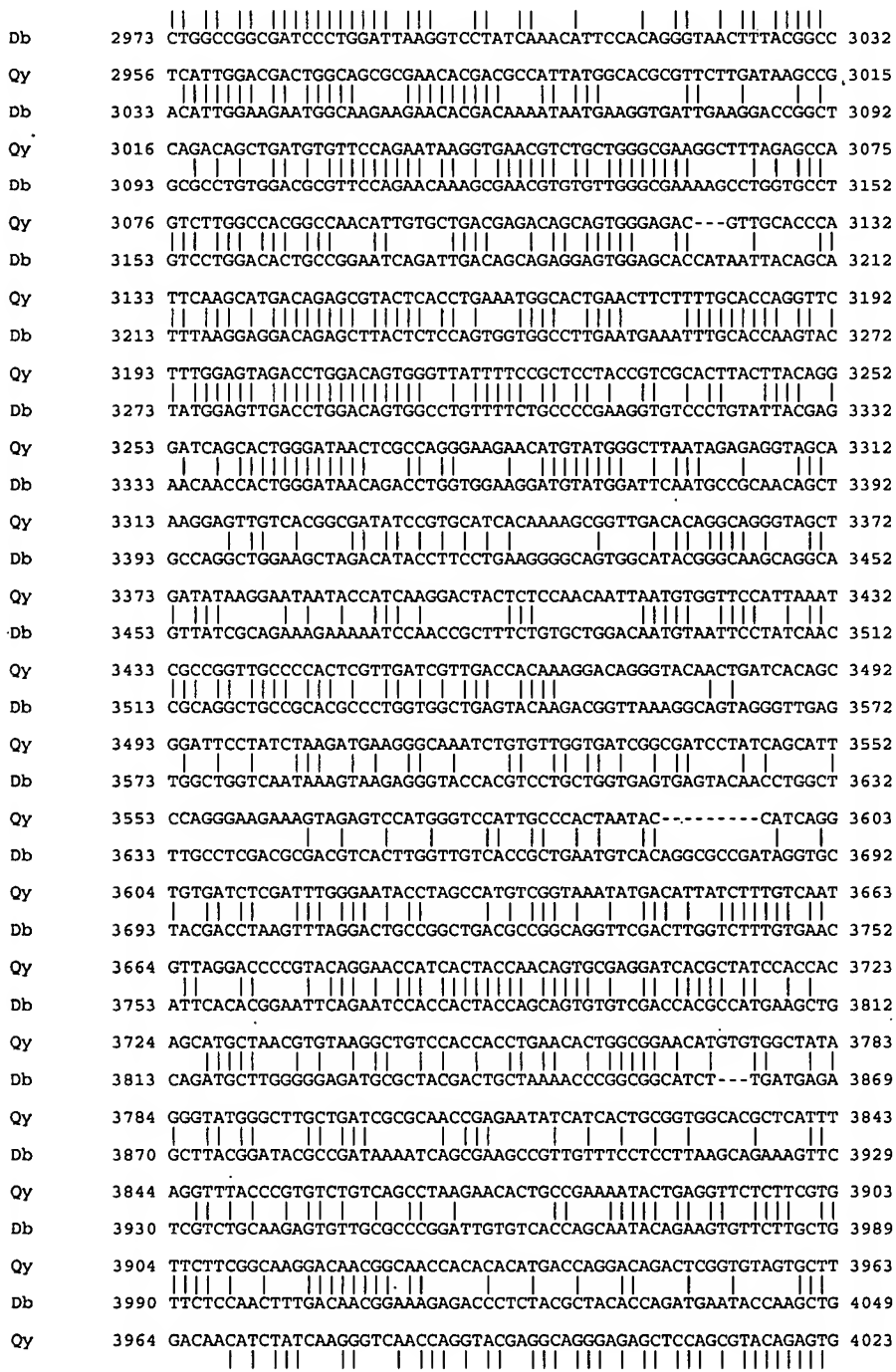
RESULT 6
US-09-994-412-3
; Sequence 3, Application US/09994412
; Publication No. US20030059943A1
; GENERAL INFORMATION:
; APPLICANT: Certa, Ulrich
; APPLICANT: Lundstrom, Kenneth
; TITLE OF INVENTION: Inhibition of Expression of a Target Gene
; FILE REFERENCE: 20787
; CURRENT APPLICATION NUMBER: US/09/994,412
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 10610
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pSFV2gen(PD) vector
US-09-994-412-3

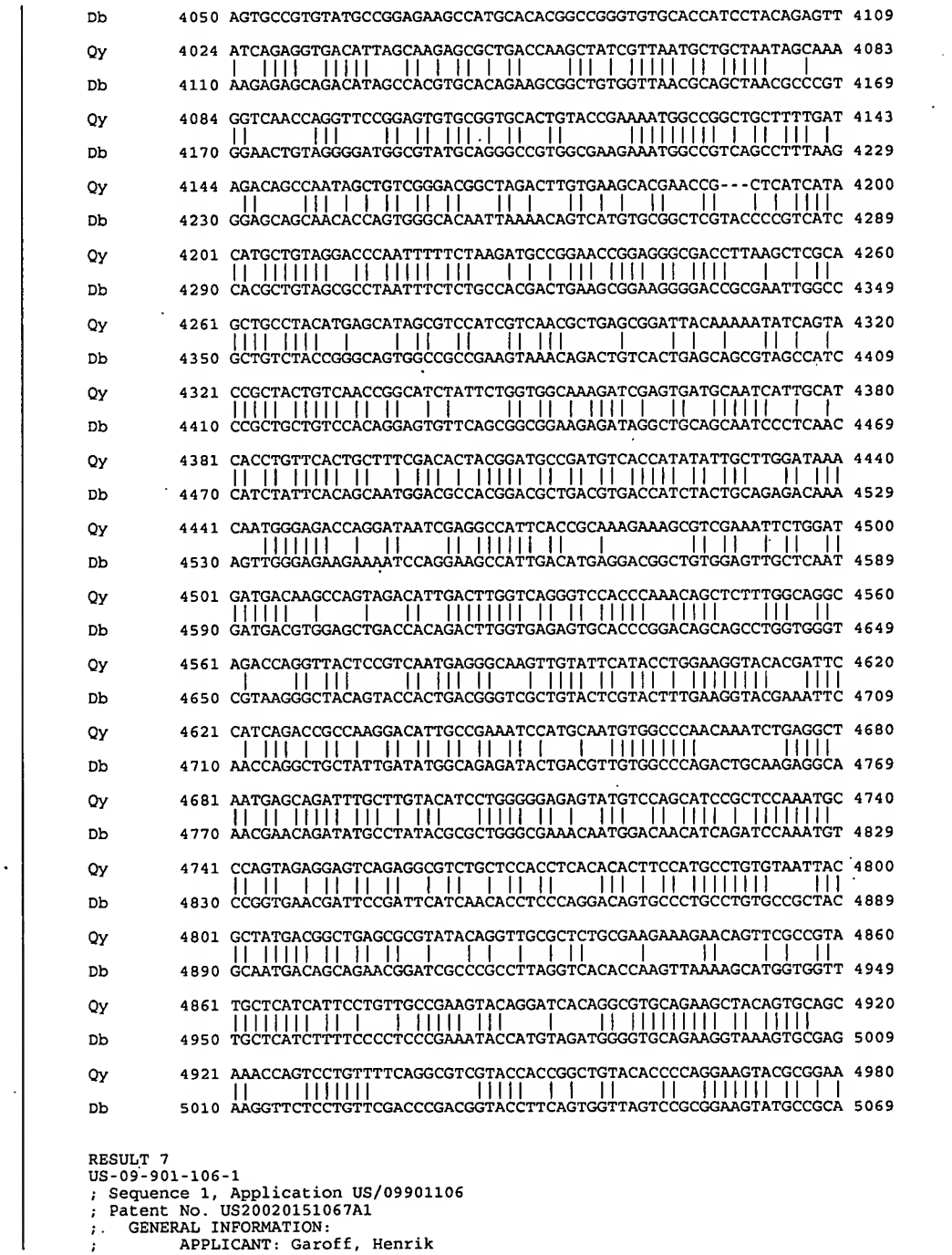
Query Match 31.3%; Score 1567.2; DB 11; Length 10610;
Best Local Similarity 58.4%; Pred. No. 0;
Matches 2906; Conservative 0; Mismatches 2038; Indels 36; Gaps 8;











RESULT 7
US-09-901-106-1
; Sequence 1, Application US/09901106
; Patent No. US20020151067A1
;. GENERAL INFORMATION:
; APPLICANT: Garoff, Henrik

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;                 Liljestrom, Peter
;       TITLE OF INVENTION: DNA Expression Systems Based on
;                           Alphaviruses
;       NUMBER OF SEQUENCES: 27
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Birch, Stewart, Kolasch & Birch
;            STREET: P.O. Box 747
;            CITY: Falls Church
;            STATE: Virginia
;            COUNTRY: USA
;            ZIP: 22040-0747
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/901,106
;            FILING DATE: 10-Jul-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/07/920,281C
;            FILING DATE: 13-AUG-1992
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Murphy Jr., Gerald M.
;            REGISTRATION NUMBER: 28,977
;            REFERENCE/DOCKET NUMBER: 828-103P
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 703-241-1300
;            TELEFAX: 703-241-2848
;            TELEX: 248345
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 11517 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: RNA (genomic)
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
;       ORIGINAL SOURCE:
;            ORGANISM: Semliki Forest Virus
;       FEATURE:
;            NAME/KEY:  -
;            LOCATION:  1..11517
;            OTHER INFORMATION:  /label= genome
;            /note= "Semliki Forest Virus complete nucleotide
;            sequence, presented as a cloned DNA sequence; see
;            Figure 5."
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;            LOCATION:  87..7379
;            OTHER INFORMATION:  /product= "SFV polyprotein"
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;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-901-106-1

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Qy         91 CCACAATTTGAGATCGAAGCAAGGCAGGTCACTGACAATGACCATGCCAATGCCAGAGCG 150
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Qy        151 TTTTCGCATGTGGCAACAAAGCTCATTGAGAGCGAAGTCGACCGGGACCAAGTTATCTTG 210
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Qy        211 GACATTGGAAGTGCGCCCGTCAGACATGCACATTCCAATCACCGCTATCATTGTATCTGC 270
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Qy        271 CCTATGATAAGCGCTGAAGACCCGGACAGACTACAACGGTATGCAGAAAGACT------T 324
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Qy        325 AAGAAAAGTGACATTACCGACAAGAACATAGCCTCTAAGGCGGCAGACCTGCTGGAAGTC 384
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Qy        445 TACTTTGGAAGTGTAGCAGTATACCAAGATGTGTACGCAGTCCATGCACCGACATCAATC 504
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Qy        565 TTTATGTACAAAAACATGGCAGGTTCCTACCCTACTTACAACACGAACTGGGCTGACGAG 624
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Qy        625 AGAGTATTGGAAGCACGTAACATTGGCCTCGGTAACTCAGATCTTCAGGAGAGCAGGCTT 684
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Db        756 GGCAAACTGTCCATTCTCCGCAAGAAGCAATTGAAACCTTGCGACACAGTCATGTTCTCG 815

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Qy        865 GAAGGGTACGTCATCAAAAAGATAACGATCAGCCCAGGACTATACGGTAAAGTTGAGAAC 924
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Db       1236 CTGCTTCCGATTGTGGCCGTCGCATTTAGCAAGTGGGCGAGGGAATACAAGGCAGACCTT 1295

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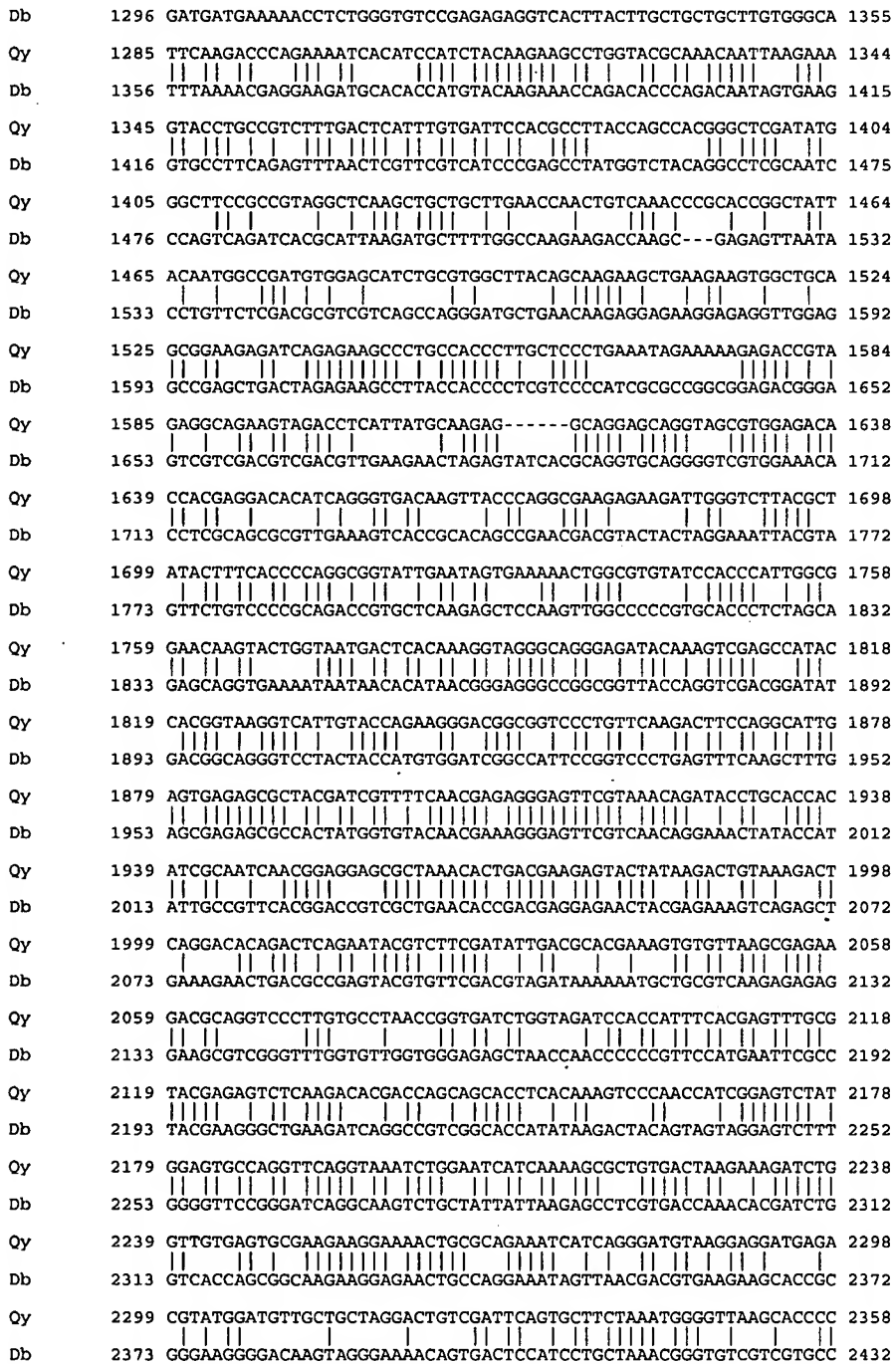
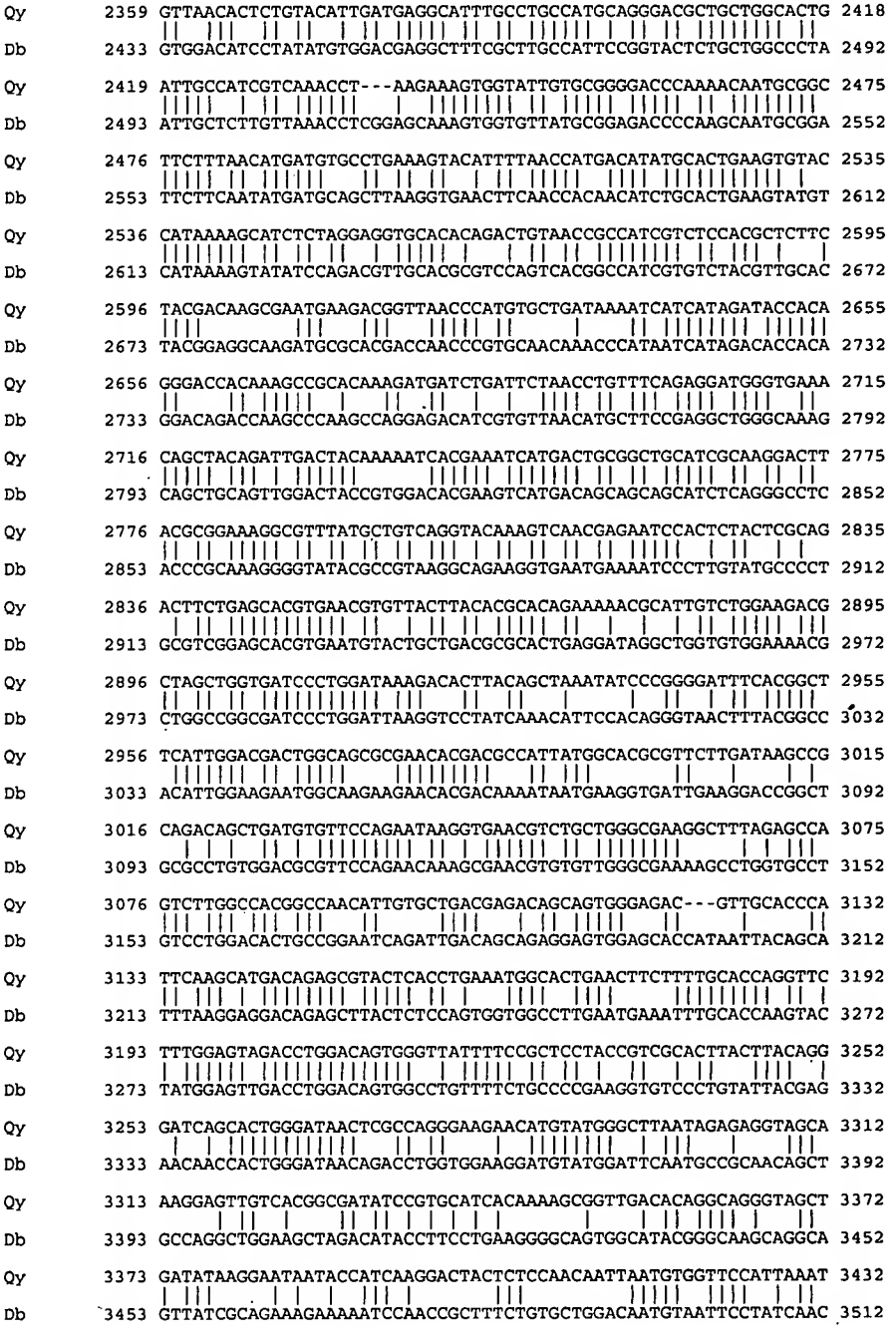
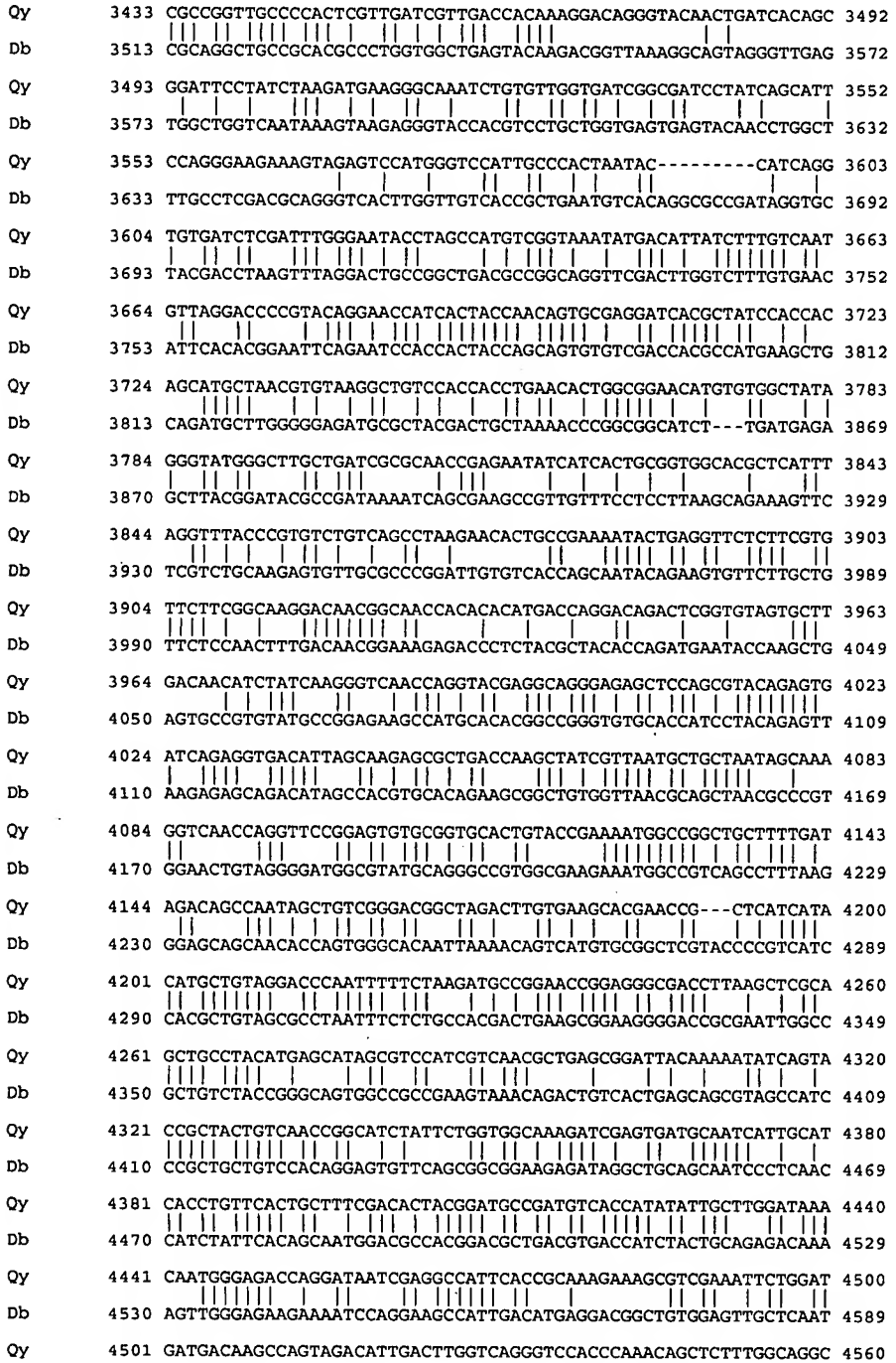
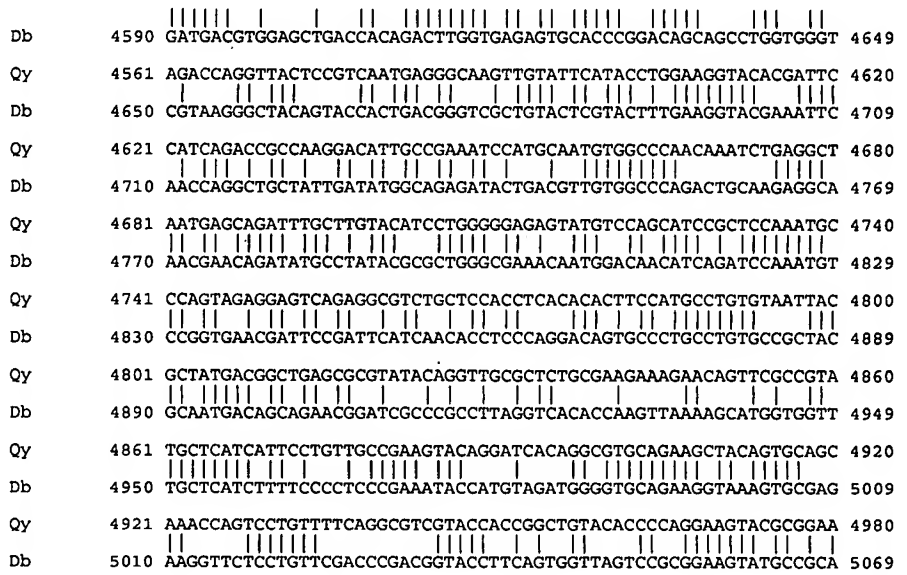


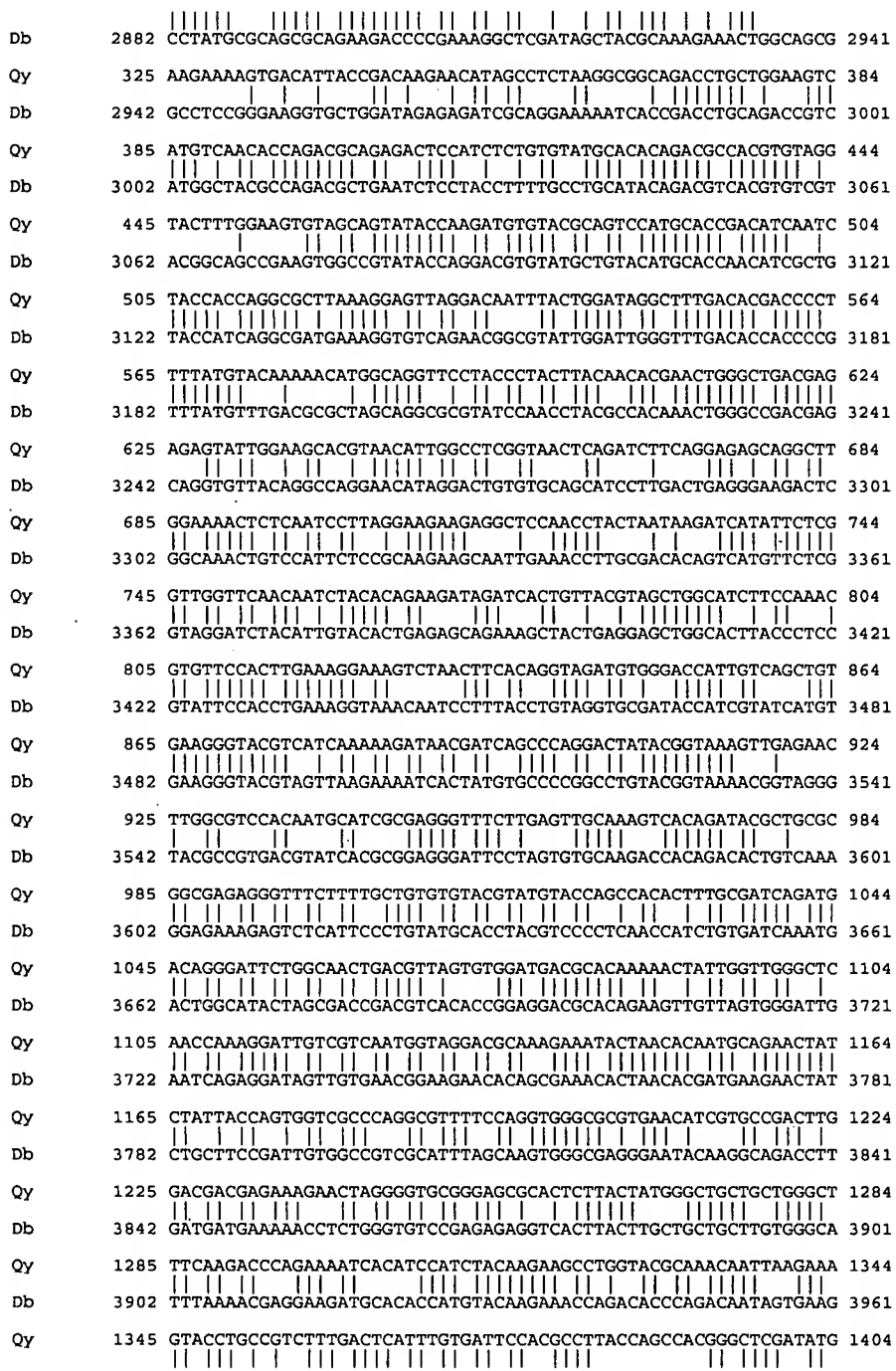






RESULT 8
US-09-190-246-1
; Sequence 1, Application US/09190246
; Publication No. US20030180257A1
; GENERAL INFORMATION:
; APPLICANT: Parrington, Mark
; APPLICANT: Li, Xiaomao
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: ALPHAVIRUS VECTORS FOR PARAMYXOVIRUS VACCINES
; FILE REFERENCE: Parrington et al.
; CURRENT APPLICATION NUMBER: US/09/190,246
; CURRENT FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 15538
; TYPE: DNA
; ORGANISM: Semliki Forest virus
US-09-190-246-1

Query Match 31.3%; Score 1564; DB 12; Length 15538;
Best Local Similarity 58.3%; Pred. No. 0;
Matches 2904; Conservative 0; Mismatches 2040; Indels 36; Gaps 8;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Qy 1999 CAGGACACAGACTCAGAATACGTCTTCGATATTGACGCACGAAAGTGTGTTAAGCGAGAA 2058
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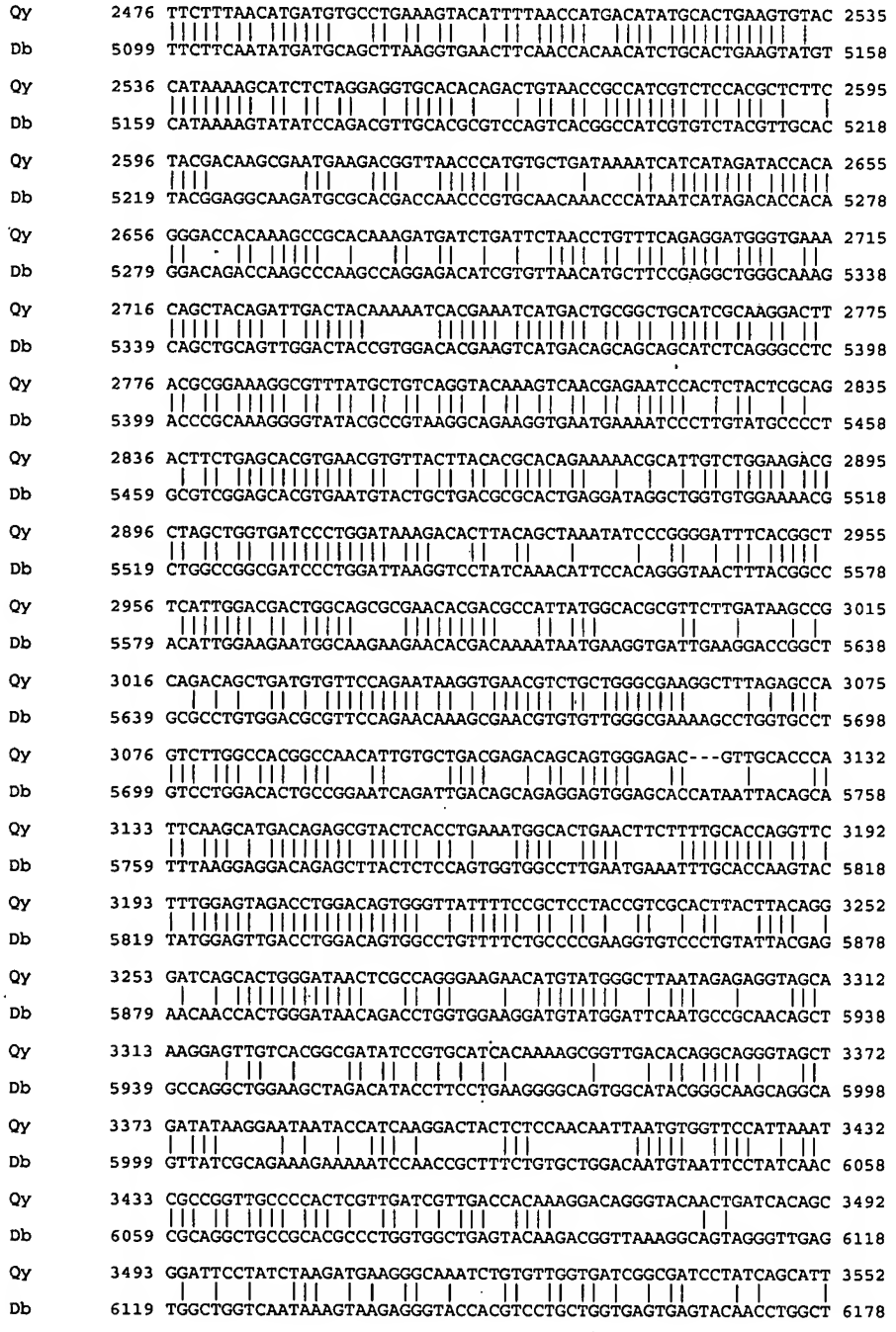
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RESULT 9
US-09-190-246-4
; Sequence 4, Application US/09190246
; Publication No. US20030180257A1
; GENERAL INFORMATION:
;  APPLICANT: Parrington, Mark
;  APPLICANT: Li, Xiaomao
;  APPLICANT: Klein, Michel
;  TITLE OF INVENTION: ALPHAVIRUS VECTORS FOR PARAMYXOVIRUS VACCINES
;  FILE REFERENCE: Parrington et al.
;  CURRENT APPLICATION NUMBER: US/09/190,246
;  CURRENT FILING DATE: 1998-11-13
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 8100
;   TYPE: DNA
;   ORGANISM: Semliki Forest virus
US-09-190-246-4

  Query Match             29.5%;  Score 1473.8;  DB 12;  Length 8100;
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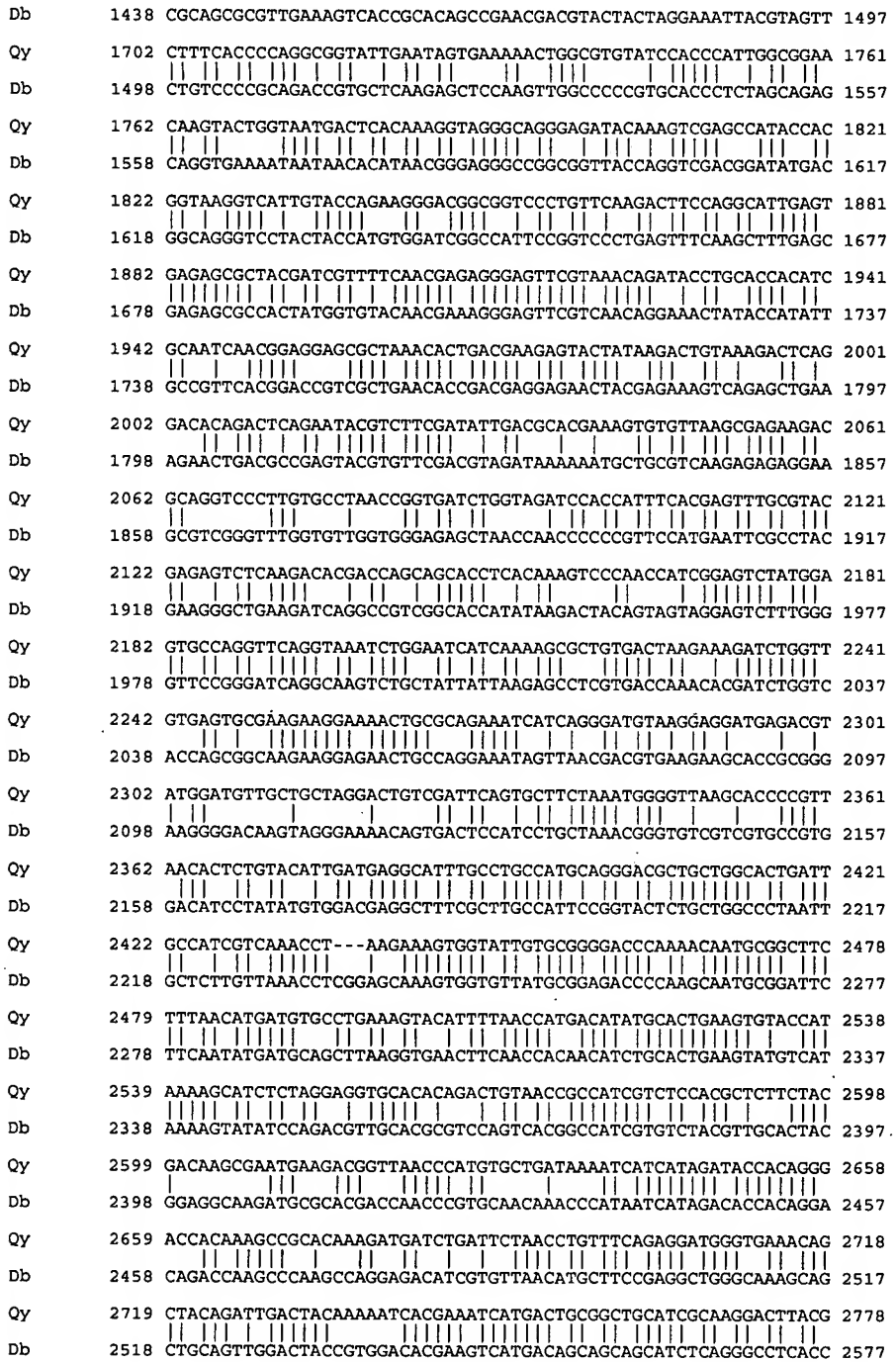
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Qy       4264 GCCTACATGAGCATAGCGTCCATCGTCAACGCTGAGCGGATTACAAAAATATCAGTACCG 4323
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Qy       4324 CTACTGTCAACCGGCATCTATTCTGGTGGCAAAGATCGAGTGATGCAATCATTGCATCAC 4383
Db       4135 CTGCTGTCCACAGGAGTGTTCAGCGGCGGAAGAGATAGGCTGCAGCAATCCCTCAACCAT 4194

Qy       4384 CTGTTCACTGCTTTCGACACTACGGATGCCGATGTCACCATATATTGCTTGGATAAACAA 4443
Db       4195 CTATTCACAGCAATGGACGCCACGGACGCTGACGTGACCATCTACTGCAGAGACAAAAGT 4254

Qy       4444 TGGGAGACCAGGATAATCGAGGCCATTCACCGCAAAGAAAGCGTCGAAATTCTGGATGAT 4503
Db       4255 TGGGAGAAGAAAATCCAGGAAGCCATTGACATGAGGACGGCTGTGGAGTTGCTCAATGAT 4314

Qy       4504 GACAAGCCAGTAGACATTGACTTGGTCAGGGTCCACCCAAACAGCTCTTTGGCAGGCAGA 4563
Db       4315 GACGTGGAGCTGACCACAGACTTGGTGAGAGTGCACCCGGACAGCAGCCTGGTGGGTCGT 4374

Qy       4564 CCAGGTTACTCCGTCAATGAGGGCAAGTTGTATTCATACCTGGAAGGTACACGATTCCAT 4623
Db       4375 AAGGGCTACAGTACCACTGACGGGTCGCTGTACTCGTACTTTGAAGGTACGAAATTCAAC 4434

Qy       4624 CAGACCGCCAAGGACATTGCCGAAATCCATGCAATGTGGCCCAACAAATCTGAGGCTAAT 4683
Db       4435 CAGGCTGCTATTGATATGGCAGAGATACTGACGTTGTGGCCCAGACTGCAAGAGGCAAAC 4494

Qy       4684 GAGCAGATTTGCTTGTACATCCTGGGGGAGAGTATGTCCAGCATCCGCTCCAAATGCCCA 4743
Db       4495 GAACAGATATGCCTATACGCGCTGGGCGAAACAATGGACAACATCAGATCCAAATGTCCG 4554

Qy       4744 GTAGAGGAGTCAGAGGCGTCTGCTCCACCTCACACACTTCCATGCCTGTGTAATTACGCT 4803
Db       4555 GTGAACGATTCCGATTCATCAACACCTCCCAGGACAGTGCCCTGCCTGTGCCGCTACGCA 4614

Qy       4804 ATGACGGCTGAGCGCGTATACAGGTTGCGCTCTGCGAAGAAAGAACAGTTCGCCGTATGC 4863
Db       4615 ATGACAGCAGAACGGATCGCCCGCCTTAGGTCACACCAAGTTAAAAGCATGGTGGTTTGC 4674

Qy       4864 TCATCATTCCTGTTGCCGAAGTACAGGATCACAGGCGTGCAGAAGCTACAGTGCAGCAAA 4923
Db       4675 TCATCTTTTCCCCTCCCGAAATACCATGTAGATGGGGTGCAGAAGGTAAAGTGCGAGAAG 4734

Qy       4924 CCAGTCCTGTTTTCAGGCGTCGTACCACCGGCTGTACACCCCAGGAAGTACGCGGAA 4980
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Db       4735 GTTCTCCTGTTCGACCCGACGGTACCTTCAGTGGTTAGTCCGCGGAAGTATGCCGCA 4791
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RESULT 10
US-09-507-362-102
; Sequence 102, Application US/09507362
; Publication No. US20030096397A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W.
; Polo, John M.
; Belli, Barbara A.
; Schlesinger, Sondra
; Dryga, Sergey A.
; Frolov, Ilya
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
; WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
; SYNTHESIS
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group PLLC
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/507,362
; FILING DATE: 18-Feb-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.457D6 /1196.011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8000 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 102:
US-09-507-362-102

Query Match 26.0%; Score 1300.4; DB 11; Length 8000;
Best Local Similarity 56.0%; Pred. No. 0;
Matches 2819; Conservative 0; Mismatches 2131; Indels 80; Gaps 16;

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Qy         23 ATATGGAAAGAATTCACGTTGACTTAGATGCTGACAGCCCGTATGTCAAGTCGTTACAGC 82
Db         64 AGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGCAAA 123

Qy         83 GGACGTTTCCACAATTTGAGATCGAAGCAAGGCAGGTCACTGACAATGACCATGCCAATG 142
Db        124 AAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTAATG 183

Qy        143 CCAGAGCGTTTTCGCATGTGGCAACAAAGCTCATTGAGAGCGAAGTCGACCGGGACCAAG 202
Db        184 CCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAGCGA 243

Qy        203 TTATCTTGGACATTGGAAGTGCGCCCGTCAGACATGCACATTCCAATCACCGCTATCATT 262
Db        244 CGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATCATT 303

Qy        263 GTATCTGCCCTATGATAAGCGCTGAAGACCCGGACAGACTACAACGGTATGCAGAAAGAC 322
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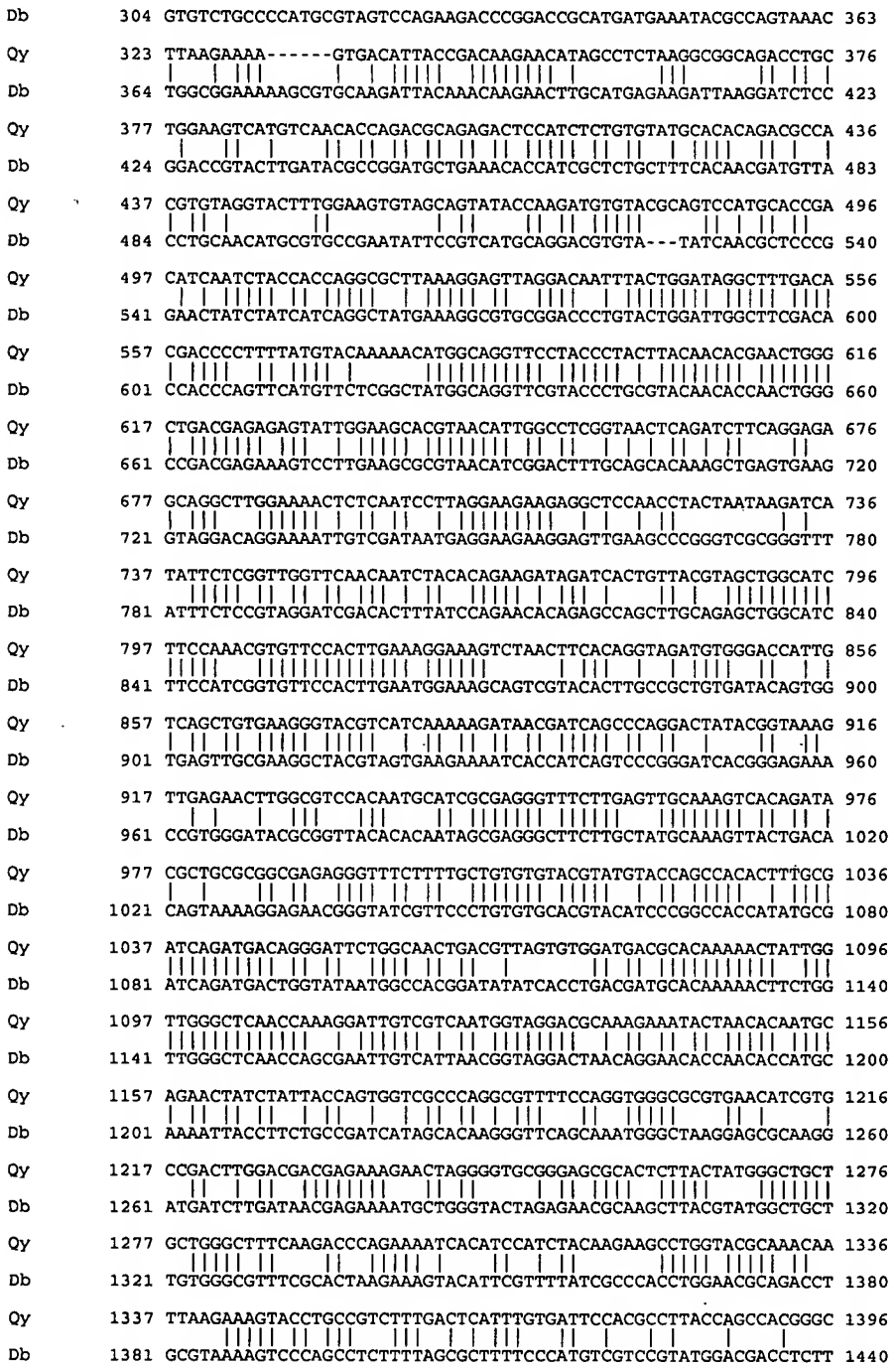

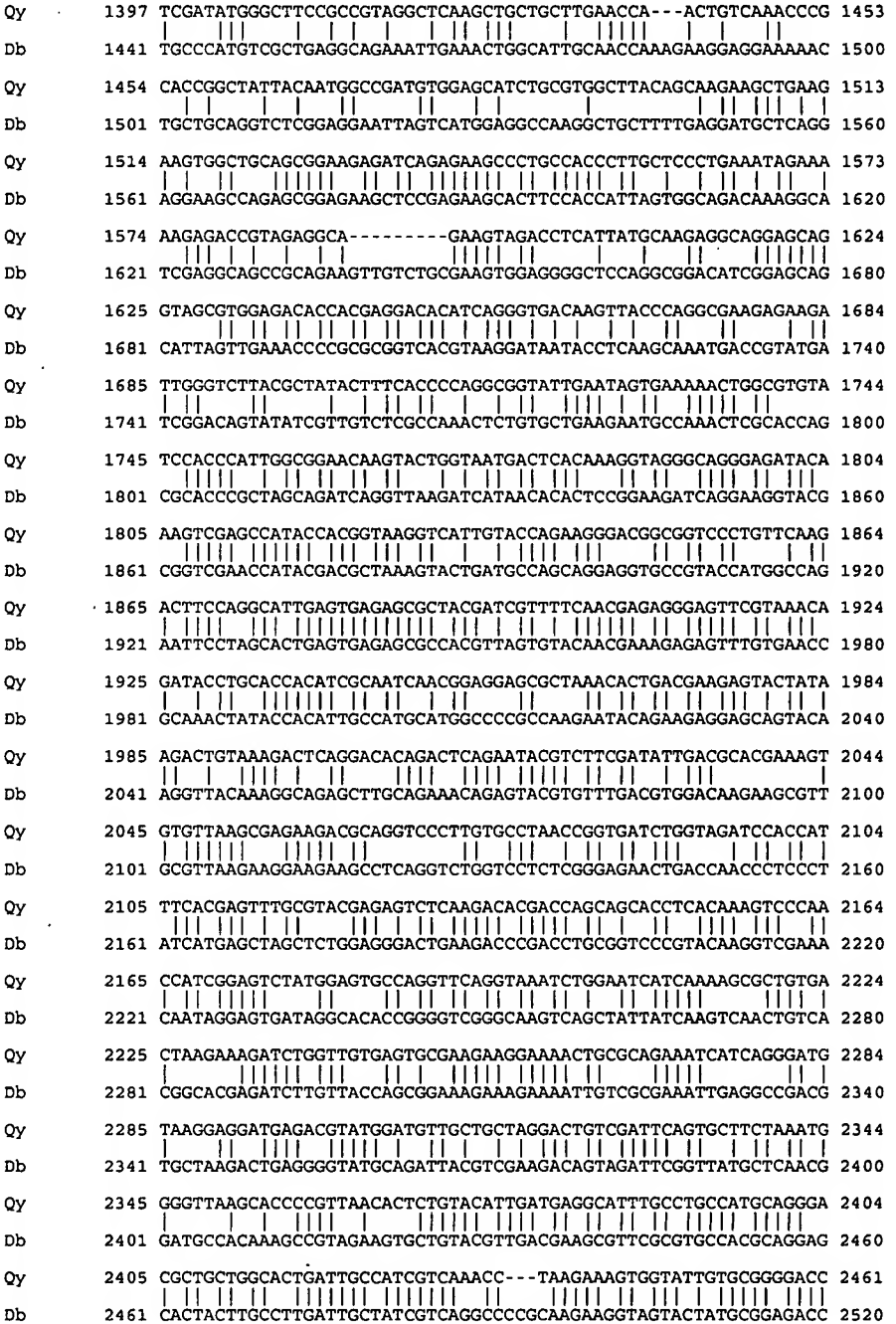

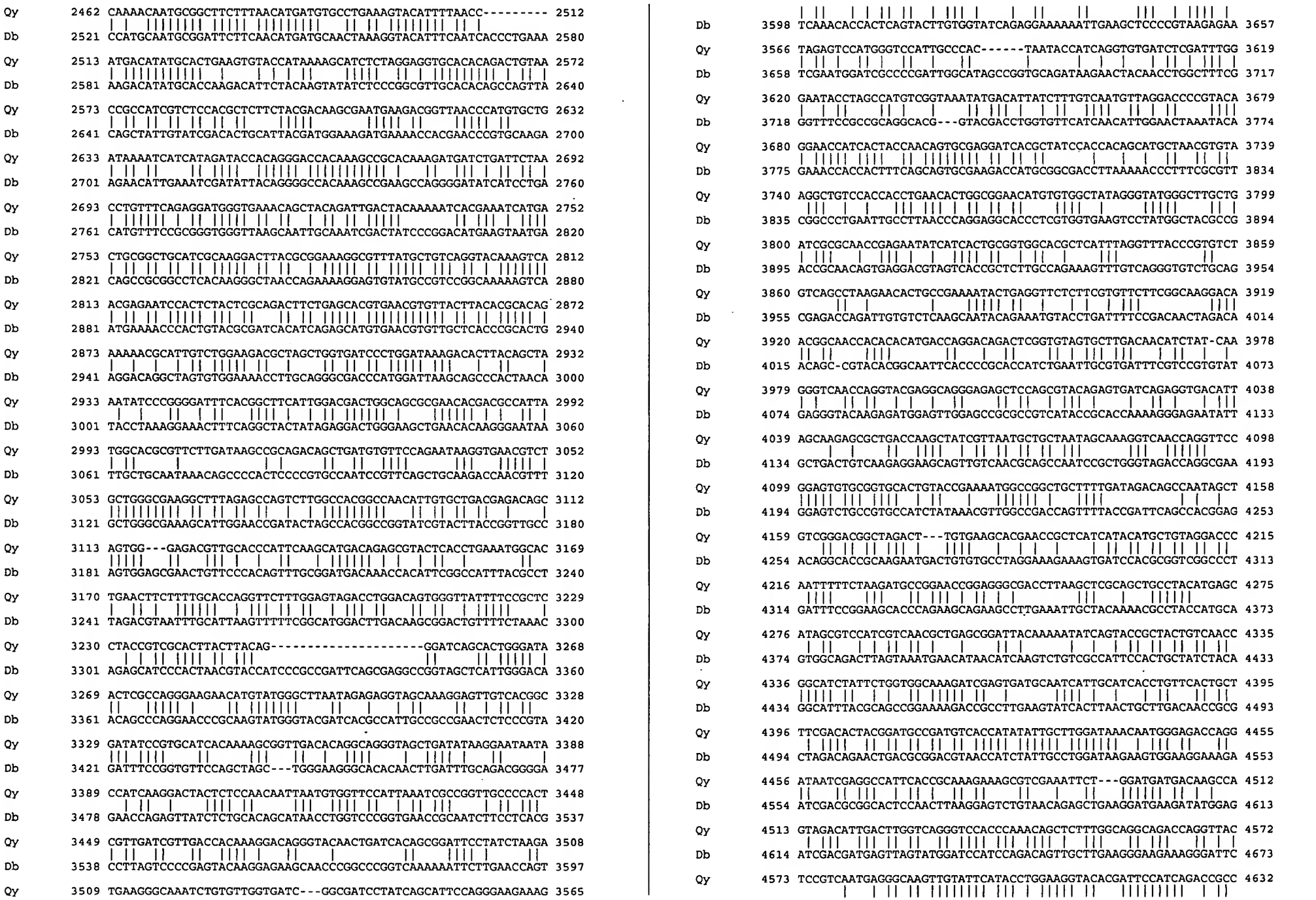

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Qy       4633 AAGGACATTGCCGAAATCCATGCAATGTGGCCCAACAAATCTGAGGCTAATGAGCAGATT 4692

Db       4734 AAAGACATGGCGGAGATAAAGGTCCTGTTCCCTAATGACCAGGAAAGTAATGAACAACTG 4793

Qy       4693 TGCTTGTACATCCTGGGGGAGAGTATGTCCAGCATCCGCTCCAAATGCCCAGTAGAGGAG 4752

Db       4794 TGTGCCTACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGGTCGACCAT 4853

Qy       4753 TCAGAGGCGTCTGCTCCACCTCACACACTTCCATGCCTGTGTAATTACGCTATGACGGCT 4812

Db       4854 AACCCGTCGTCTAGCCCGCCCAAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCA 4913

Qy       4813 GAGCGCGTATACAGGTTGCGCTCTGCGAAGAAAGAACAGTTCGCCGTATGCTCATCATTC 4872

Db       4914 GAAAGGGTCCACAGACTTAGAAGCAATAACGTCAAAGAAGTTACAGTATGCTCCTCCACC 4973

Qy       4873 CTGTTGCCGAAGTACAGGATCACAGGCGTGCAGAAGCTACAGTGCAGCAAACCAGTCCTG 4932

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Qy       4933 TTTTCAGGCGTCGTACCACCGGCTGTACACCCCAGGAAGTACGCGGAAAT 4982

Db       5034 TTTAATCCGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGT 5083
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RESULT 11
US-09-507-362-103
; Sequence 103, Application US/09507362
; Publication No. US20030096397A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W.
; Polo, John M.
; Belli, Barbara A.
; Schlesinger, Sondra
; Dryga, Sergey A.
; Frolov, Ilya
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
; WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
; SYNTHESIS
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group PLLC
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/507,362
; FILING DATE: 18-Feb-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.457D6 /1196.011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11740 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-09-507-362-103

Query Match 26.0%; Score 1300.4; DB 11; Length 11740;
Best Local Similarity 56.0%; Pred. No. 0;
Matches 2819; Conservative 0; Mismatches 2131; Indels 80; Gaps 16;

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Qy         23 ATATGGAAAGAATTCACGTTGACTTAGATGCTGACAGCCCGTATGTCAAGTCGTTACAGC 82

Db         64 AGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGCAAA 123

Qy         83 GGACGTTTCCACAATTTGAGATCGAAGCAAGGCAGGTCACTGACAATGACCATGCCAATG 142

Db        124 AAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTAATG 183

Qy        143 CCAGAGCGTTTTCGCATGTGGCAACAAAGCTCATTGAGAGCGAAGTCGACCGGGACCAAG 202

Db        184 CCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAGCGA 243

Qy        203 TTATCTTGGACATTGGAAGTGCGCCCGTCAGACATGCACATTCCAATCACCGCTATCATT 262

Db        244 CGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATCATT 303

Qy        263 GTATCTGCCCTATGATAAGCGCTGAAGACCCGGACAGACTACAACGGTATGCAGAAAGAC 322

Db        304 GTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTAAAC 363

Qy        323 TTAAGAAAA------GTGACATTACCGACAAGAACATAGCCTCTAAGGCGGCAGACCTGC 376

Db        364 TGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATCTCC 423

Qy        377 TGGAAGTCATGTCAACACCAGACGCAGAGACTCCATCTCTGTGTATGCACACAGACGCCA 436

Db        424 GGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATGTTA 483

Qy        437 CGTGTAGGTACTTTGGAAGTGTAGCAGTATACCAAGATGTGTACGCAGTCCATGCACCGA 496

Db        484 CCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTA---TATCAACGCTCCCG 540

Qy        497 CATCAATCTACCACCAGGCGCTTAAAGGAGTTAGGACAATTTACTGGATAGGCTTTGACA 556

Db        541 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 600

Qy        557 CGACCCCTTTTATGTACAAAAACATGGCAGGTTCCTACCCTACTTACAACACGAACTGGG 616

Db        601 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 660

Qy        617 CTGACGAGAGAGTATTGGAAGCACGTAACATTGGCCTCGGTAACTCAGATCTTCAGGAGA 676

Db        661 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 720

Qy        677 GCAGGCTTGGAAAACTCTCAATCCTTAGGAAGAAGAGGCTCCAACCTACTAATAAGATCA 736

Db        721 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 780

Qy        737 TATTCTCGGTTGGTTCAACAATCTACACAGAAGATAGATCACTGTTACGTAGCTGGCATC 796

Db        781 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 840

Qy        797 TTCCAAACGTGTTCCACTTGAAAGGAAAGTCTAACTTCACAGGTAGATGTGGGACCATTG 856

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Qy        857 TCAGCTGTGAAGGGTACGTCATCAAAAAGATAACGATCAGCCCAGGACTATACGGTAAAG 916

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Qy        917 TTGAGAACTTGGCGTCCACAATGCATCGCGAGGGTTTCTTGAGTTGCAAAGTCACAGATA 976

Db        961 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1020

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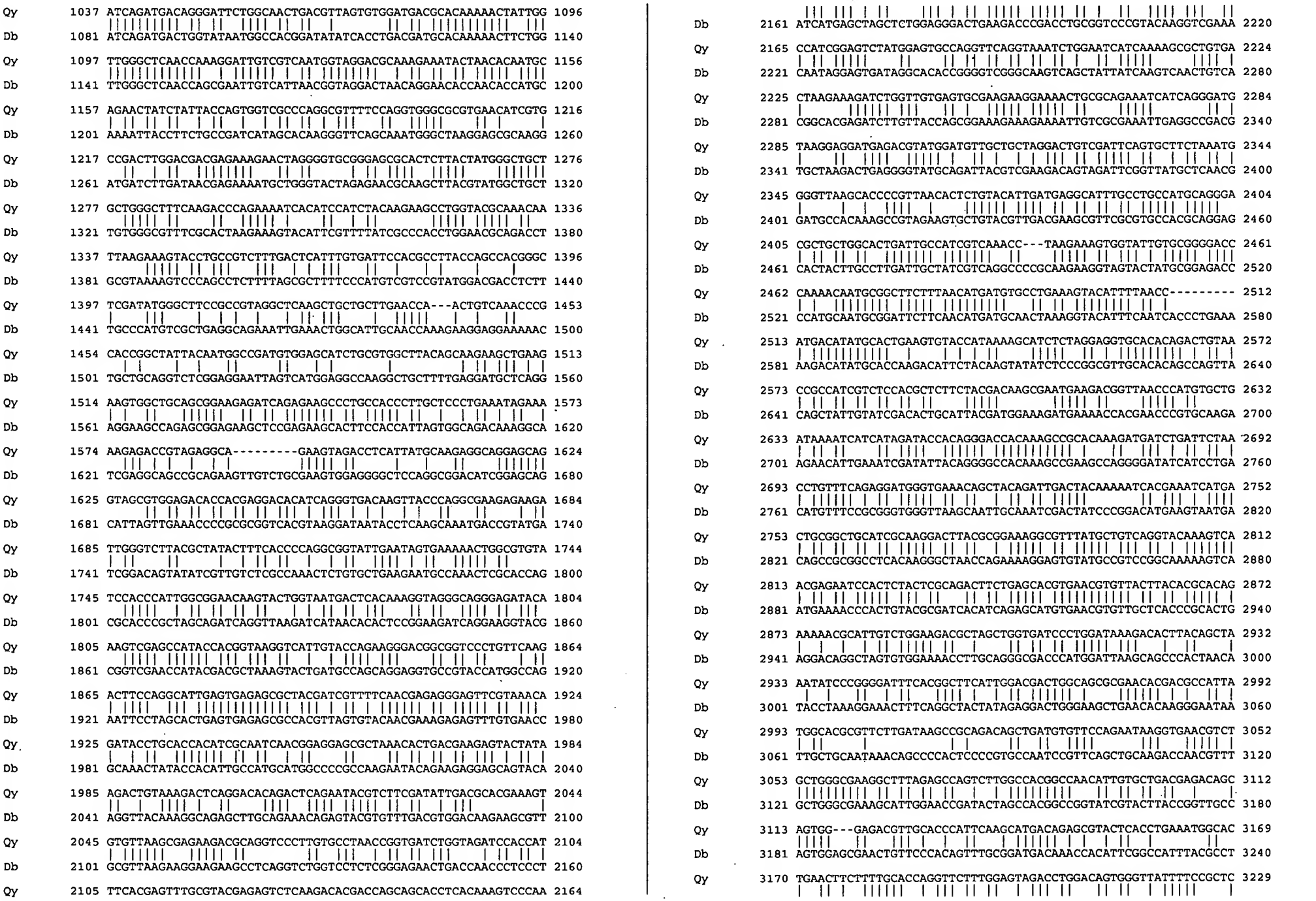

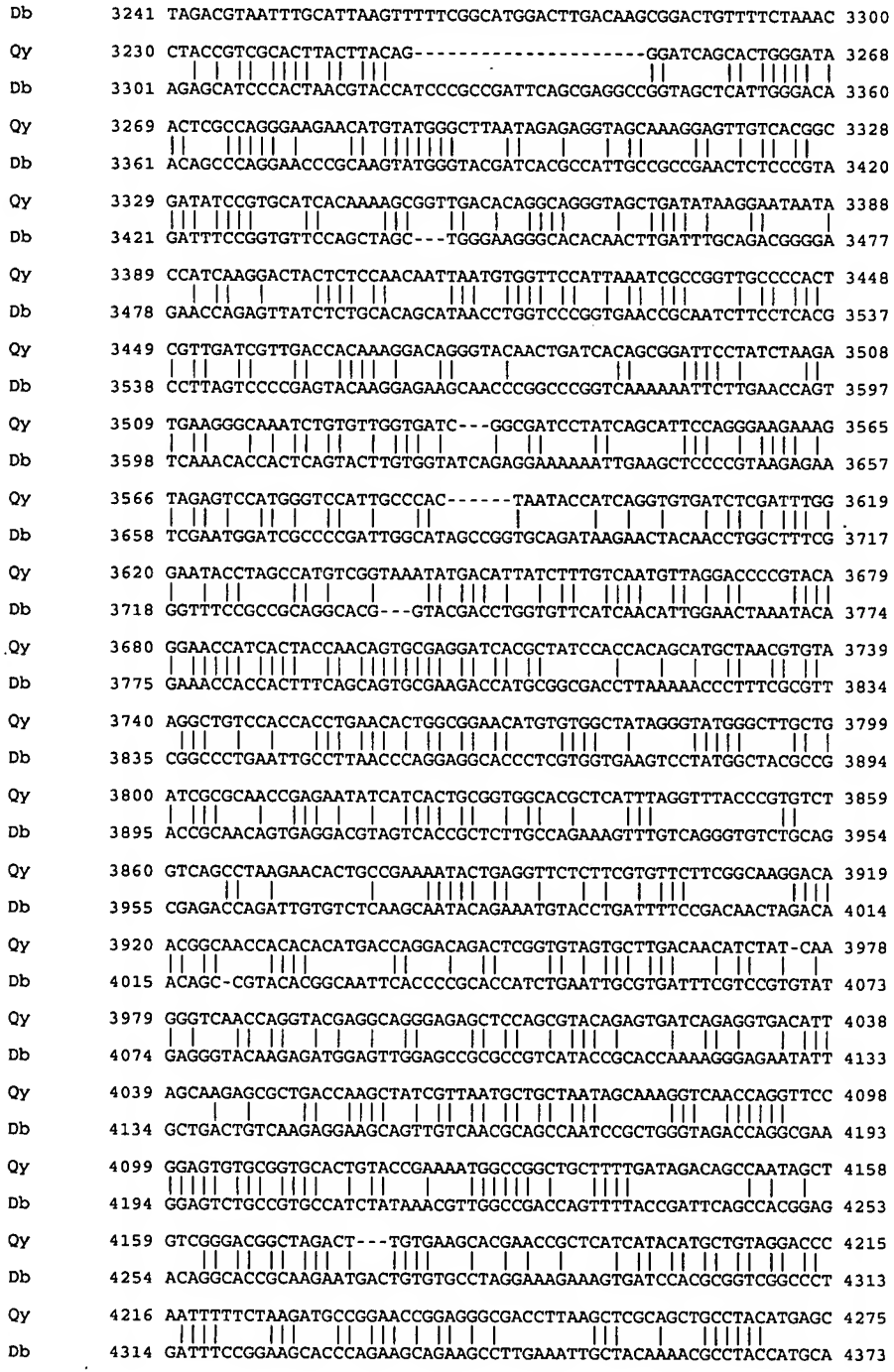

RESULT 12
US-09-507-362-101
; Sequence 101, Application US/09507362
; Publication No. US20030096397A1
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr., Thomas W.
; Polo, John M.
; Belli, Barbara A.
; Schlesinger, Sondra
; Dryga, Sergey A.
; Frolov, Ilya
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
; WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
; SYNTHESIS
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group PLLC
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:

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;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/507,362
;             FILING DATE: 18-Feb-2000
;             CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;             NAME: McMasters, David D.
;             REGISTRATION NUMBER: 33,963
;             REFERENCE/DOCKET NUMBER: 930049.457D6 /1196.011
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (206) 622-4900
;             TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 101:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 8000 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-09-507-362-101

  Query Match             25.9%;  Score 1295.6;  DB 11;  Length 8000;
  Best Local Similarity   56.0%;  Pred. No. 0;
  Matches 2816;  Conservative    0;  Mismatches 2134;  Indels   80;  Gaps   16;

Qy         23 ATATGGAAAGAATTCACGTTGACTTAGATGCTGACAGCCCGTATGTCAAGTCGTTACAGC 82
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Db         64 AGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTGCAACTGAAAA 123

Qy         83 GGACGTTTCCACAATTTGAGATCGAAGCAAGGCAGGTCACTGACAATGACCATGCCAATG 142
                |  || || ||||||||| | | ||||  ||||||||||   ||||||||||| ||||
Db        124 AAAGCTTCCCGCAATTTGAGGTAGTAGCACAGCAGGTCACTCCAAATGACCATGCTAATG 183

Qy        143 CCAGAGCGTTTTCGCATGTGGCAACAAAGCTCATTGAGAGCGAAGTCGACCGGGACCAAG 202
              ||||||| |||||||| |||| |  || || || |||   || ||
Db        184 CCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAGCGA 243

Qy        203 TTATCTTGGACATTGGAAGTGCGCCCGTCAGACATGCACATTCCAATCACCGCTATCATT 262
              |||||||||||  || || || || |   |       |||| | ||||  |||||||
Db        244 CGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATCATT 303

Qy        263 GTATCTGCCCTATGATAAGCGCTGAAGACCCGGACAGACTACAACGGTATGCAGAAAGAC 322
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Db        304 GTGTCTGCCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAAATACGCCAGTAAAC 363

Qy        323 TTAAGAAAA------GTGACATTACCGACAAGAACATAGCCTCTAAGGCGGCAGACCTGC 376
              |    | |||      |  | |||||  ||||||| |       |||     || || |
Db        364 TGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATCTCC 423

Qy        377 TGGAAGTCATGTCAACACCAGACGCAGAGACTCCATCTCTGTGTATGCACACAGACGCCA 436
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Db        424 GGACCGTACTTGATACGCCGGATGCTGAAACACCATCGCTCTGCTTTCACAACGATGTTA 483

Qy        437 CGTGTAGGTACTTTGGAAGTGTAGCAGTATACCAAGATGTGTACGCAGTCCATGCACCGA 496
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Qy        497 CATCAATCTACCACCAGGCGCTTAAAGGAGTTAGGACAATTTACTGGATAGGCTTTGACA 556
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Db        541 GAACTATCTATCATCAGGCTATGAAAGGCGTGCGGACCCTGTACTGGATTGGCTTCGACA 600

Qy        557 CGACCCCTTTTATGTACAAAAACATGGCAGGTTCCTACCCTACTTACAACACGAACTGGG 616
              | ||||  || |||| |      ||||||||||| |||||| | |||||||| |||||||
Db        601 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTACCCTGCGTACAACACCAACTGGG 660

Qy        617 CTGACGAGAGAGTATTGGAAGCACGTAACATTGGCCTCGGTAACTCAGATCTTCAGGAGA 676
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Db        661 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGCACAAAGCTGAGTGAAG 720

Qy        677 GCAGGCTTGGAAAACTCTCAATCCTTAGGAAGAAGAGGCTCCAACCTACTAATAAGATCA 736

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Db        721 GTAGGACAGGAAAATTGTCGATAATGAGGAAGAAGGAGTTGAAGCCCGGGTCGCGGGTTT 780

Qy        737 TATTCTCGGTTGGTTCAACAATCTACACAGAAGATAGATCACTGTTACGTAGCTGGCATC 796
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Db        781 ATTTCTCCGTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 840

Qy        797 TTCCAAACGTGTTCCACTTGAAAGGAAAGTCTAACTTCACAGGTAGATGTGGGACCATTG 856
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Db        841 TTCCATCGGTGTTCCACTTGAATGGAAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG 900

Qy        857 TCAGCTGTGAAGGGTACGTCATCAAAAAGATAACGATCAGCCCAGGACTATACGGTAAAG 916
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Db        901 TGAGTTGCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGGATCACGGGAGAAA 960

Qy        917 TTGAGAACTTGGCGTCCACAATGCATCGCGAGGGTTTCTTGAGTTGCAAAGTCACAGATA 976
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Db        961 CCGTGGGATACGCGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAGTTACTGACA 1020

Qy        977 CGCTGCGCGGCGAGAGGGTTTCTTTTGCTGTGTGTACGTATGTACCAGCCACACTTTGCG 1036
              | |    || ||  |||| || ||  |||||| |||||  | || |||||  | ||||
Db       1021 CAGTAAAAGGAGAACGGGTATCGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1080

Qy       1037 ATCAGATGACAGGGATTCTGGCAACTGACGTTAGTGTGGATGACGCACAAAAACTATTGG 1096
              |||||||||| || ||  |||| || ||  |        || || ||||||||||  |||
Db       1081 ATCAGATGACTGGTATAATGGCCACGGATATATCACCTGACGATGCACAAAAACTTCTGG 1140

Qy       1097 TTGGGCTCAACCAAAGGATTGTCGTCAATGGTAGGACGCAAAGAAATACTAACACAATGC 1156
              |||||||||||  | |||||| | || |||||||||  | || || || ||||| ||||
Db       1141 TTGGGCTCAACCAGCGAATTGTCATTAACGGTAGGACTAACAGGAACACCAACACCATGC 1200

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Db       1201 AAAATTACCTTCTGCCGATCATAGCACAAGGGTTCAGCAAATGGGCTAAGGAGCGCAAGG 1260

Qy       1217 CCGACTTGGACGACGAGAAAGAACTAGGGGTGCGGGAGCGCACTCTTACTATGGGCTGCT 1276
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Db       1261 ATGATCTTGATAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 1320

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Db       1321 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTTATCGCCCACCTGGAACGCAGACCT 1380

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Db       1381 GCGTAAAAGTCCCAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGGACGACCTCTT 1440

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Qy       1454 CACCGGCTATTACAATGGCCGATGTGGAGCATCTGCGTGGCTTACAGCAAGAAGCTGAAG 1513
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Db       1501 TGCTGCAGGTCTCGGAGGAATTAGTCATGGAGGCCAAGGCTGCTTTTGAGGATGCTCAGG 1560

Qy       1514 AAGTGGCTGCAGCGGAAGAGATCAGAGAAGCCCTGCCACCCTTGCTCCCTGAAATAGAAA 1573
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Db       1561 AGGAAGCCAGAGCGGAGAAGCTCCGAGAAGCACTTCCACCATTAGTGGCAGACAAAGGCA 1620

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Db       1621 TCGAGGCAGCCGCAGAAGTTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATCGGAGCAG 1680

Qy       1625 GTAGCGTGGAGACACCACGAGGACACATCAGGGTGACAAGTTACCCAGGCGAAGAGAAGA 1684
              || || || || || || ||| | ||| | | | | ||    ||      | ||
Db       1681 CATTAGTTGAAACCCCGCGCGGTCACGTAAGGATAATACCTCAAGCAAATGACCGTATGA 1740

Qy       1685 TTGGGTCTTACGCTATACTTTCACCCCAGGCGGTATTGAATAGTGAAAAACTGGCGTGTA 1744
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Qy       1745 TCCACCCATTGGCGGAACAAGTACTGGTAATGACTCACAAAGGTAGGGCAGGGAGATACA 1804
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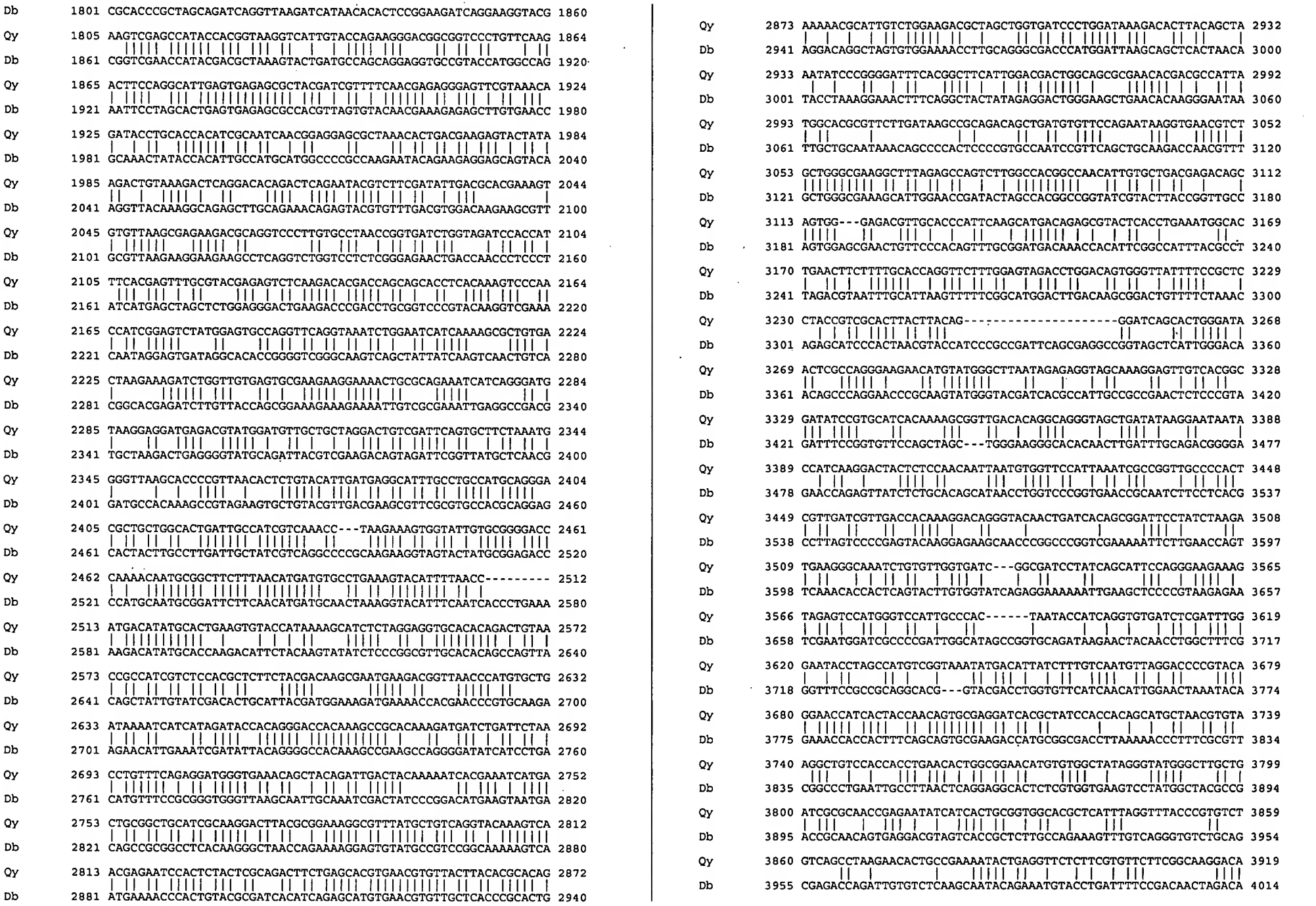

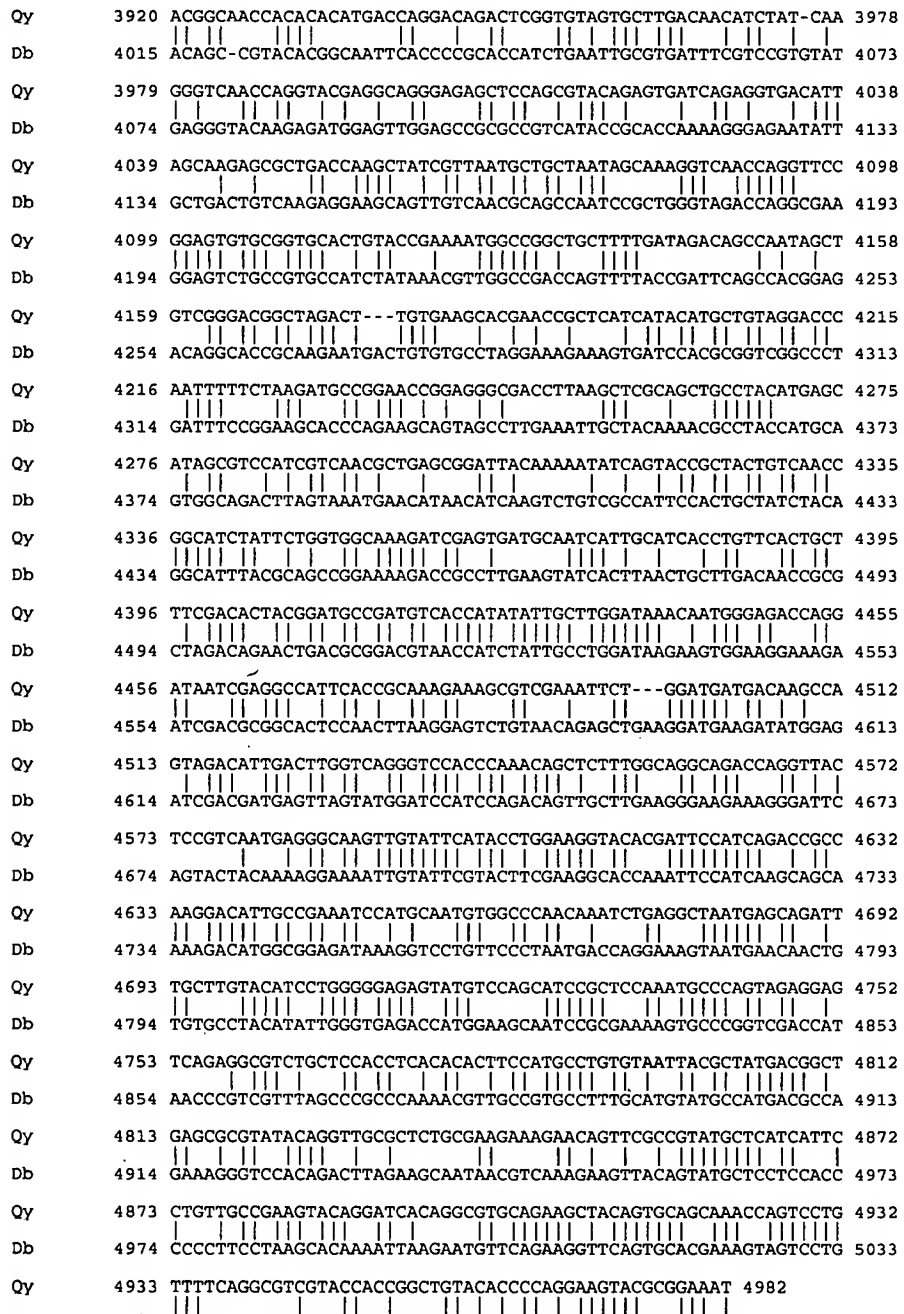

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Qy       3979 GGGTCAACCAGGTACGAGGCAGGGAGAGCTCCAGCGTACAGAGTGATCAGAGGTGACATT 4038
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Qy       4039 AGCAAGAGCGCTGACCAAGCTATCGTTAATGCTGCTAATAGCAAAGGTCAACCAGGTTCC 4098
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Qy       4159 GTCGGGACGGCTAGACT---TGTGAAGCACGAACCGCTCATCATACATGCTGTAGGACCC 4215
Db       4254 ACAGGCACCGCAAGAATGACTGTGTGCCTAGGAAAGAAAGTGATCCACGCGGTCGGCCCT 4313

Qy       4216 AATTTTTCTAAGATGCCGGAACCGGAGGGCGACCTTAAGCTCGCAGCTGCCTACATGAGC 4275
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Qy       4276 ATAGCGTCCATCGTCAACGCTGAGCGGATTACAAAAATATCAGTACCGCTACTGTCAACC 4335
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Qy       4336 GGCATCTATTCTGGTGGCAAAGATCGAGTGATGCAATCATTGCATCACCTGTTCACTGCT 4395
Db       4434 GGCATTTACGCAGCCGGAAAAGACCGCCTTGAAGTATCACTTAACTGCTTGACAACCGCG 4493

Qy       4396 TTCGACACTACGGATGCCGATGTCACCATATATTGCTTGGATAAACAATGGGAGACCAGG 4455
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Qy       4513 GTAGACATTGACTTGGTCAGGGTCCACCCAAACAGCTCTTTGGCAGGCAGACCAGGTTAC 4572
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Qy       4573 TCCGTCAATGAGGGCAAGTTGTATTCATACCTGGAAGGTACACGATTCCATCAGACCGCC 4632
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Qy       4633 AAGGACATTGCCGAAATCCATGCAATGTGGCCCAACAAATCTGAGGCTAATGAGCAGATT 4692
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Qy       4753 TCAGAGGCGTCTGCTCCACCTCACACACTTCCATGCCTGTGTAATTACGCTATGACGGCT 4812
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Qy       4813 GAGCGCGTATACAGGTTGCGCTCTGCGAAGAAAGAACAGTTCGCCGTATGCTCATCATTC 4872
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RESULT 13
US-09-733-042-1
; Sequence 1, Application US/09733042
; Patent No. US20020168709A1
; GENERAL INFORMATION:
;  APPLICANT:   Hennecke, Frank
;  APPLICANT:  Renner, Wolfgang A.
;  TITLE OF INVENTION:   Replicon Based Activation of Endogenous Genes
;  FILE REFERENCE:   1700.0100001
;  CURRENT APPLICATION NUMBER: US/09/733,042
;  CURRENT FILING DATE:  2000-12-11
;  PRIOR APPLICATION NUMBER:   US 60/169,988
;  PRIOR FILING DATE:   1999-12-10
;  NUMBER OF SEQ ID NOS:   49
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 11282
;   TYPE: DNA
;   ORGANISM: pCYTts
US-09-733-042-1

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  Best Local Similarity   56.0%;  Pred. No. 0;
  Matches 2816;  Conservative    0;  Mismatches 2134;  Indels   80;  Gaps   16;

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Qy         83 GGACGTTTCCACAATTTGAGATCGAAGCAAGGCAGGTCACTGACAATGACCATGCCAATG 142
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Qy        143 CCAGAGCGTTTTCGCATGTGGCAACAAAGCTCATTGAGAGCGAAGTCGACCGGGACCAAG 202
Db       1076 CCAGAGCATTTTCGCATCTGGCCAGTAAACTAATCGAGCTGGAGGTTCCTACCACAGCGA 1135

Qy        203 TTATCTTGGACATTGGAAGTGCGCCCGTCAGACATGCACATTCCAATCACCGCTATCATT 262
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Qy        263 GTATCTGCCCTATGATAAGCGCTGAAGACCCGGACAGACTACAACGGTATGCAGAAAGAC 322
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Qy        323 TTAAGAAAA------GTGACATTACCGACAAGAACATAGCCTCTAAGGCGGCAGACCTGC 376
Db       1256 TGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAGATTAAGGATCTCC 1315

Qy        377 TGGAAGTCATGTCAACACCAGACGCAGAGACTCCATCTCTGTGTATGCACACAGACGCCA 436
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Qy        437 CGTGTAGGTACTTTGGAAGTGTAGCAGTATACCAAGATGTGTACGCAGTCCATGCACCGA 496
Db       1376 CCTGCAACATGCGTGCCGAATATTCCGTCATGCAGGACGTGTA---TATCAACGCTCCCG 1432

Qy        497 CATCAATCTACCACCAGGCGCTTAAAGGAGTTAGGACAATTTACTGGATAGGCTTTGACA 556
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Qy        557 CGACCCCTTTTATGTACAAAAACATGGCAGGTTCCTACCCTACTTACAACACGAACTGGG 616
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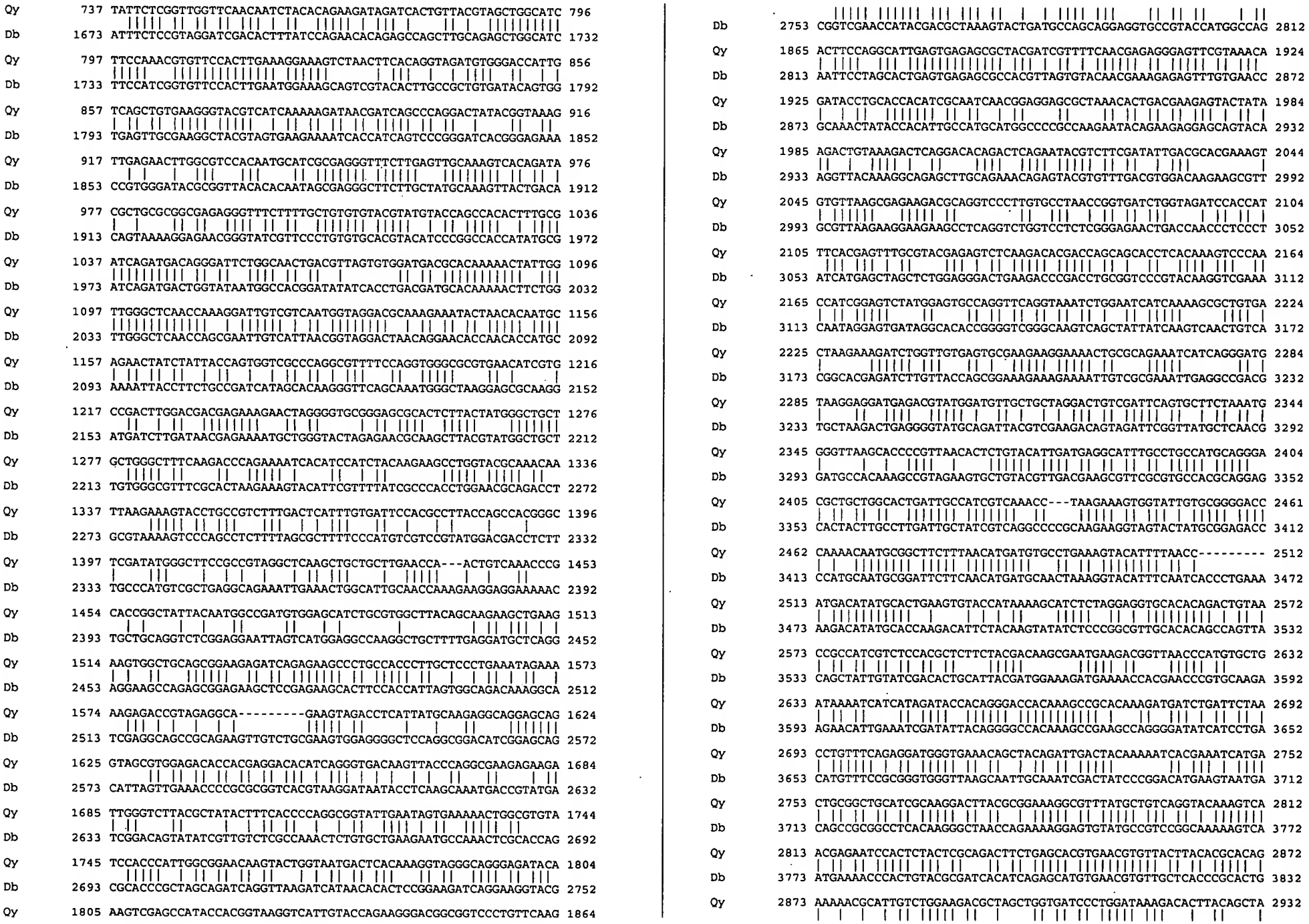

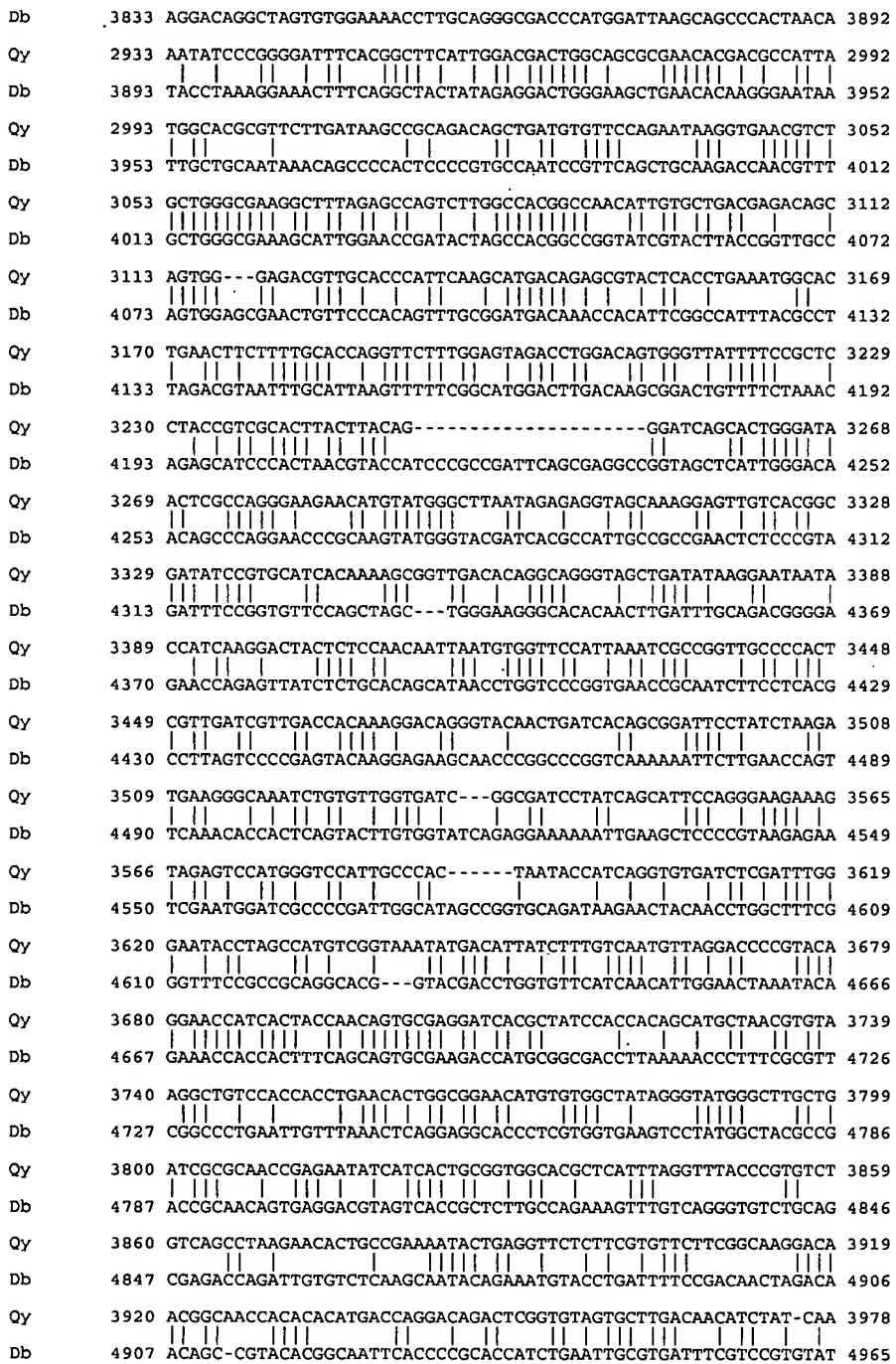

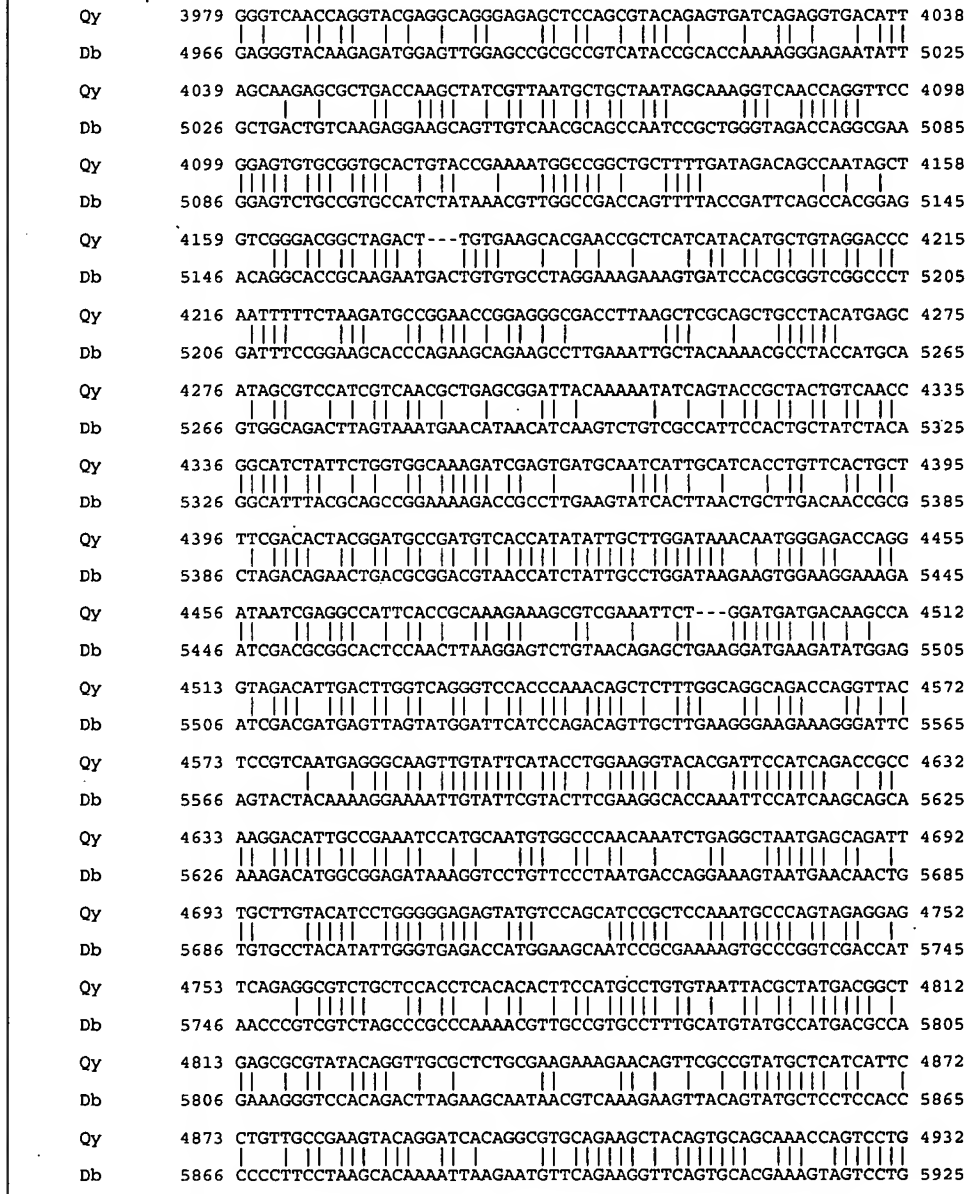

RESULT 14
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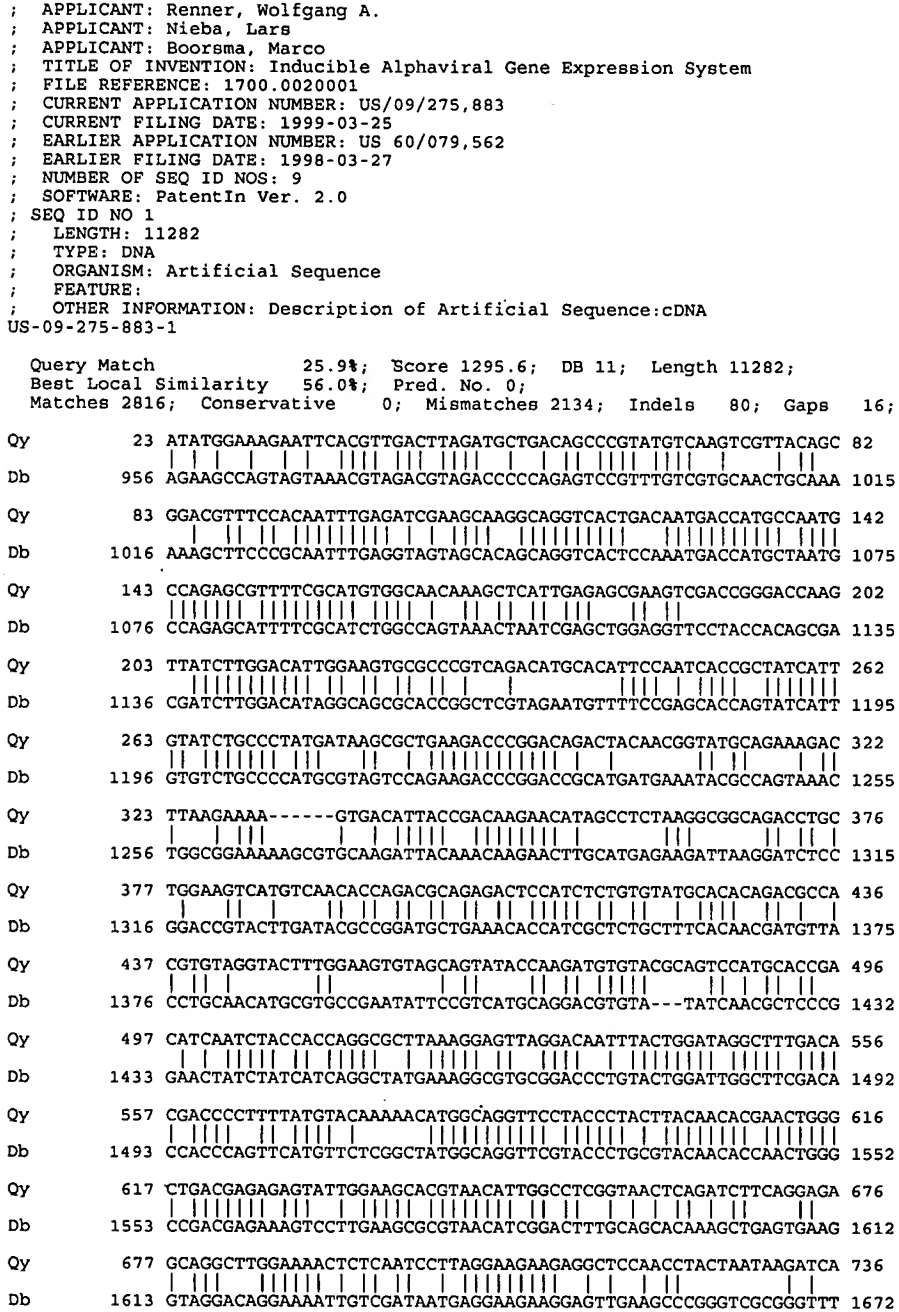
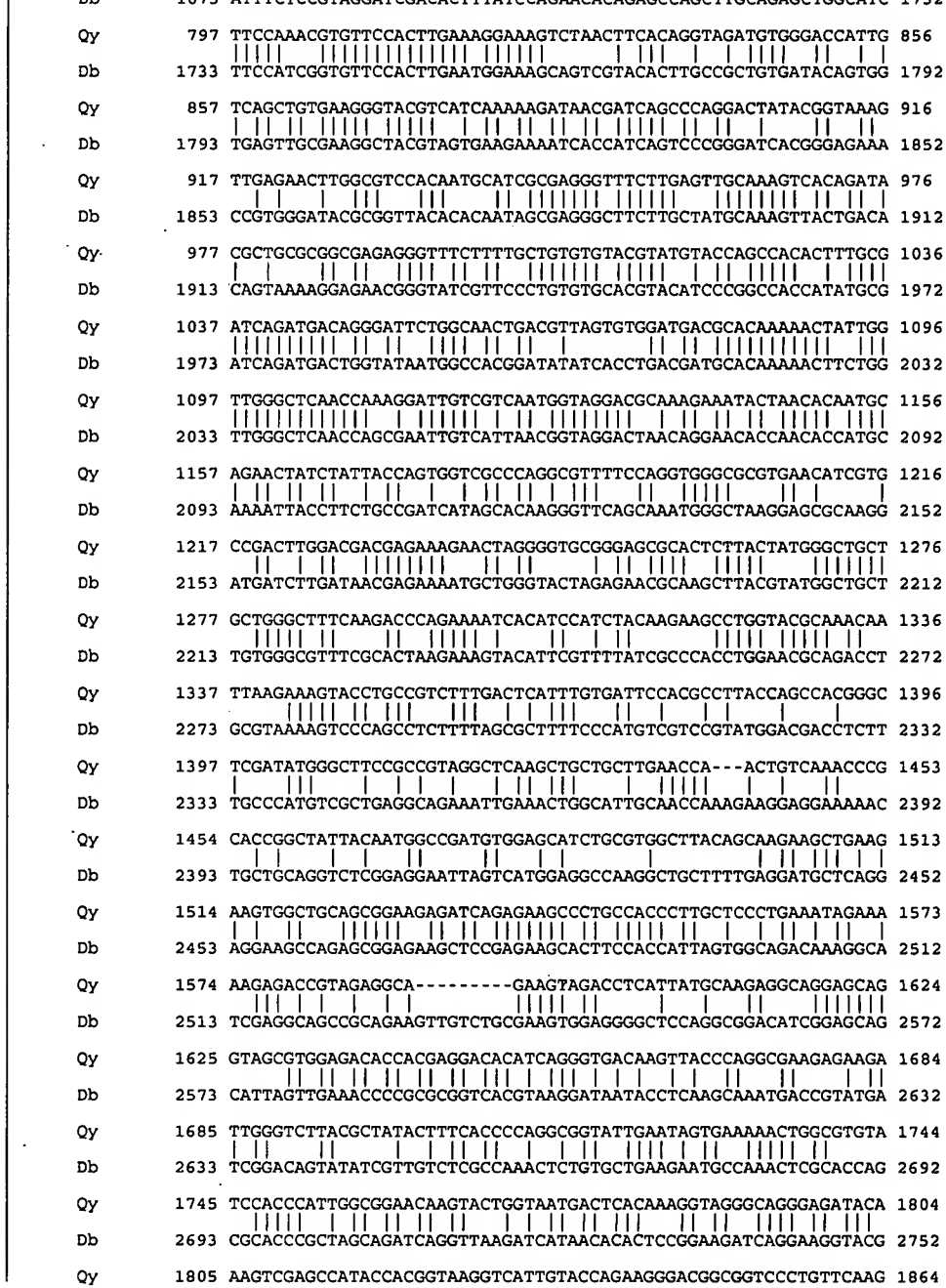
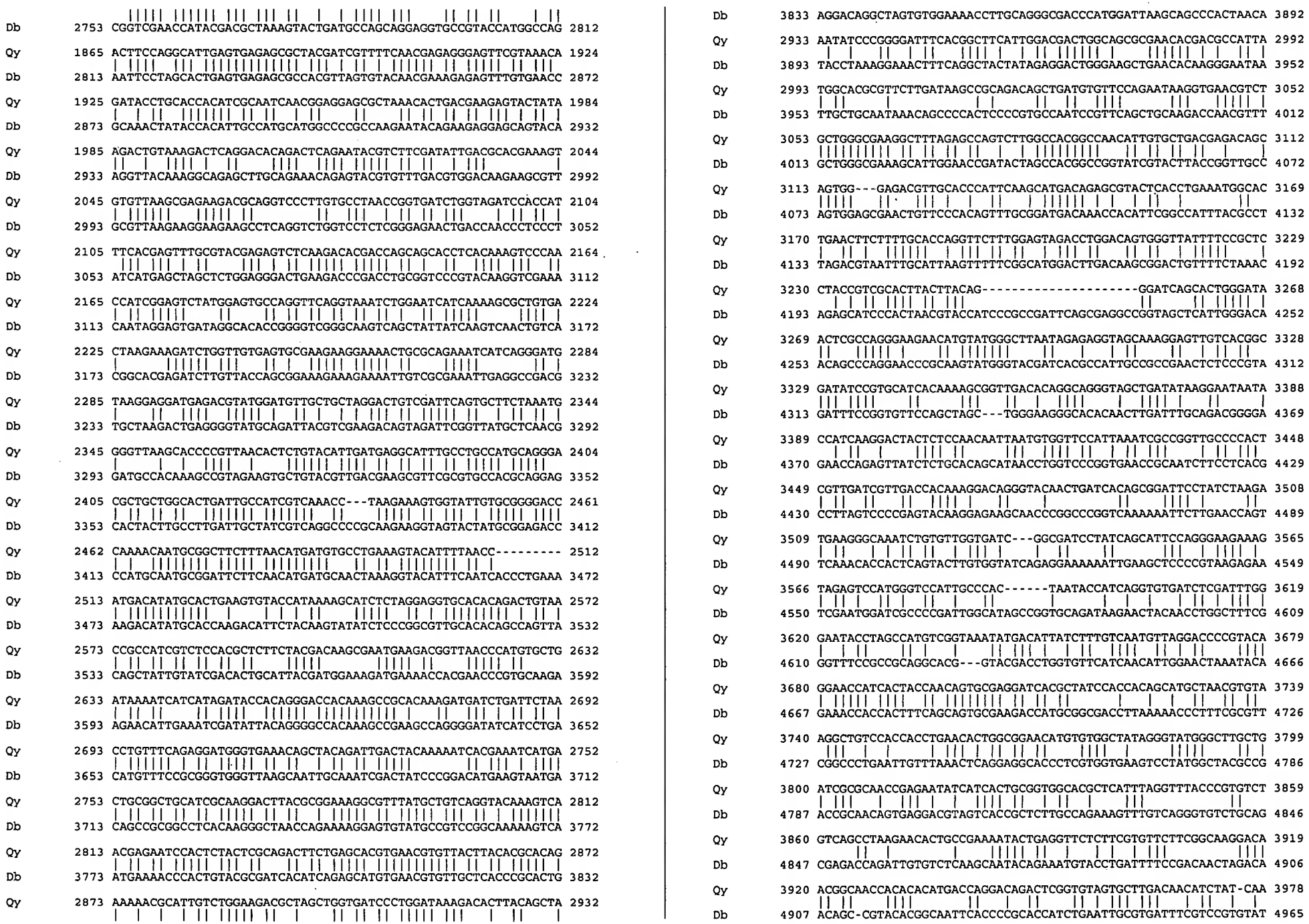
; Sequence 1, Application US/09275883

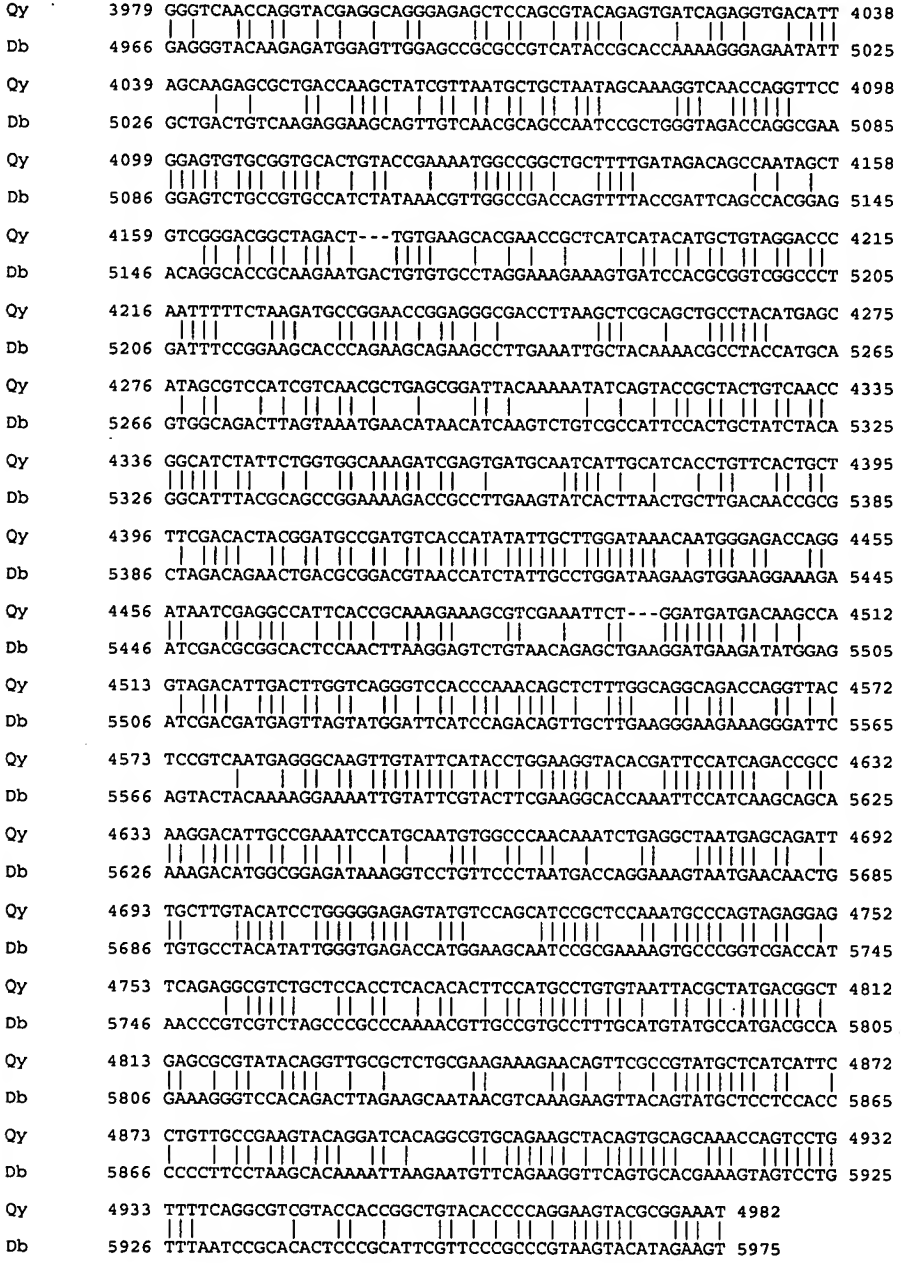
; Publication No. US20030053988A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Nieba, Lars
; APPLICANT: Boorsma, Marco
; TITLE OF INVENTION: Inducible Alphaviral Gene Expression System
; FILE REFERENCE: 1700.0020001
; CURRENT APPLICATION NUMBER: US/09/275,883
; CURRENT FILING DATE: 1999-03-25
; EARLIER APPLICATION NUMBER: US 60/079,562
; EARLIER FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 11282
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:cDNA
US-09-275-883-1

Query Match 25.9%; Score 1295.6; DB 11; Length 11282;
Best Local Similarity 56.0%; Pred. No. 0;
Matches 2816; Conservative 0; Mismatches 2134; Indels 80; Gaps 16;









RESULT 15
US-10-123-101-51
; Sequence 51, Application US/10123101

; Publication No. US20030148262A1
; GENERAL INFORMATION:
; APPLICANT: POLO, John
; APPLICANT: PERRI, Silvia
; APPLICANT: THUDIUM, Kent
; TITLE OF INVENTION: CHIMERIC ALPHAVIRUS REPLICON PARTICLES
; FILE REFERENCE: 2300-17924 / PP17924.002
; CURRENT APPLICATION NUMBER: US/10/123,101
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 60/295,451
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 705
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEE nsP fragment oligo 1
US-10-123-101-51

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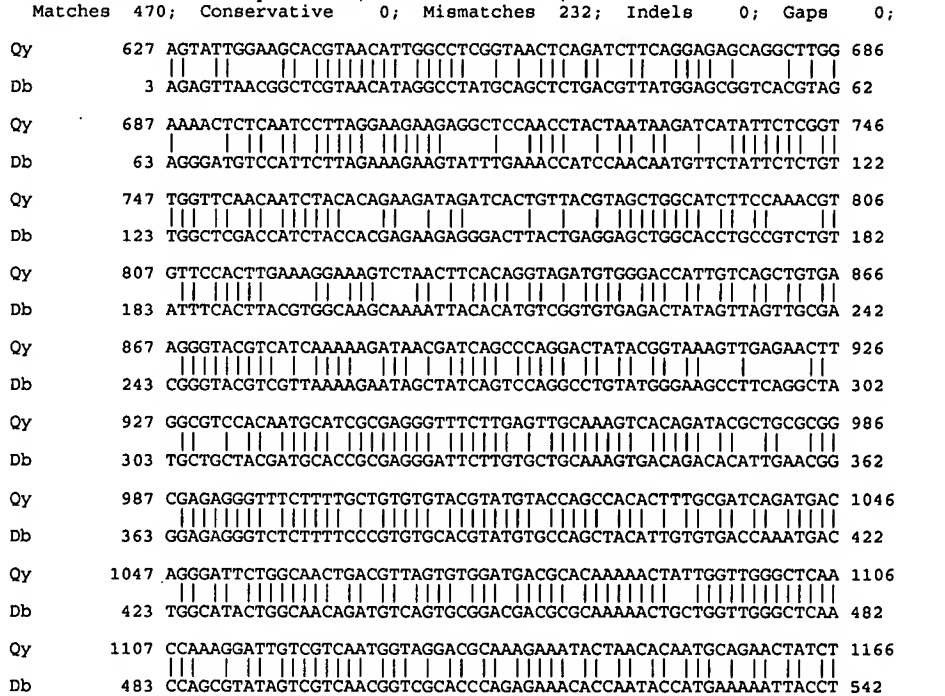
Best Local Similarity 67.0%; Pred. No. 1e-97;
Matches 470; Conservative 0; Mismatches 232; Indels 0; Gaps 0;



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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Maximum Match 100%
Listing first 45 summaries

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; Patent No. 6261570
;  GENERAL INFORMATION:
;    APPLICANT:  Michael D. Parker
;    APPLICANT:  Jonathan F. Smith
;    APPLICANT:  Bruce Crise
;    APPLICANT:  Mark Steve Oberste
;    APPLICANT:  Shannon Schmura
;    TITLE OF INVENTION:  Live Attenuated Virus Vaccines for Eastern Equine Encephalitis
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Charles H. Harris
;      STREET:  USA MRMC -  MRMC-JA
;      CITY:  FORT DETRICK, FREDERICK
;      STATE:  MARYLAND
;      COUNTRY:  USA
;      ZIP:  21702-5012
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Macintosh 7.5
;      SOFTWARE:  Microsoft Word 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/991,840A
;      FILING DATE:  December 16, 1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  Provisional Application 60/047162,
;      FILING DATE:  May 20, 1997
;      APPLICATION NUMBER:  Provisional Application 60/053,652
;      FILING DATE:  July 24, 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Charles H. Harris
;      REGISTRATION NUMBER:  34,616
;      REFERENCE/DOCKET NUMBER:  003/058/SAP RIID 96-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 619-2065
;      TELEFAX:  (301) 619-5034
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11492 base pairs
;      TYPE:  Nucleic acid
;      STRANDEDNESS:  Double
;      TOPOLOGY:  Linear
;    FEATURE:  OTHER INFORMATION:  N at all occurences is = unknown:
;    FEATURE:  OTHER INFORMATION: K at all
;    FEATURE:  occurences is = G or T
US-08-991-840A-1
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Query Match 89.8%; Score 4492; DB 3; Length 11492;
Best Local Similarity 95.8%; Pred. No. 0;
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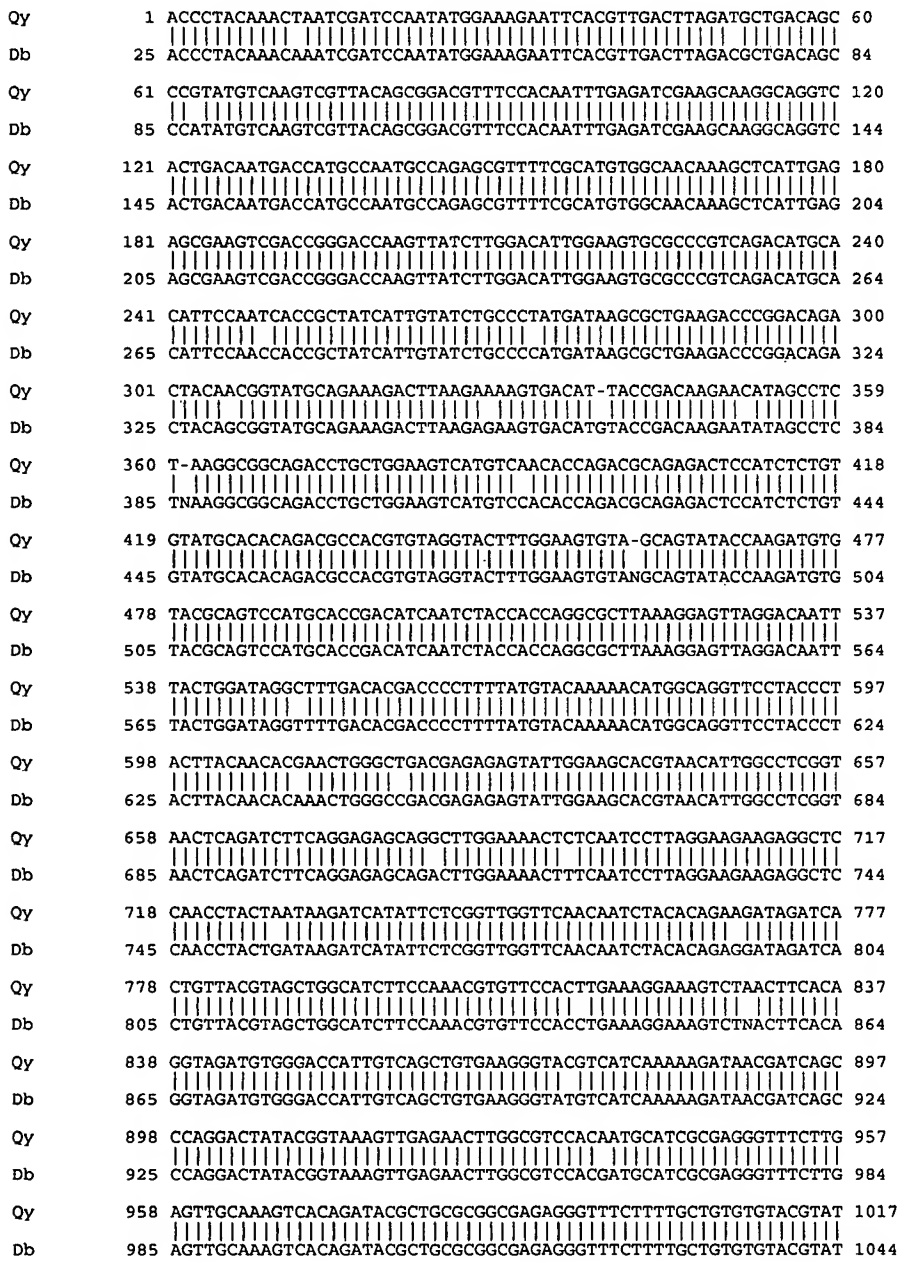

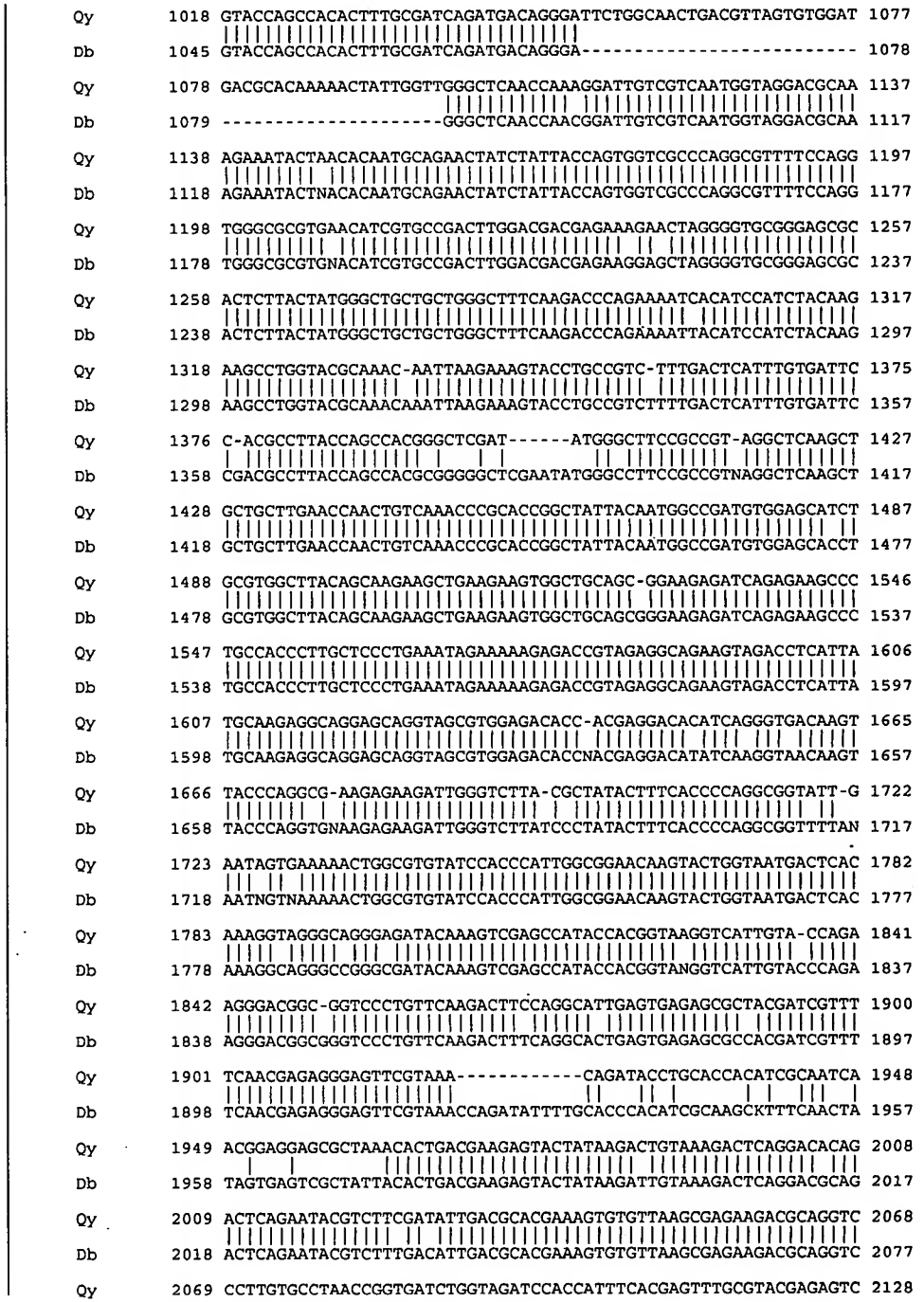

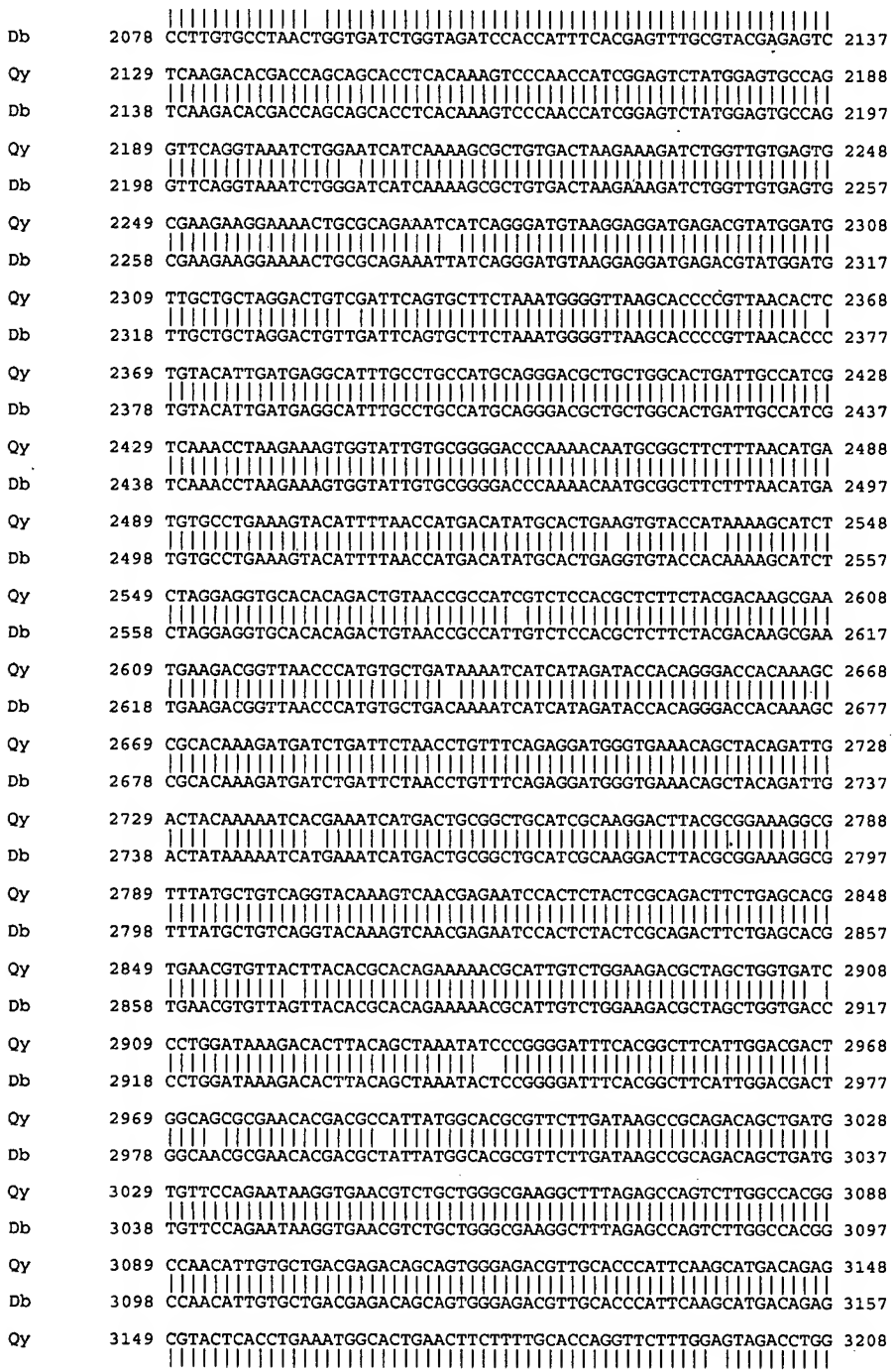
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Db 2318 TTGCTGCTAGGACTGTTGATTCAGTGCTTCTAAATGGGGTTAAGCACCCCGTTAACACCC 2377
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Db 2438 TCAAACCTAAGAAAGTGGTATTGTGCGGGGACCCAAAACAATGCGGCTTCTTTAACATGA 2497
Qy 2489 TGTGCCTGAAAGTACATTTTAACCATGACATATGCACTGAAGTGTACCATAAAAGCATCT 2548
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Db 2918 CCTGGATAAAGACACTTACAGCTAAATACTCCGGGGATTTCACGGCTTCATTGGACGACT 2977
Qy 2969 GGCAGCGCGAACACGACGCCATTATGGCACGCGTTCTTGATAAGCCGCAGACAGCTGATG 3028
Db 2978 GGCAACGCGAACACGACGCTATTATGGCACGCGTTCTTGATAAGCCGCAGACAGCTGATG 3037
Qy 3029 TGTTCCAGAATAAGGTGAACGTCTGCTGGGCGAAGGCTTTAGAGCCAGTCTTGGCCACGG 3088
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Qy 3449 CGTTGATCGTTGACCACAAAGGACAGGGTACAACTGATCACAGCGGATTCCTATCTAAGA 3508
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Qy 4169 CTAGACTTGTGAAGCACGAACCGCTCATCATACATGCTGTAGGACCCAATTTTTCTAAGA 4228
Db 4178 CTAGACTTGTGAAGCACGAACCGCTCATCATACATGCTGTAGGACCGAATTTTTCTAAGA 4237
Qy 4229 TGCCGGAACCGGAGGGCGACCTTAAGCTCGCAGCTGCCTACATGAGCATAGCGTCCATCG 4288
Db 4238 TGCCGGAACGAGAGGGCGACCTTAAGCTCGCAGCTGCCTACATGAGCATAGCGTCCATCG 4297

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Qy       4289 TCAACGCTGAGCGGATTACAAAAATATCAGTACCGCTACTGTCAACCGGCATCTATTCTG 4348
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Db       4298 TCAACGCTGAGCGGATTACTAAAATATCAGTACCGCTACTGTCAACTGGCATCTATTCTG 4357

Qy       4349 GTGGCAAAGATCGAGTGATGCAATCATTGCATCACCTGTTCACTGCTTTCGACACTACGG 4408
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Db       4358 GTGGCAAAGATCGAGTGATGCAATCATTGCATCACTTGTTCACTGCTTTCGACACTACGG 4417

Qy       4409 ATGCCGATGTCACCATATATTGCTTGGATAAACAATGGGAGACCAGGATAATCGAGGCCA 4468
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Qy       4469 TTCACCGCAAAGAAAGCGTCGAAATTCTG---GATGATGACAAGCCAGTAGACATTGACT 4525
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Qy       4646 AAATCCATGCAATGTGGCCCAACAAATCTGAGGCTAATGAGCAGATTTGCTTGTACATCC 4705
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Db       4658 AAATCCATGCAATGTGGCCCAACAAATCTGAGGCTAATGAGCAGATTTGCTTGTACATCC 4717

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Qy       4766 CTCCACCTCACACACTTCCATGCCTGTGTAATTACGCTATGACGGCTGAGCGCGTATACA 4825
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Qy       4946 TACCACCGGCTGTACACCCCAGGAAGTACGCGGAAATAATTCTAGAAACGCCACC 5000
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Db       4958 TACCACCGGCTGTACACCCCAGGAAGTACGCGGAAATAATTCTAGAAACGCCACC 5012
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RESULT 2
US-09-454-721A-3
; Sequence 3, Application US/09454721A
; Patent No. 6296854
; GENERAL INFORMATION:
;  APPLICANT:   Peter Pushko
;  APPLICANT:  Michael D. Parker
;  APPLICANT:  Jonathan F. Smith
;  APPLICANT:  Burce J. Crise
;  TITLE OF INVENTION:  Live Attenuated Venezuelan Equine Encephalitis Vaccine
;  FILE REFERENCE:  Army 146
; CURRENT APPLICATION NUMBER: US/09/454,721A
;  CURRENT FILING DATE:  1999-12-07
;  PRIOR APPLICATION NUMBER:  US 60/111,330
;  PRIOR FILING DATE:  1998-12-07
;  NUMBER OF SEQ ID NOS:  3
;  SOFTWARE:  Microsoft Word
; SEQ ID NO 3
;   LENGTH: 11459
;   TYPE: DNA
;   ORGANISM: Venezuelan Equine Encephalitis Virus
;   FEATURE:
US-09-454-721A-3
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  Best Local Similarity   64.5%;  Pred. No. 0;
  Matches 3219;  Conservative    0;  Mismatches 1745;  Indels   24;  Gaps    3;

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Db         30 AATTACCTACCCAAAATGGAGAAAGTTCACGTTGACATCGAGGAAGACAGCCCATTCCTC 89

Qy         70 AAGTCGTTACAGCGGACGTTTCCACAATTTGAGATCGAAGCAAGGCAGGTCACTGACAAT 129
              |   | || |||||||  || || || |||||| | ||||| | ||||||||||||| |||
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Db        390 ATGAAGGAGCTCGCCGCCGTCATGAGCGACCCTGACCTGGAAACTGAGACTATGTGCCTC 449

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Qy        544 ATAGGCTTTGACACGACCCCTTTTATGTACAAAAACATGGCAGGTTCCTACCCTACTTAC 603
              |||||||||||||| ||||||||||||   || ||| |||| ||  | || ||  | |||
Db        570 ATAGGCTTTGACACCACCCCTTTTATGTTTAAGAACTTGGCTGGAGCATATCCATCATAC 629

Qy        604 AACACGAACTGGGCTGACGAGAGAGTATTGGAAGCACGTAACATTGGCCTCGGTAACTCA 663
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Qy        664 GATCTTCAGGAGAGCAGGCTTGGAAAACTCTCAATCCTTAGGAAGAAGAGGCTCCAACCT 723
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Db        690 GACGTTATGGAGCGGTCACGTAGAGGGATGTCCATTCTTAGAAAGAAGTATTTGAAACCA 749

Qy        724 ACTAATAAGATCATATTCTCGGTTGGTTCAACAATCTACACAGAAGATAGATCACTGTTA 783
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Db        750 TCCAACAATGTTCTATTCTCTGTTGGCTCGACCATCTACCACGAGAAGAGGGACTTACTG 809

Qy        784 CGTAGCTGGCATCTTCCAAACGTGTTCCACTTGAAAGGAAAGTCTAACTTCACAGGTAGA 843
              | |||||||| || ||    || || |||||     || |||   || | |||| || |
Db        810 AGGAGCTGGCACCTGCCGTCTGTATTTCACTTACGTGGCAAGCAAAATTACACATGTCGG 869

Qy        844 TGTGGGACCATTGTCAGCTGTGAAGGGTACGTCATCAAAAAGATAACGATCAGCCCAGGA 903
              |||| ||| || || || || || ||||||||| | ||||  ||| | ||||| |||||
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Qy        904 CTATACGGTAAAGTTGAGAACTTGGCGTCCACAATGCATCGCGAGGGTTTCTTGAGTTGC 963
              || ||. || ||    |      || ||  | || ||||| |||||||| |||||| | |||
Db        930 CTGTATGGGAAGCCTTCAGGCTATGCTGCTACGATGCACCGCGAGGGATTCTTGTGCTGC 989

Qy        964 AAAGTCACAGATACGCTGCGCGGCGAGAGGGTTTCTTTTGCTGTGTGTACGTATGTACCA 1023
              ||||| ||||| ||  ||  ||| |||||||| |||||| | ||||| |||||||| |||
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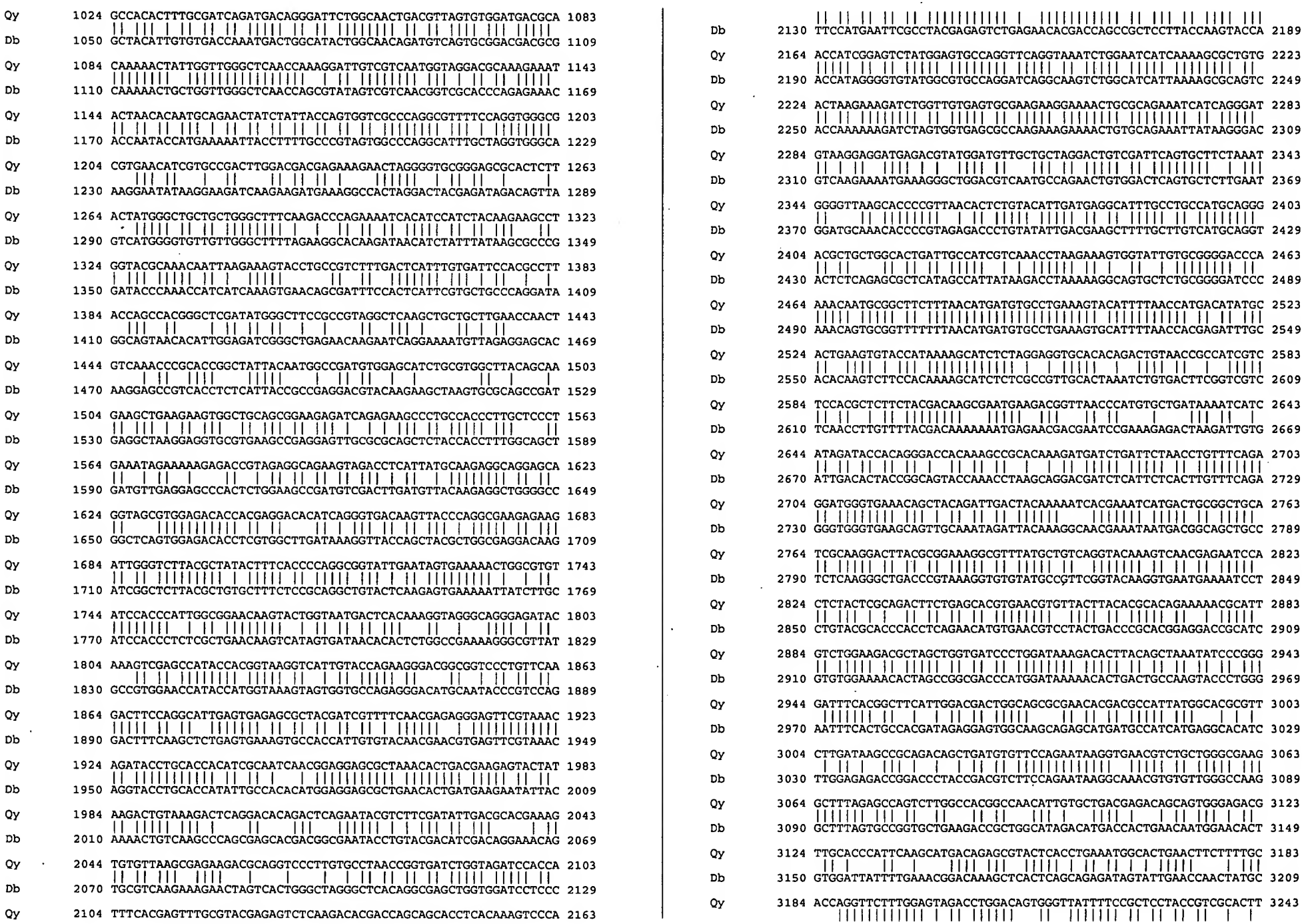

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Db       3270 TCCATTAGGAATAATCACTGGGATAACTCCCCGTCGCCTAACATGTACGGGCTGAATAAA 3329
Qy       3304 GAGGTAGCAAAGGAGTTGTCACGGCGATATCCGTGCATCACAAAAGCGGTTGACACAGGC 3363
Db       3330 GAAGTGGTCCGTCAGCTCTCTCGCAGGTACCCACAACTGCCTCGGGCAGTTGCCACTGGA 3389
Qy       3364 AGGGTAGCTGATATAAGGAATAATACCATCAAGGACTACTCTCCAACAATTAATGTGGTT 3423
Db       3390 AGAGTCTATGACATGAACACTGGTACACTGCGCAATTATGATCCGCGCATAAACCTAGTA 3449
Qy       3424 CCATTAAATCGCCGGTTGCCCCACTCGTTGATCGTTGACCACAAAGGACAGGGTACAACT 3483
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Qy       3604 TGTGATCTCGATTTGGGAATACCTAGCCATGTCGGTAAATATGACATTATCTTTGTCAAT 3663
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Qy       3664 GTTAGGACCCCGTACAGGAACCATCACTACCAACAGTGCGAGGATCACGCTATCCACCAC 3723
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Qy       3784 GGGTATGGGCTTGCTGATCGCGCAACCGAGAATATCATCACTGCGGTGGCACGCTCATTT 3843
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Db       4170 TTACAGCCGATCGAAGTAGGAAAAGCGCGACTGGTCAAAGGTGCAGCTAAACATATCATT 4229
Qy       4201 CATGCTGTAGGACCCAATTTTTCTAAGATGCCGGAACCGGAGGGCGACCTTAAGCTCGCA 4260
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Qy       4321 CCGCTACTGTCAACCGGCATCTATTCTGGTGGCAAAGATCGAGTGATGCAATCATTGCAT 4380
Db       4350 CCACTGTTGTCCACCGGCATCTTTTCCGGAAACAAAGATCGACTAACCCAATCATTGAAC 4409
Qy       4381 CACCTGTTCACTGCTTTCGACACTACGGATGCCGATGTCACCATATATTGCTTGGATAAA 4440
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Qy       4441 CAATGGGAGACCAGGATAATCGAGGCCATTCACCGCAAAGAAAGCGTCGAAATTCTGGA- 4499
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Db       4590 AGTTCTTTGGCTGGAAGGAAGGGCTACAGCACAAGCGATGGCAAAACTTTCTCATATTTG 4649
Qy       4606 GAAGGTACACGATTCCATCAGACCGCCAAGGACATTGCCGAAATCCATGCAATGTGGCCC 4665
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Qy       4666 AACAAATCTGAGGCTAATGAGCAGATTTGCTTGTACATCCTGGGGGAGAGTATGTCCAGC 4725
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Qy       4966 AGGAAGTA 4973
Db       5010 AGGAAGTA 5017
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RESULT 3
US-08-991-840A-2
; Sequence 2, Application US/08991840A
; Patent No. 6261570
; GENERAL INFORMATION:
; APPLICANT: Michael D. Parker
; APPLICANT: Jonathan F. Smith
; APPLICANT: Bruce Crise
; APPLICANT: Mark Steve Oberste
; APPLICANT: Shannon Schmura
; TITLE OF INVENTION: Live Attenuated Virus Vaccines for Eastern Equine Encephalitis
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: USA MRMC - MRMC-JA
; CITY: FORT DETRICK, FREDERICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5

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;      SOFTWARE:  Microsoft Word 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/991,840A
;      FILING DATE:  December 16, 1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  Provisional Application 60/047162,
;      FILING DATE:  May 20, 1997
;      APPLICATION NUMBER:  Provisional Application 60/053,652
;      FILING DATE:  July 24, 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Charles H. Harris
;      REGISTRATION NUMBER:  34,616
;      REFERENCE/DOCKET NUMBER:  003/058/SAP RIID 96-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 619-2065
;      TELEFAX:  (301) 619-5034
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11464 base pairs
;      TYPE:  Nucleic acid
;      STRANDEDNESS:  Double
;      TOPOLOGY:  Unknown
US-08-991-840A-2

  Query Match             41.5%;  Score 2074.8;  DB 3;  Length 11464;
  Best Local Similarity   64.1%;  Pred. No. 0;
  Matches 3202;  Conservative    0;  Mismatches 1772;  Indels   24;  Gaps    4;

Qy          1 ACCCTACAAACTAATCGATCCAATATGGAAAGAATTCACGTTGACTTAGATGCTGACAGC 60
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Db         20 AGCCCAAACCAATAACTACCCAAAATGGAGAAAGTTCACGTTGACATCGAGGAAGATAGT 79

Qy         61 CCGTATGTCAAGTCGTTACAGCGGACGTTTCCACAATTTGAGATCGAAGCAAGGCAGGTC 120
              ||  |   |||   | ||||| ||||  || || || |||||| | ||||| | |||||||
Db         80 CCCTTCCTCAGAGCATTACAACGGAGCTTCCCGCAGTTTGAGGTAGAAGCCAAGCAGGTC 139

Qy        121 ACTGACAATGACCATGCCAATGCCAGAGCGTTTTCGCATGTGGCAACAAAGCTCATTGAG 180
              || || |||||||||||| || ||||||||||||||||||| ||||| | ||  | || |||
Db        140 ACAGATAATGACCATGCTAACGCCAGAGCGTTTTCGCATTTGGCATCGAAATTGATCGAG 199

Qy        181 AGCGAAGTCGACCGGGACCAAGTTATCTTGGACATTGGAAGTGCGCCCGTCAGACATGCA 240
              |  || || || |    | |    ||| | ||||||||||||||||| | | |
Db        200 ACGGAGGTGGAACCATCCGATACGATCCTAGACATTGGAAGTGCGCCTGCCCGCAGAATG 259

Qy        241 CATTCCAATCACCGCTATCATTGTATCTGCCCTATGATAAGCGCTGAAGACCCGGACAGA 300
              ||||||| ||     || ||||| ||||| || |||| | | || ||||| |||||||||
Db        260 TATTCCAAGCATAAGTACCATTGCATCTGTCCGATGAAATGTGCAGAAGATCCGGACAGA 319

Qy        301 CTACAACGGTATGCAGAAAGACTTAAGAAAAGT------GACATTACCGACAAGAACATA 354
              ||       |||||||  |  || ||||| |         || ||||| || ||| |  |
Db        320 CTGTTTAAGTATGCAGCCAAGCTGAAGAAGAACTGTAAAGAGATTACAGATAAGGAACTG 379

Qy        355 GCCTCTAAGGCGGCAGACCTGCTGGAAGTCATGTCAACACCAGACGCAGAGACTCCATCT 414
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Db        380 GACAAGAAGATGAAGGAGCTTGCGGAAGTCATGAGCGACCCTGATCTCGAAACTGAAACG 439

Qy        415 CTGTGTATGCACACAGACGCCACGTGTAGGTACTTTGGAAGTGTAGCAGTATACCAAGAT 474
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Db        440 ATTTGCCTTCACGACGATGAAACCTGTCGATTTGAGGGTCAAGTCGCAGTGTATCAGGAT 499

Qy        475 GTGTACGCAGTCCATGCACCGACATCAATCTACCACCAGGCGCTTAAAGGAGTTAGGACA 534
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Qy        535 ATTTACTGGATAGGCTTTGACACGACCCCTTTTATGTACAAAAACATGGCAGGTTCCTAC 594
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Db        680 TGCAGCTCCGATGTGATGGAGCGGTCACGTAGAGGGATGTCCATCCTCAGAAAGAAATTT 739

Qy        715 CTCCAACCTACTAATAAGATCATATTCTCGGTTGGTTCAACAATCTACACAGAAGATAGA 774
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Qy        775 TCACTGTTACGTAGCTGGCATCTTCCAAACGTGTTCCACTTGAAAGGAAAGTCTAACTTC 834
              |  || | || ||||| || ||   ||| || ||| |   || |||   || | |
Db        800 GACTTACTAAGGAGTTGGCACCTACCGTCCGTTTTTCACCTACGTGGTAAGCAGAATTAC 859

Qy        835 ACAGGTAGATGTGGGACCATTGTCAGCTGTGAAGGGTACGTCATCAAAAAGATAACGATC 894
              ||  || | |||| ||| || || || || || ||||||||| |||||| |||| | ||
Db        860 ACTTGTCGGTGTGAGACTATAGTTAGTTGCGACGGGTACGTCGTCAAAAGGATAGCTATT 919

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Qy        955 TTGAGTTGCAAAGTCACAGATACGCTGCGCGGCGAGAGGGTTTCTTTTGCTGTGTGTACG 1014
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Db        980 TTGTGCTGCAAGGTGACGGACACGCTTGACGGGGAGAGGGTCTCTTTCCCCGTATGCACG 1039

Qy       1015 TATGTACCAGCCACACTTTGCGATCAGATGACAGGGATTCTGGCAACTGACGTTAGTGTG 1074
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Db       1040 TACGTGCCAGCCACATTGTGCGACCAAATGACAGGCATTCTGGCAACAGATGTCAGTGCA 1099

Qy       1075 GATGACGCACAAAAACTATTGGTTGGGCTCAACCAAAGGATTGTCGTCAATGGTAGGACG 1134
              || ||||| || ||| |  ||||||||||||||||  | || |||||  |||||  | ||
Db       1100 GACGACGCGCAGAAATTGCTGGTTGGGCTCAACCAGCGAATAGTCGTAAATGGCCGCACT 1159

Qy       1135 CAAAGAAATACTAACACAATGCAGAACTATCTATTACCAGTGGTCGCCCAGGCGTTTTCC 1194
              ||||| |||||||||||||||| |||||||| |||||||| || || || || || ||| ||
Db       1160 CAAAGGAATACTAACACAATGAAGAACTATTTATTACCCGTCGTGGCACAAGCATTTGCC 1219

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Db       1220 AGATGGGCTAAAGAGTACACAGAAGATCAAGAAGATGAAAGACCATTGGGGCTTAGGGAC 1279

Qy       1255 CGCACTCTTACTATGGGCTGCTGCTGGGCTTTCAAGACCCAGAAAATCACATCCATCTAC 1314
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Qy       1315 AAGAAGCCTGGTACGCAAACAATTAAGAAAGTACCTGCCGTCTTTGACTCATTTGTGATT 1374
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Db       1460 GAGGAACCTGTGGACAGACCACCACTGATTACCGCCGACGACATACAGGAAGCCAAGAAC 1519

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Db       1520 GCGGCGGATGAGGCTAAGGAAGTCAAGGAGGCCGAAGAGCTCAGGGCAGCATTACCACCG 1579

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Db       1580 CTGTCTGCCGATGTAGAGGAACCTGCACTGGAGGCGGACGTTGACTTAATGCTGCAGGAG 1639

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Qy       1675 GAAGAGAAGATTGGGTCTTACGCTATACTTTCACCCCAGGCGGTATTGAATAGTGAAAAA 1734
              ||||| || ||||| ||||| ||  | || || || || || || ||| ||   |||||||||
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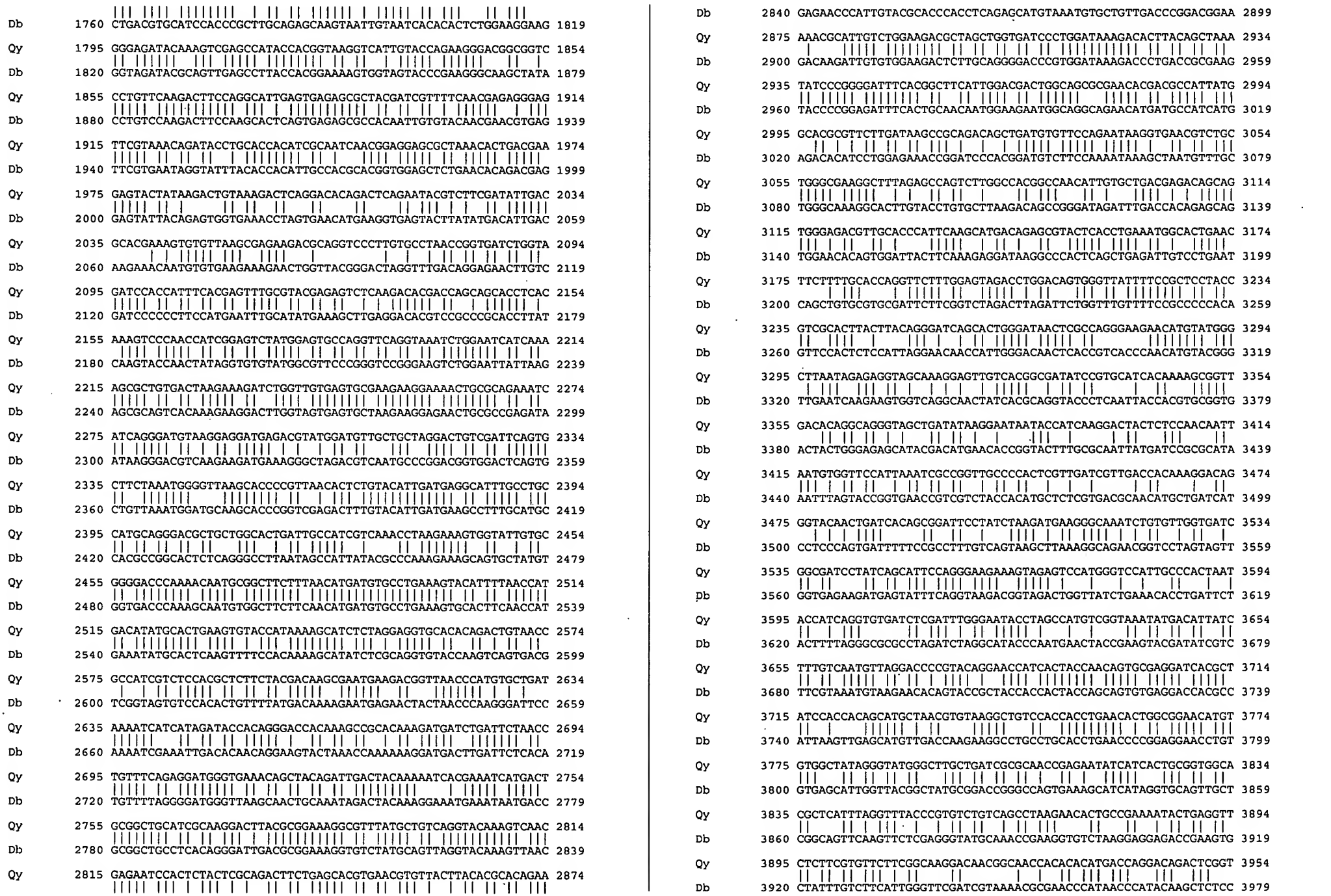

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Db       4580 CACCCTAAGAGCTCTTTGGCTGGAAGGAAAGGTTACAGCACTAGCGATGGGAAGACATTC 4639

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RESULT 4
US-07-920-281C-1
; Sequence 1, Application US/07920281C
; Patent No. 5739026
;  GENERAL INFORMATION:
;    APPLICANT:  Garoff, Henrik
;    APPLICANT:  Liljestrom, Peter
;    TITLE OF INVENTION:  DNA Expression Systems Based on
;    TITLE OF INVENTION:  Alphaviruses
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Birch, Stewart, Kolasch & Birch
;      STREET:  P.O. Box 747
;      CITY:  Falls Church
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22040-0747
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/920,281C
;      FILING DATE:  13-AUG-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy Jr., Gerald M.
;      REGISTRATION NUMBER:  28,977
;      REFERENCE/DOCKET NUMBER:  828-103P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-241-1300
;      TELEFAX:  703-241-2848
;      TELEX:  248345
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11517 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Semliki Forest Virus
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US-07-920-281C-1

  Query Match           31.3%;  Score 1564;  DB 1;  Length 11517;
  Best Local Similarity  58.3%;  Pred. No. 0;
  Matches 2904;  Conservative    0;  Mismatches 2040;  Indels   36;  Gaps    8;

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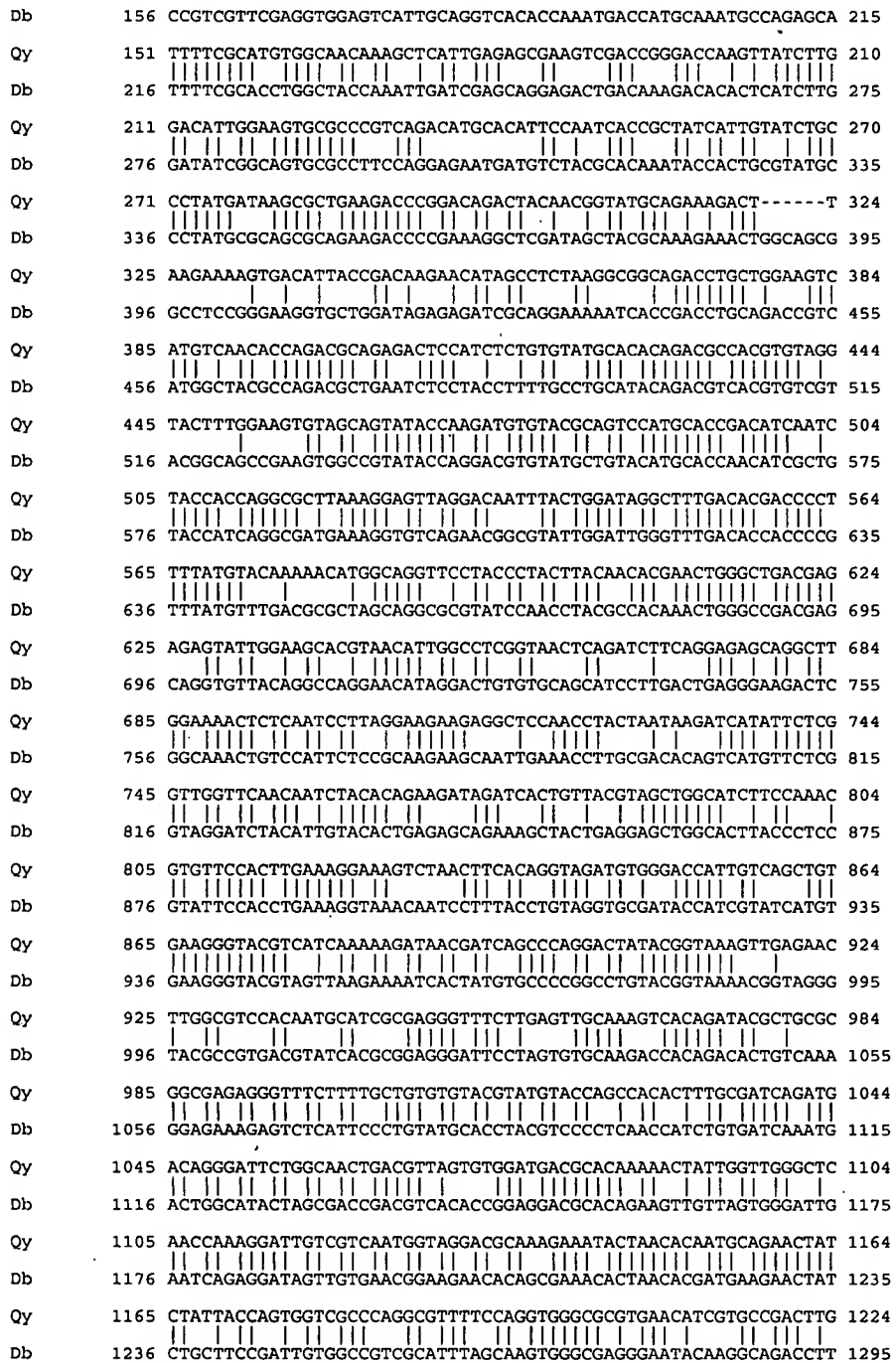
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Qy 1879 AGTGAGAGCGCTACGATCGTTTTCAACGAGAGGGAGTTCGTAAACAGATACCTGCACCAC 1938
Db 1953 AGCGAGAGCGCCACTATGGTGTACAACGAAAGGGAGTTCGTCAACAGGAAACTATACCAT 2012
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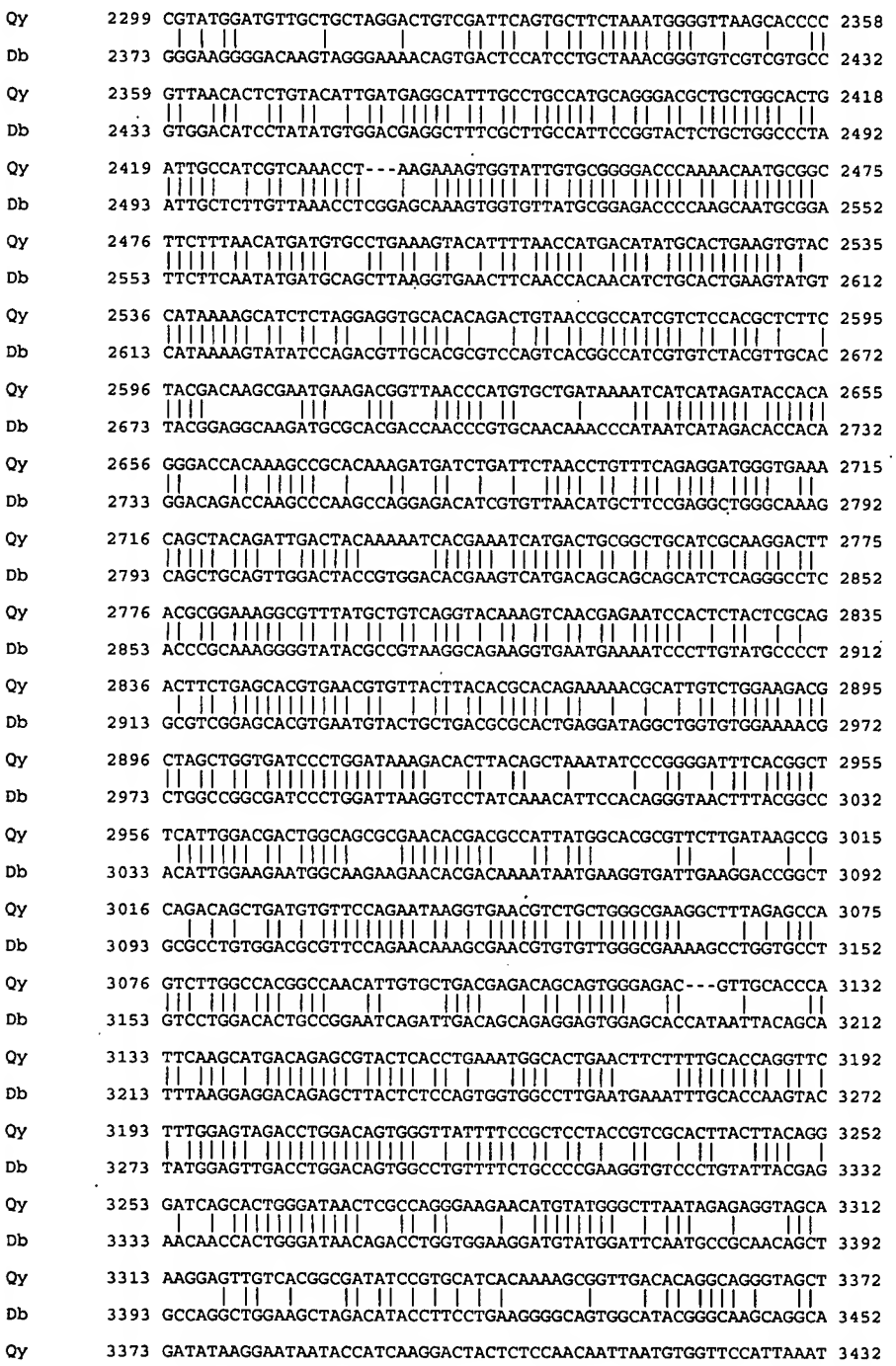
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;                   Liljestrom, Peter
;        TITLE OF INVENTION: DNA Expression Systems Based on
;                            Alphaviruses
;        NUMBER OF SEQUENCES: 27
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Birch, Stewart, Kolasch & Birch
;             STREET: P.O. Box 747
;             CITY: Falls Church
;             STATE: Virginia
;             COUNTRY: USA
;             ZIP: 22040-0747
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/466,277
;             FILING DATE: 06-Jun-1995
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 07/920,281
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Murphy Jr., Gerald M.
;             REGISTRATION NUMBER: 28,977
;             REFERENCE/DOCKET NUMBER: 828-103P
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 703-241-1300
;             TELEFAX: 703-241-2848
;             TELEX: 248345
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;             LENGTH: 11517 base pairs
;             TYPE: nucleic acid
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;             TOPOLOGY: linear
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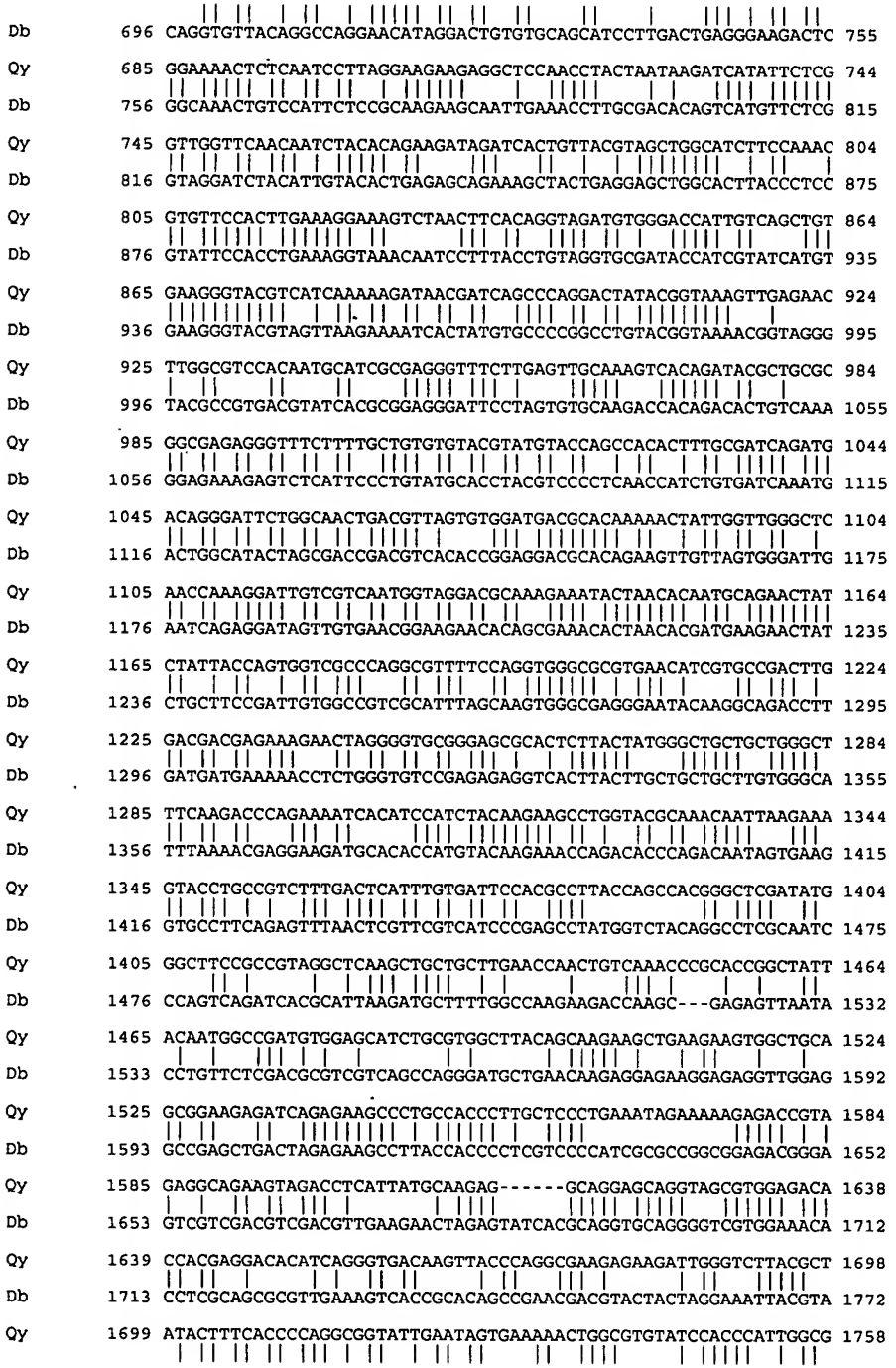
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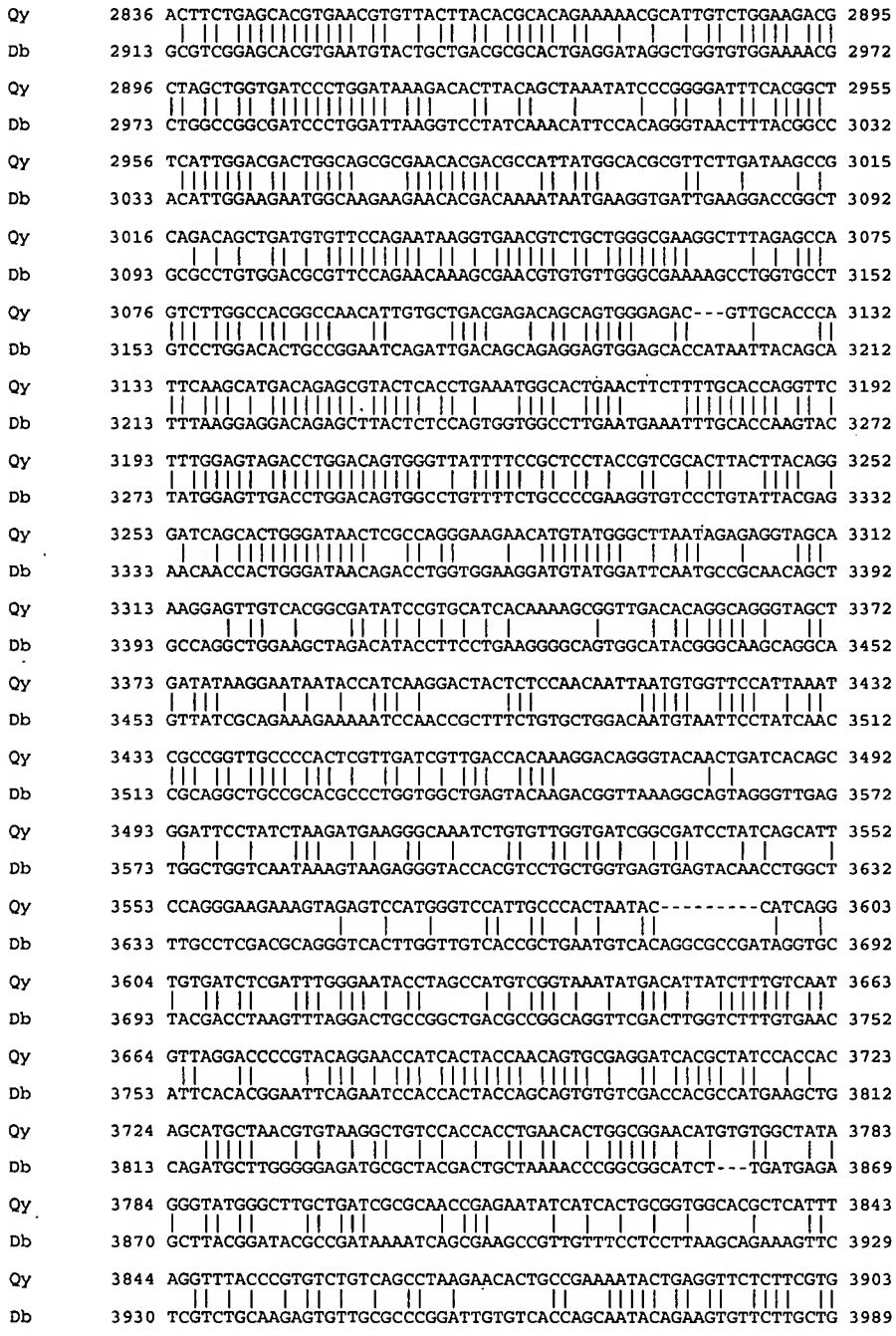

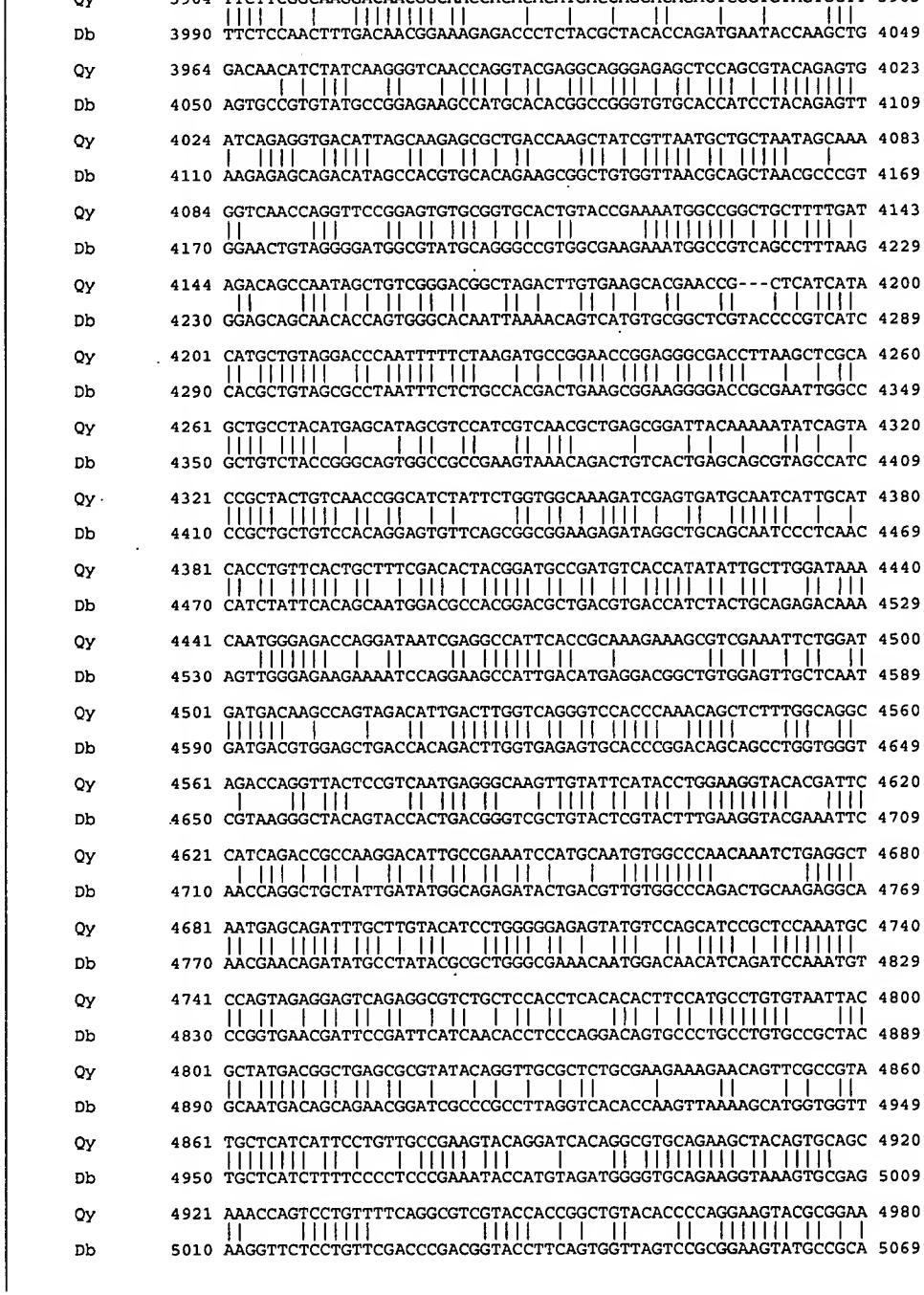

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; Patent No. 6475780
; GENERAL INFORMATION:
;  APPLICANT: Parrington, Mark
;  APPLICANT:  Li, Xiaomao
;  APPLICANT:  Klein, Michel H.
;  TITLE OF INVENTION: ALPHAVIRUS VECTORS FOR PARAMYXOVIRUS VACCINES
;  FILE REFERENCE: 1038-1042 MIS
;  CURRENT APPLICATION NUMBER: US/09/554,337
;  CURRENT FILING DATE:  2000-10-20
;  PRIOR APPLICATION NUMBER: 60/065,791
;  PRIOR FILING DATE: 1997-11-14
;  PRIOR APPLICATION NUMBER: PCT/CA98/01064
;  PRIOR FILING DATE: 1998-11-13
;  NUMBER OF SEQ ID NOS: 7
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;   ORGANISM: respiratory syncytial virus
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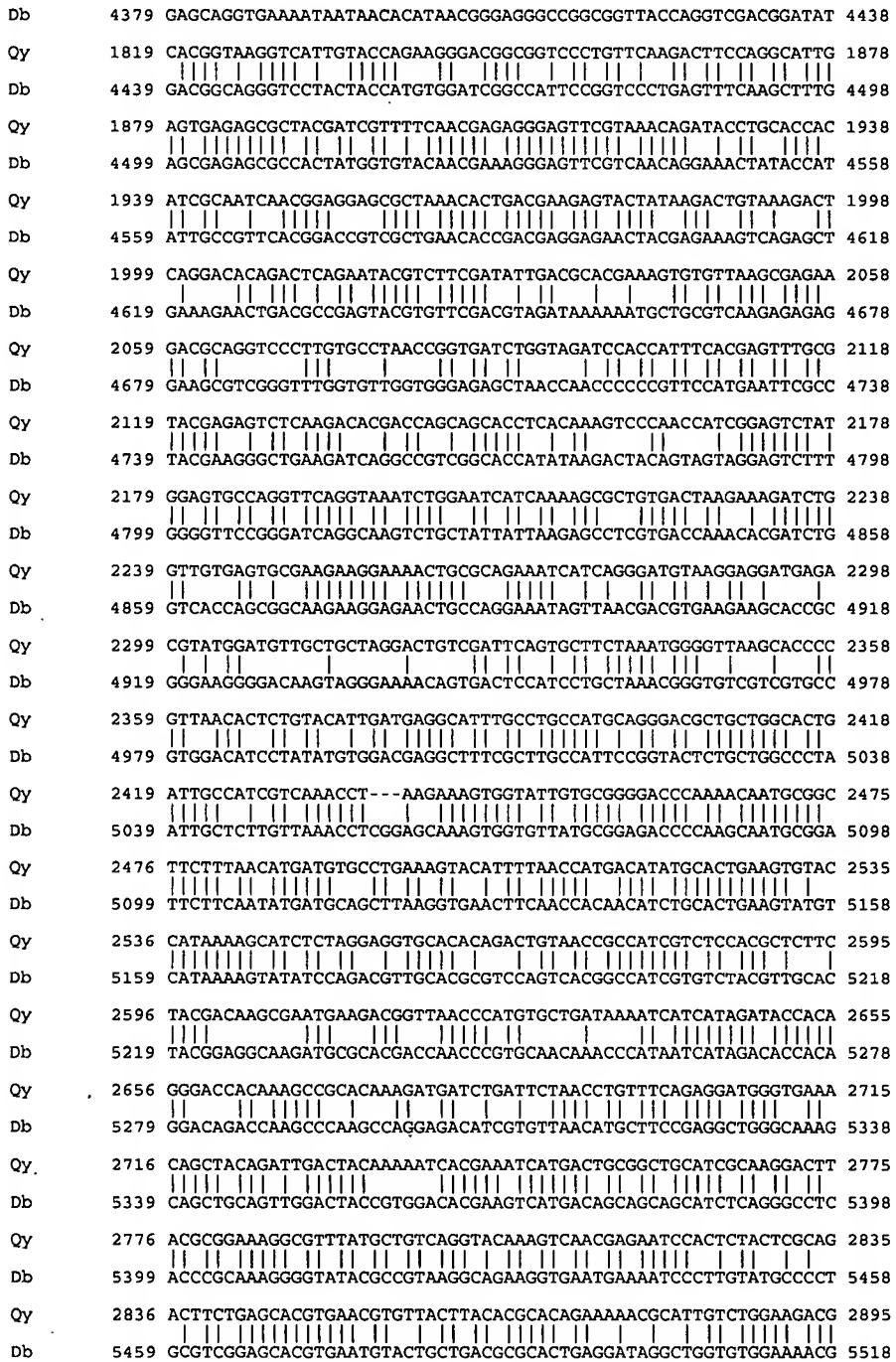
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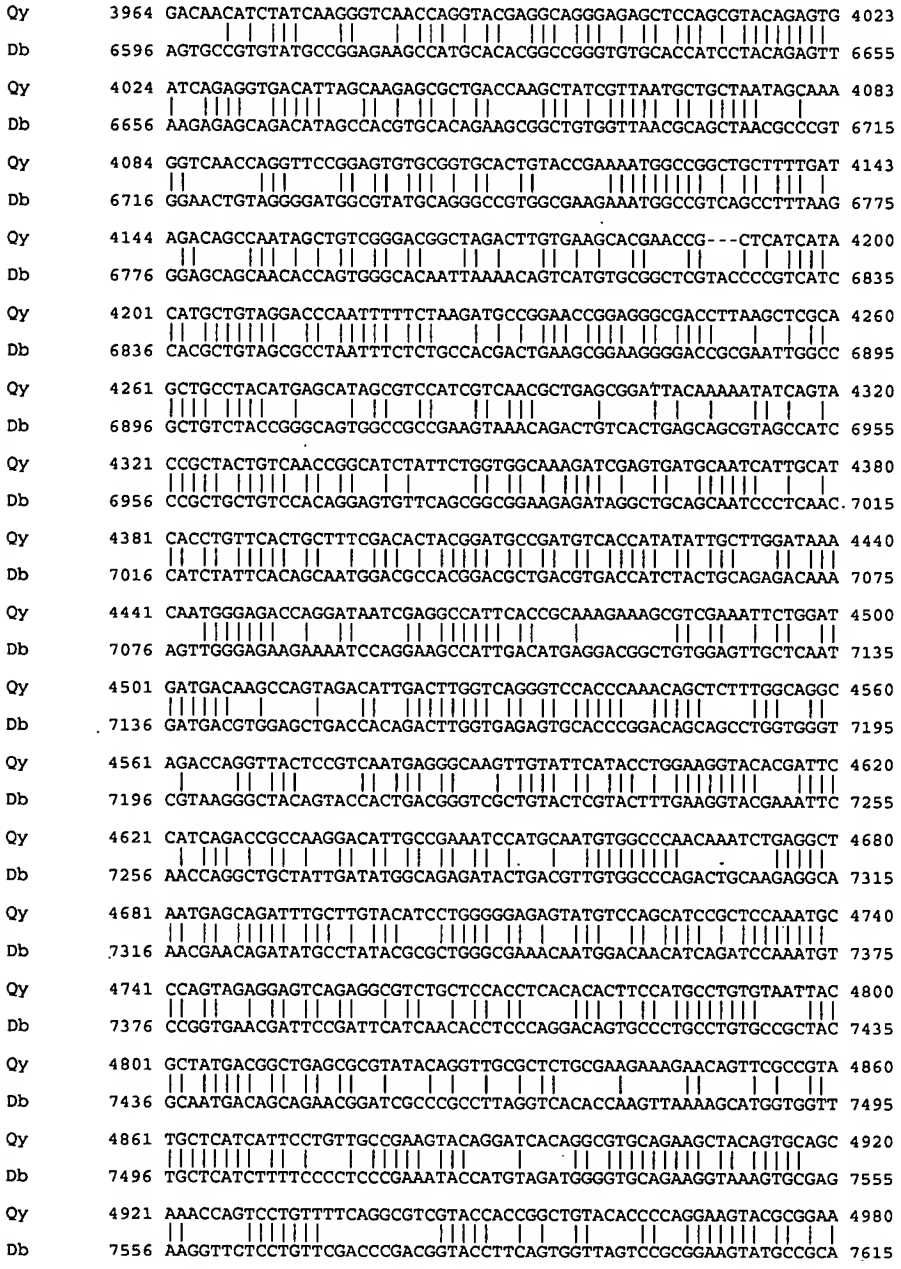

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; Sequence 4, Application US/09554337
; Patent No. 6475780

; GENERAL INFORMATION:
; APPLICANT: Parrington, Mark
; APPLICANT: Li, Xiaomao
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: ALPHAVIRUS VECTORS FOR PARAMYXOVIRUS VACCINES
; FILE REFERENCE: 1038-1042 MIS
; CURRENT APPLICATION NUMBER: US/09/554,337
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/065,791
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: PCT/CA98/01064
; PRIOR FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
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; TYPE: DNA
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US-09-554-337-4

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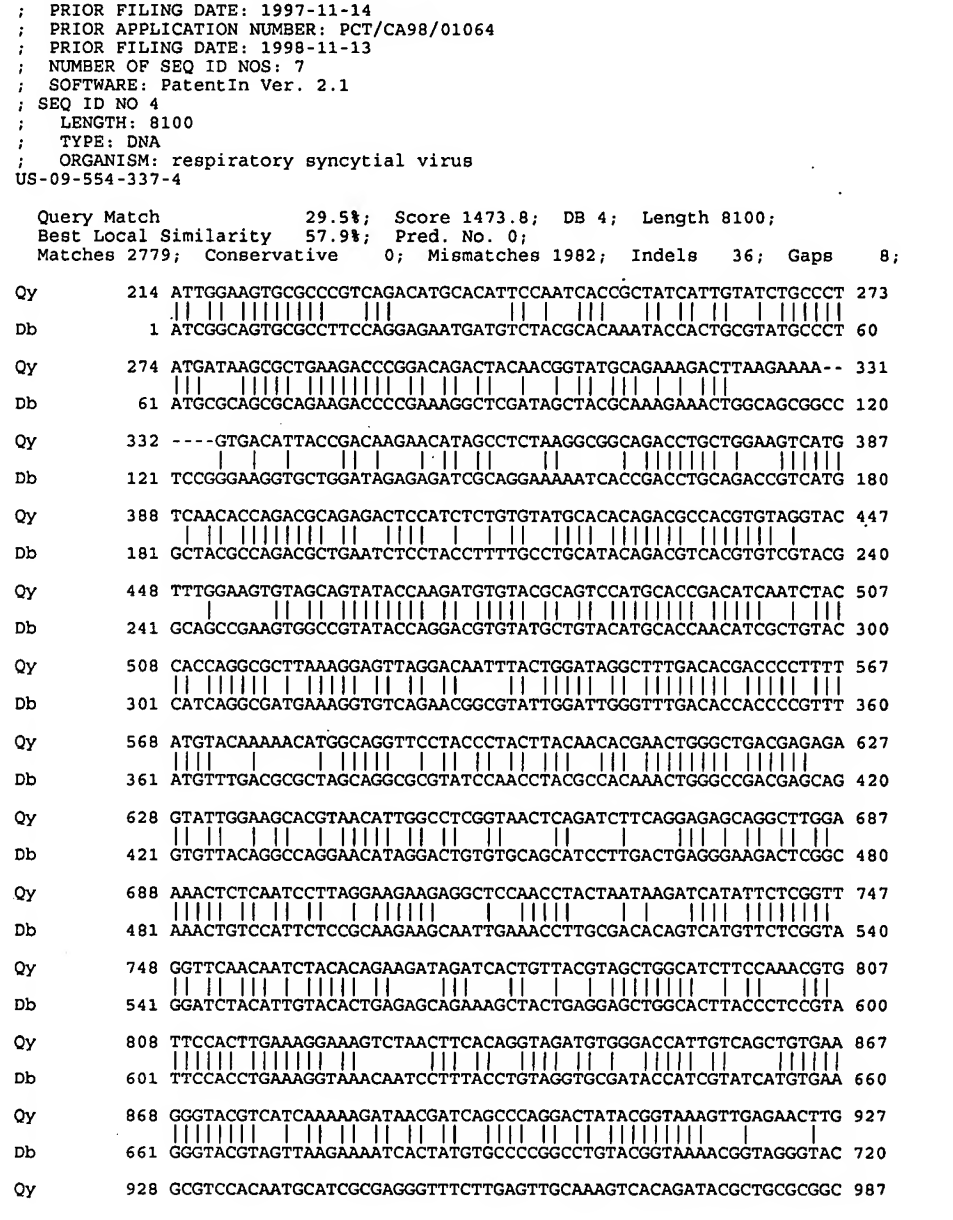

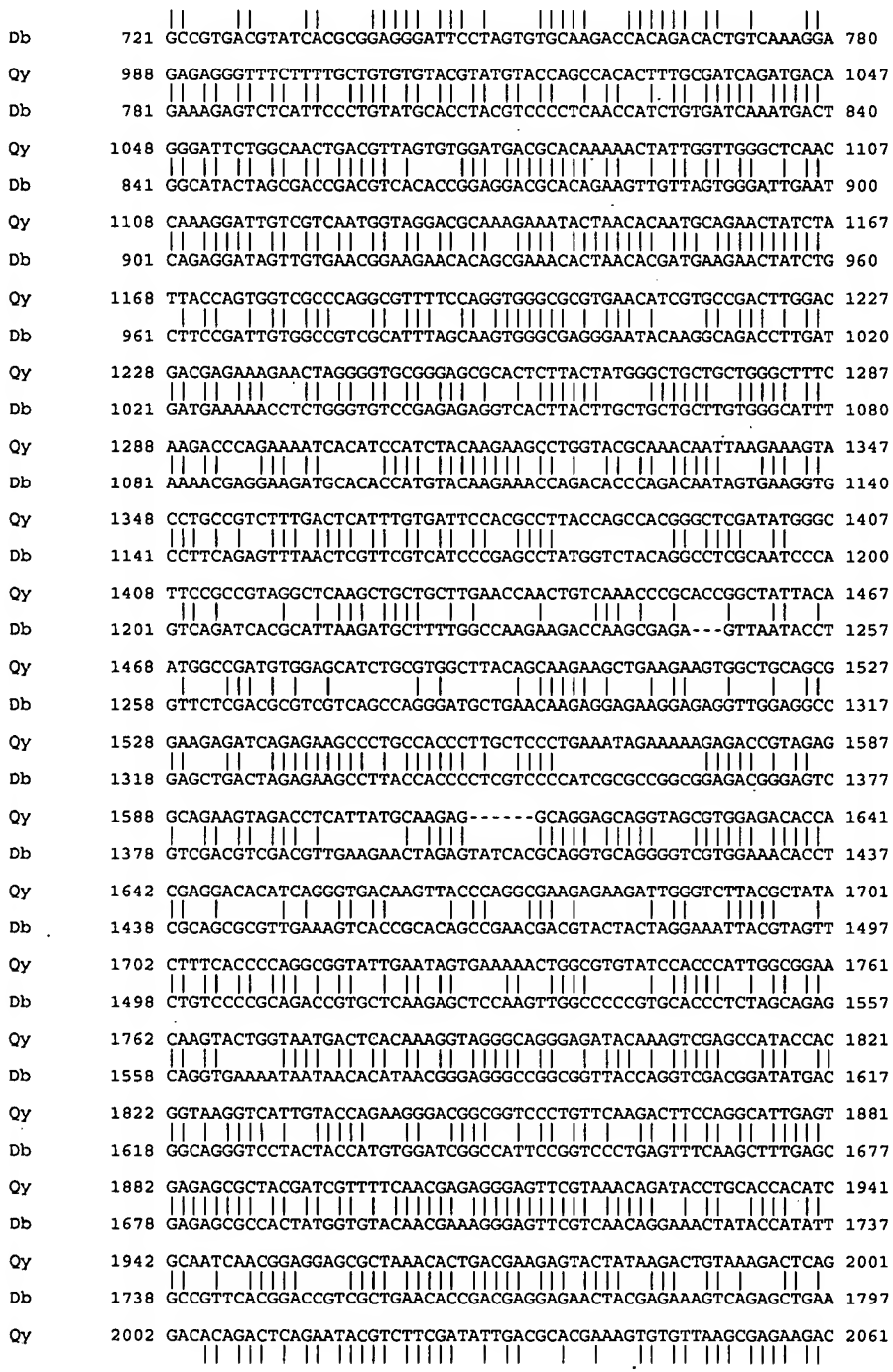
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Db 2458 CAGACCAAGCCCAAGCCAGGAGACATCGTGTTAACATGCTTCCGAGGCTGGGCAAAGCAG 2517
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Qy 2839 TCTGAGCACGTGAACGTGTTACTTACACGCACAGAAAAACGCATTGTCTGGAAGACGCTA 2898
Db 2638 TCGGAGCACGTGAATGTACTGCTGACGCGCACTGAGGATAGGCTGGTGTGGAAAACGCTG 2697
Qy 2899 GCTGGTGATCCCTGGATAAAGACACTTACAGCTAAATATCCCGGGGATTTCACGGCTTCA 2958
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Qy 2959 TTGGACGACTGGCAGCGCGAACACGACGCCATTATGGCACGCGTTCTTGATAAGCCGCAG 3018
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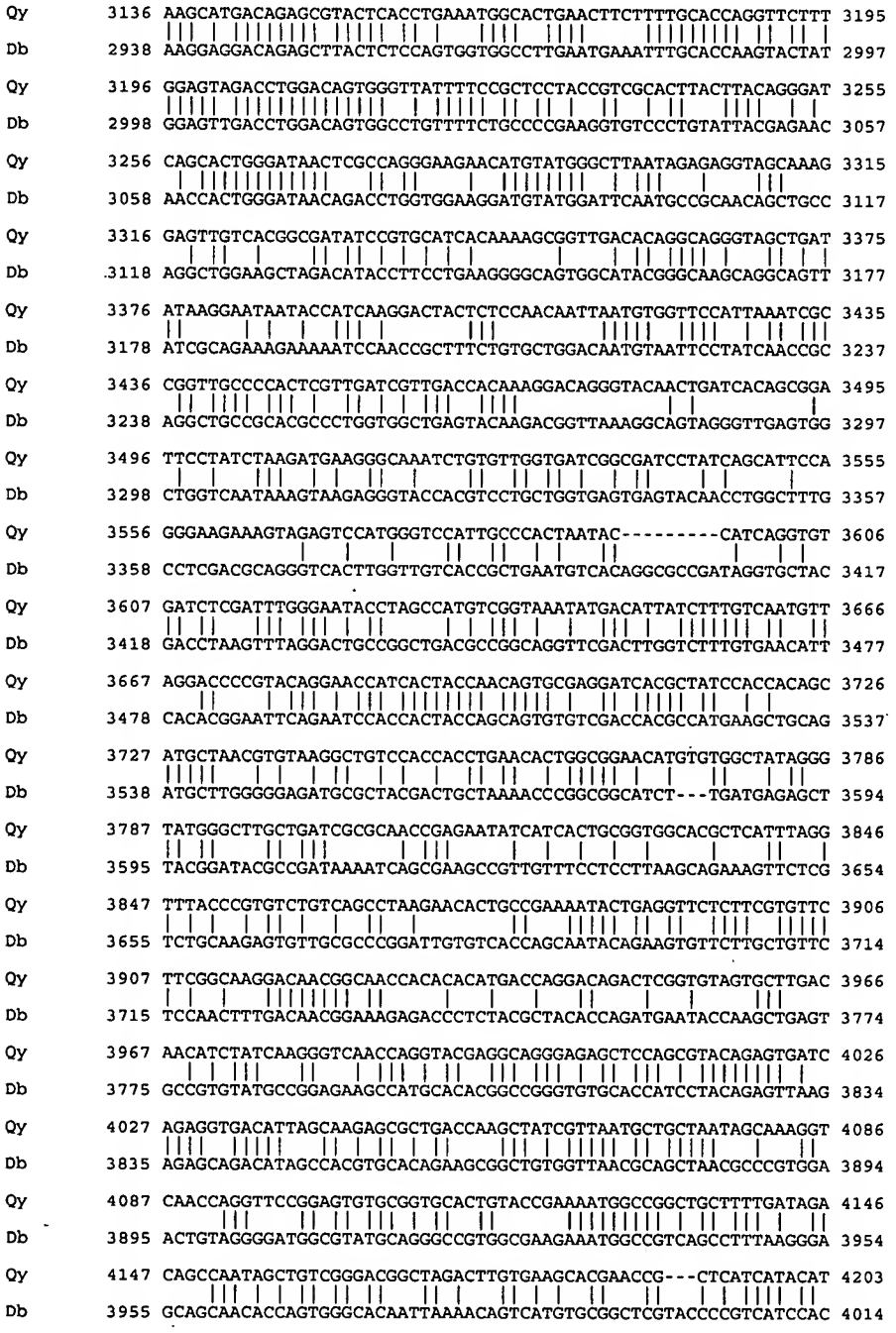

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; Sequence 1, Application US/08446932
; Patent No. 5639650
; GENERAL INFORMATION:
; APPLICANT: Johnston, Robert E.
; APPLICANT: Simpson, Dennis
; APPLICANT: Davis, Nancy L.
; TITLE OF INVENTION: cDNA Clone for South African
; TITLE OF INVENTION: Arbovirus No. 5639650 86
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: NC
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,932
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5470-118
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919) 881-3140
;      TELEFAX:  (919) 881-3175
;      TELEX:  575102
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11663 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
US-08-446-932-1

  Query Match             26.7%;  Score 1333.2;  DB 1;  Length 11663;
  Best Local Similarity   56.1%;  Pred. No. 0;
  Matches 2820;  Conservative    0;  Mismatches 2128;  Indels   80;  Gaps   13;

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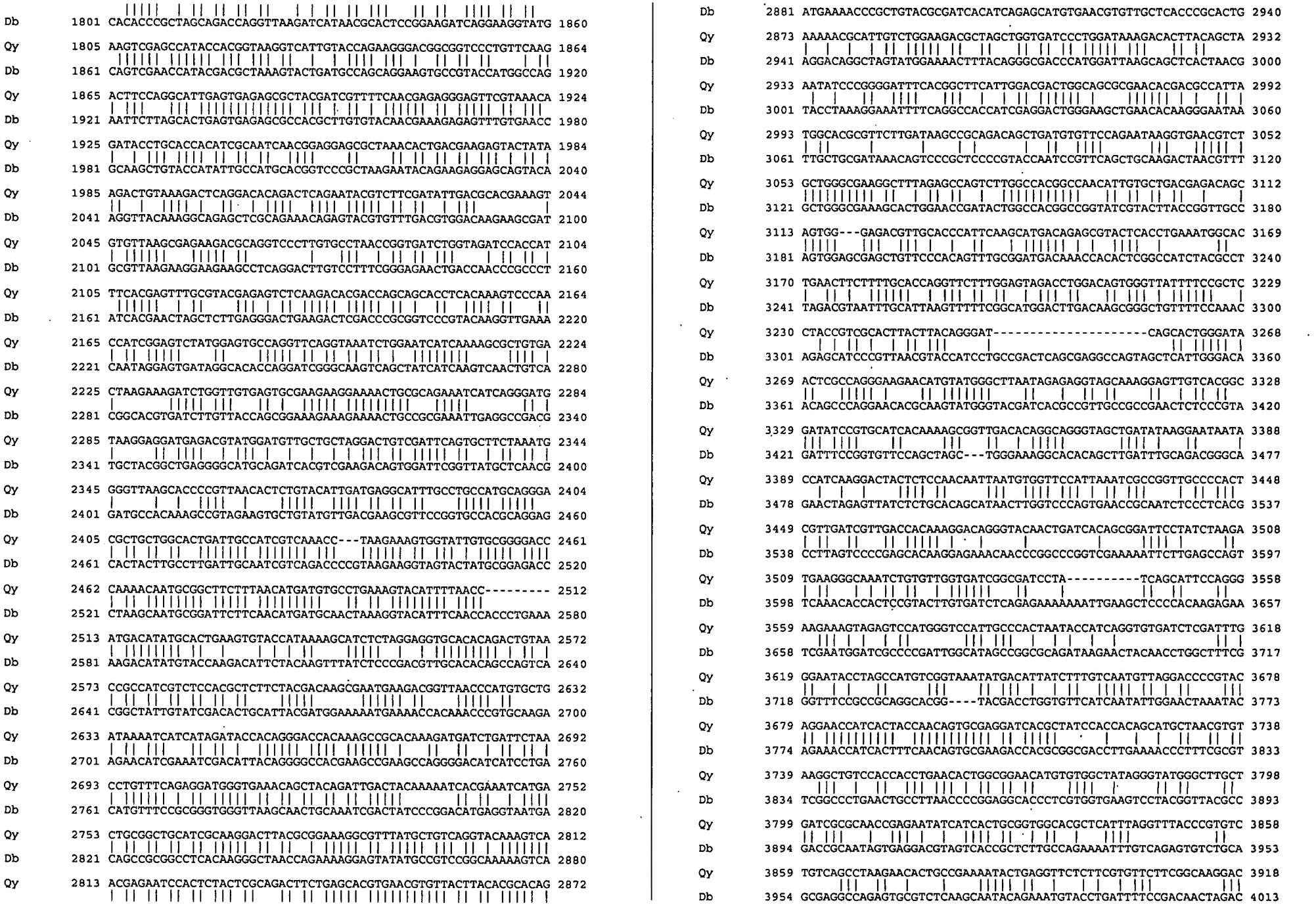

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; Sequence 1, Application US/08801263A
; Patent No. 5811407
;  GENERAL INFORMATION:
;    APPLICANT:  Johnston, Robert E.
;    APPLICANT:  Davis, Nancy L.
;    APPLICANT:  Simpson, Dennis A.
;    TITLE OF INVENTION:  System for the In Vivo Delivery and
;    TITLE OF INVENTION:  Expression of Heterologous Genes in the Bone Marrow
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell Seltzer Park & Gibson, P.A.
;      STREET:  1211 East Morehead Street
;      CITY:  Charlotte
;      STATE:  No. 5811407th Carolina
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/801,263A
;      FILING DATE:  19-FEB-1997
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5470-147
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-420-2200
;      TELEFAX:  919-881-3175
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11663 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
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;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  7608..11342
US-08-801-263A-1

  Query Match             26.7%;  Score 1333.2;  DB 1;  Length 11663;
  Best Local Similarity   56.1%;  Pred. No. 0;
  Matches 2820;  Conservative    0;  Mismatches 2128;  Indels   80;  Gaps   13;

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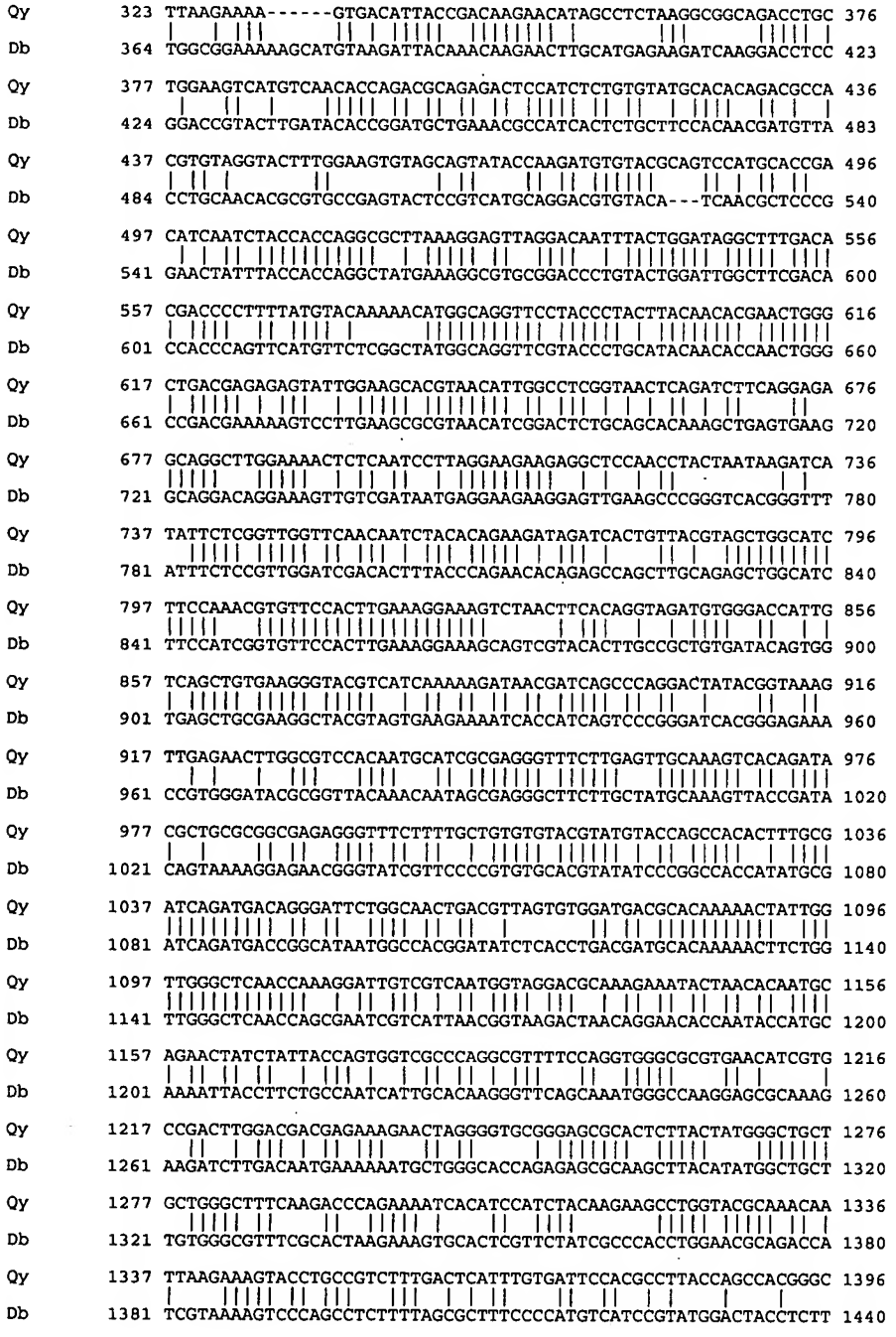
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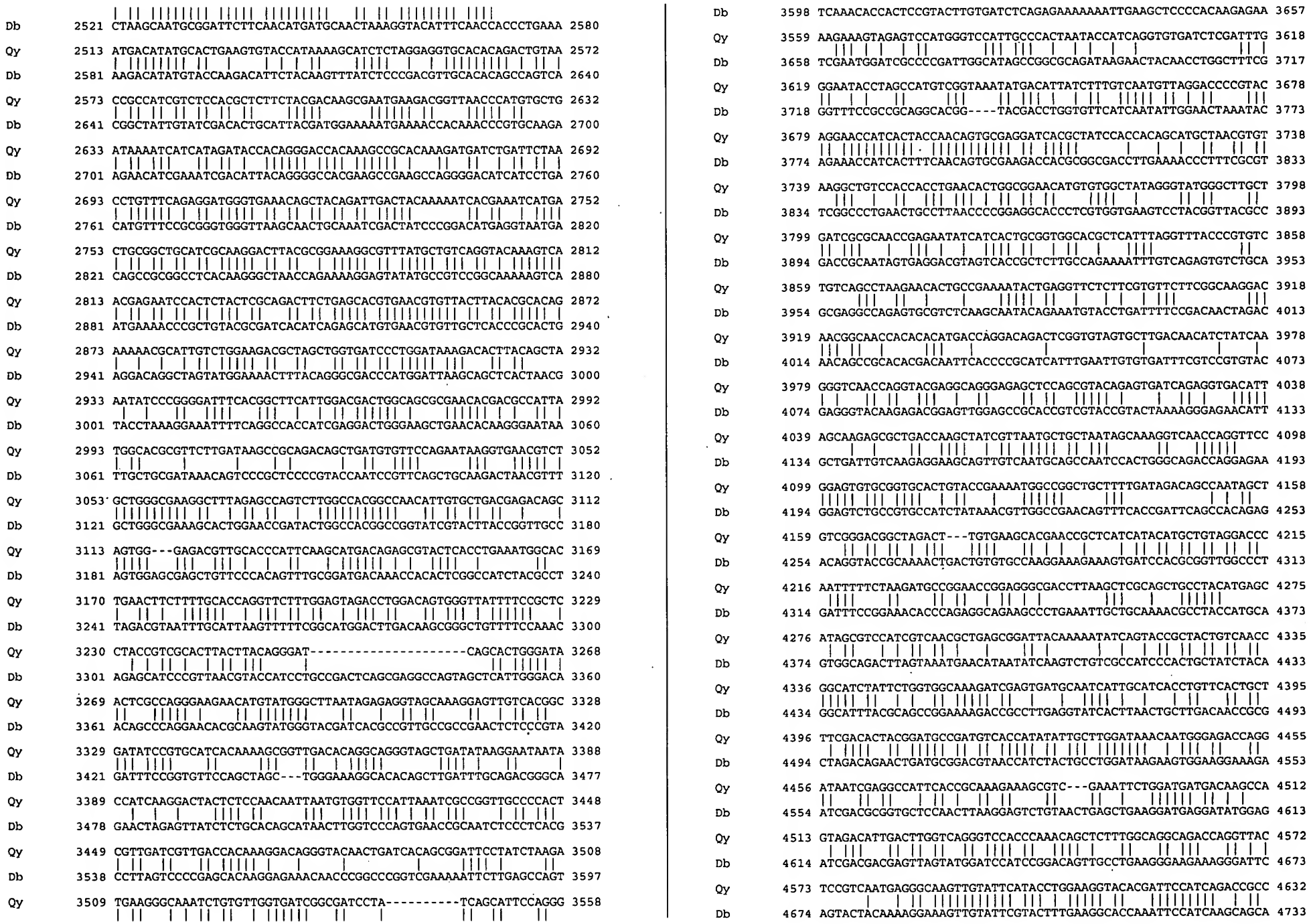

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; Sequence 7, Application US/08801263A
; Patent No. 5811407
;  GENERAL INFORMATION:
;    APPLICANT:  Johnston, Robert E.
;    APPLICANT:  Davis, Nancy L.
;    APPLICANT:  Simpson, Dennis A.
;    TITLE OF INVENTION:  System for the In Vivo Delivery and
;    TITLE OF INVENTION:  Expression of Heterologous Genes in the Bone Marrow
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell Seltzer Park & Gibson, P.A.
;      STREET:  1211 East Morehead Street
;      CITY:  Charlotte
;      STATE:  No. 5811407th Carolina
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/801,263A
;      FILING DATE:  19-FEB-1997
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5470-147
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-420-2200
;      TELEFAX:  919-881-3175
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11663 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-801-263A-7

  Query Match             26.7%;  Score 1333.2;  DB 1;  Length 11663;
  Best Local Similarity   56.1%;  Pred. No. 0;
  Matches 2820;  Conservative    0;  Mismatches 2128;  Indels   80;  Gaps   13;
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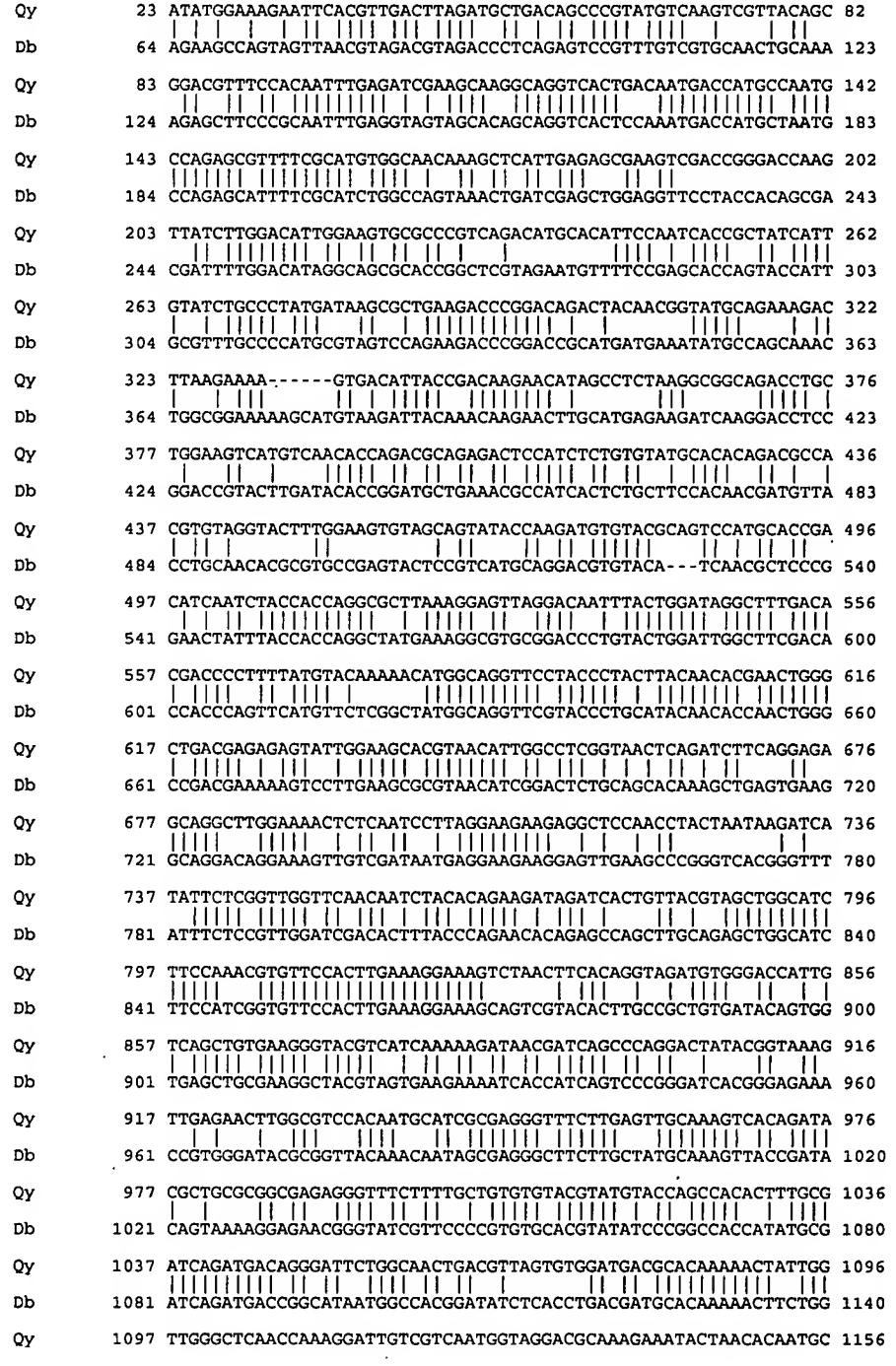

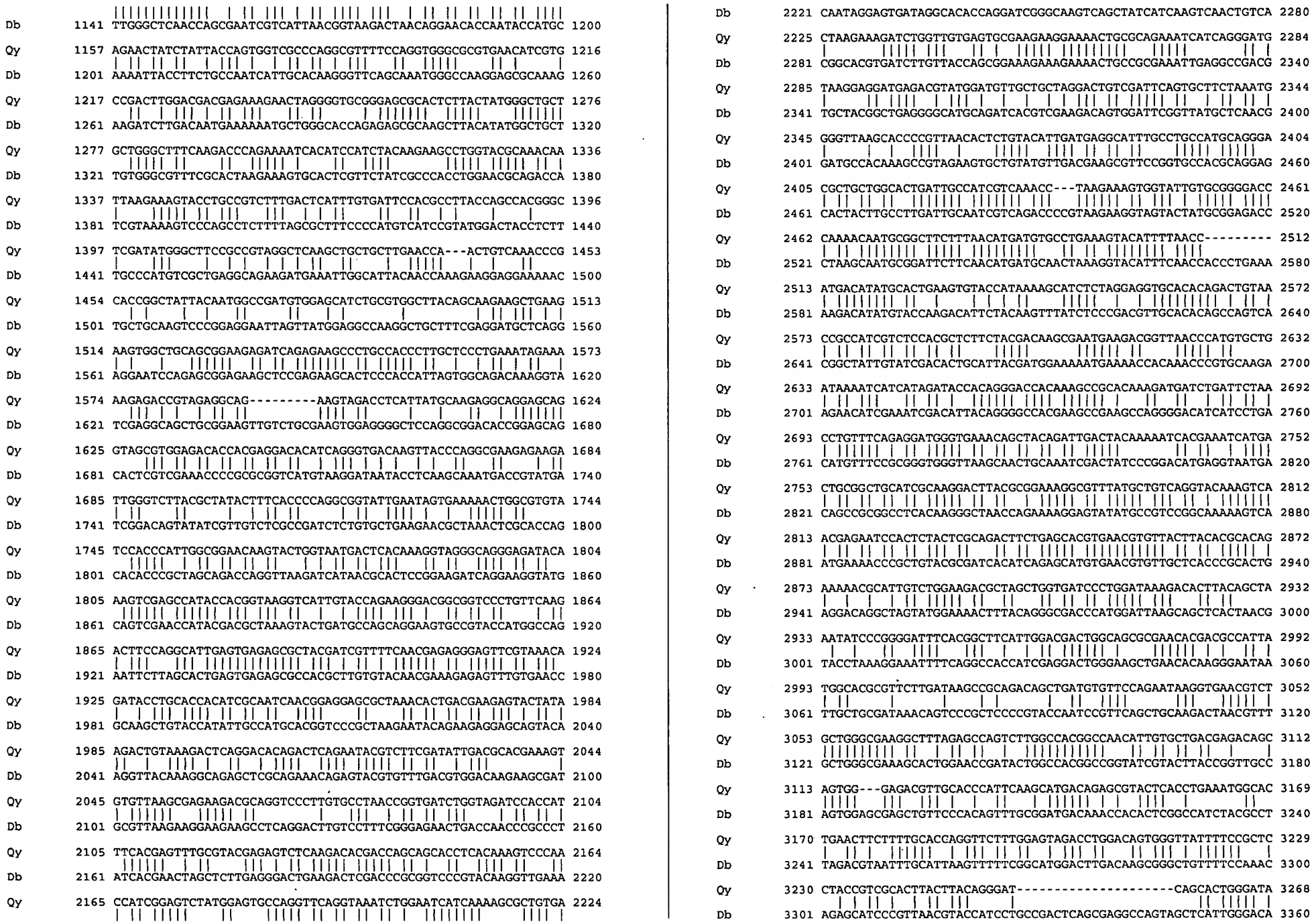

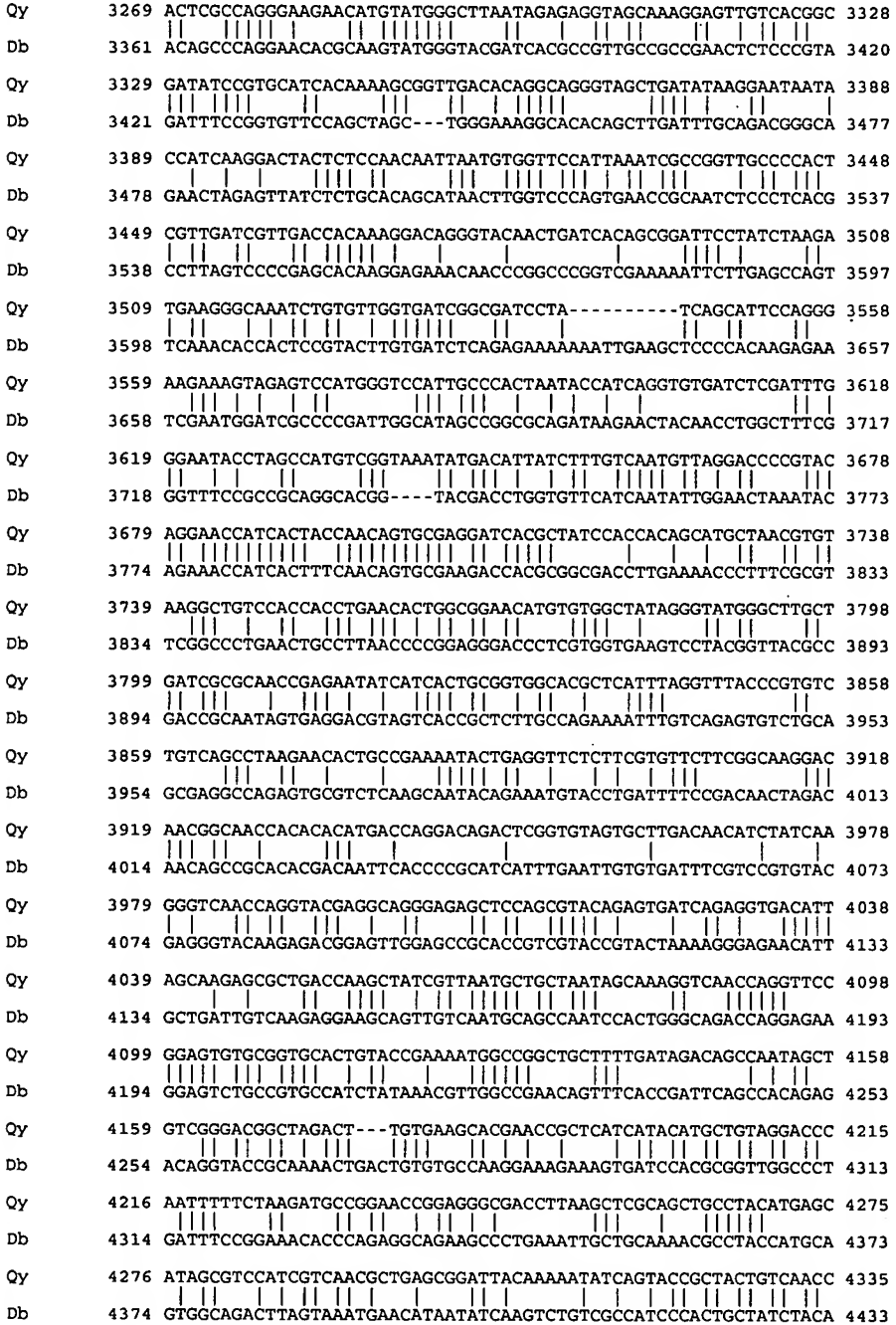

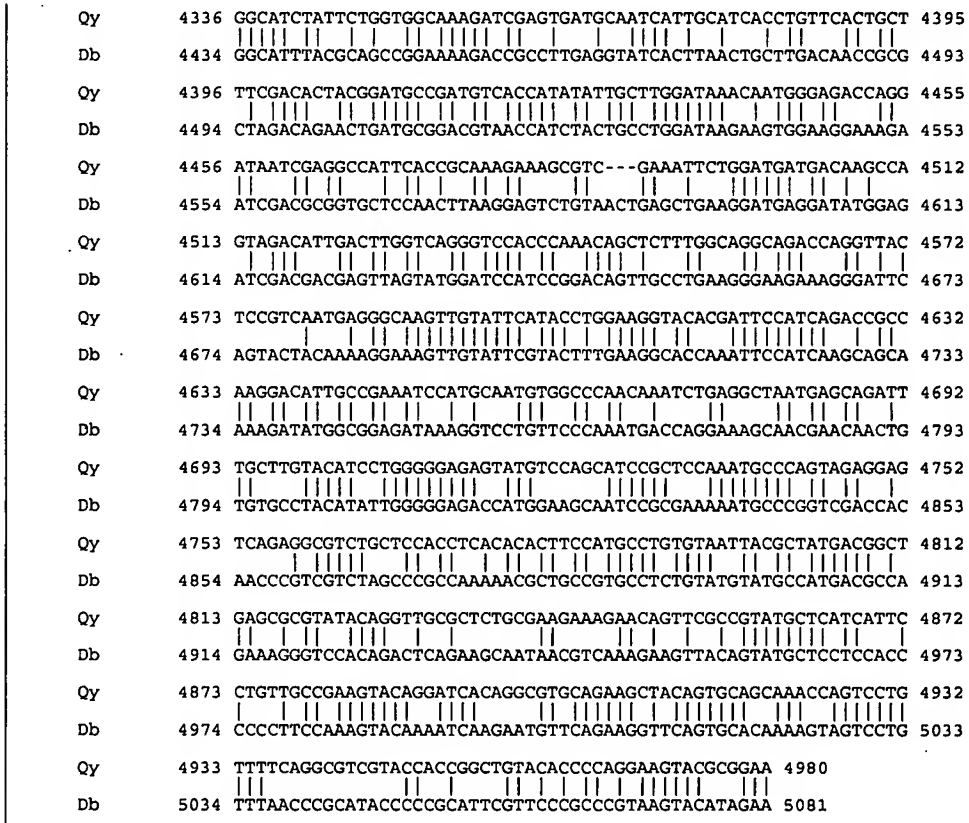

RESULT 11
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; Sequence 1, Application US/09102248
; Patent No. 6008035
; GENERAL INFORMATION:
; APPLICANT: Johnston, Robert E.
; APPLICANT: Davis, Nancy L.
; APPLICANT: Simpson, Dennis A.
; TITLE OF INVENTION: System for the In Vivo Delivery and
; TITLE OF INVENTION: Expression of Heterologous Genes in the Bone Marrow
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell Seltzer Park & Gibson, P.A.
; STREET: 1211 East Morehead Street
; CITY: Charlotte
; STATE: No. 6008035th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,248
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

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;     APPLICATION NUMBER:  US 08/801,263
;       FILING DATE:  19-FEB-1997
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Sibley, Kenneth D.
;       REGISTRATION NUMBER:  31,665
;       REFERENCE/DOCKET NUMBER:  5470-147
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  919-420-2200
;       TELEFAX:  919-881-3175
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  11663 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
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;       LOCATION:  7608..11342
US-09-102-248-1

  Query Match           26.7%;  Score 1333.2;  DB 3;  Length 11663;
  Best Local Similarity  56.1%;  Pred. No. 0;
  Matches 2820;  Conservative    0;  Mismatches 2128;  Indels   80;  Gaps   13;

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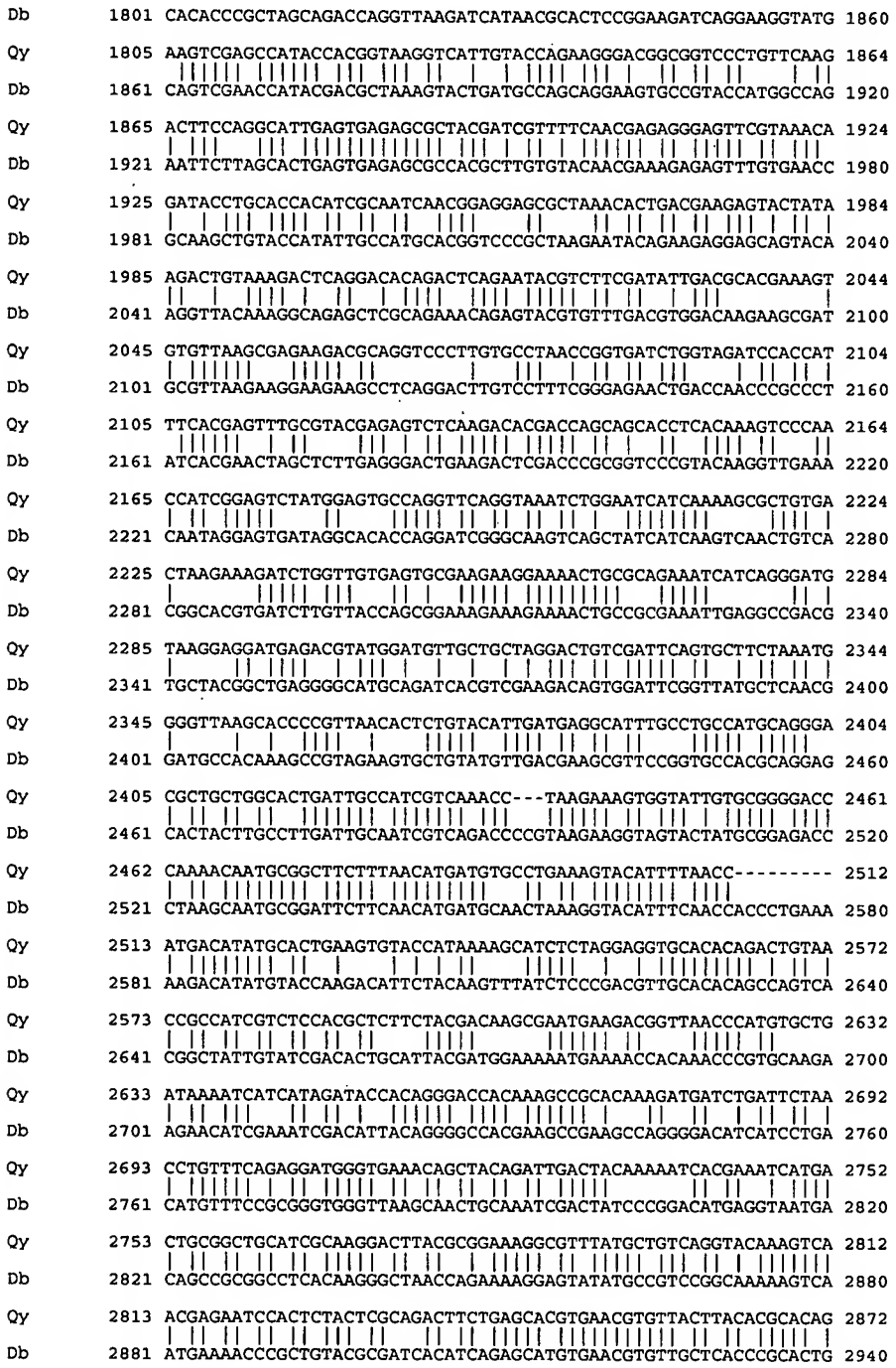
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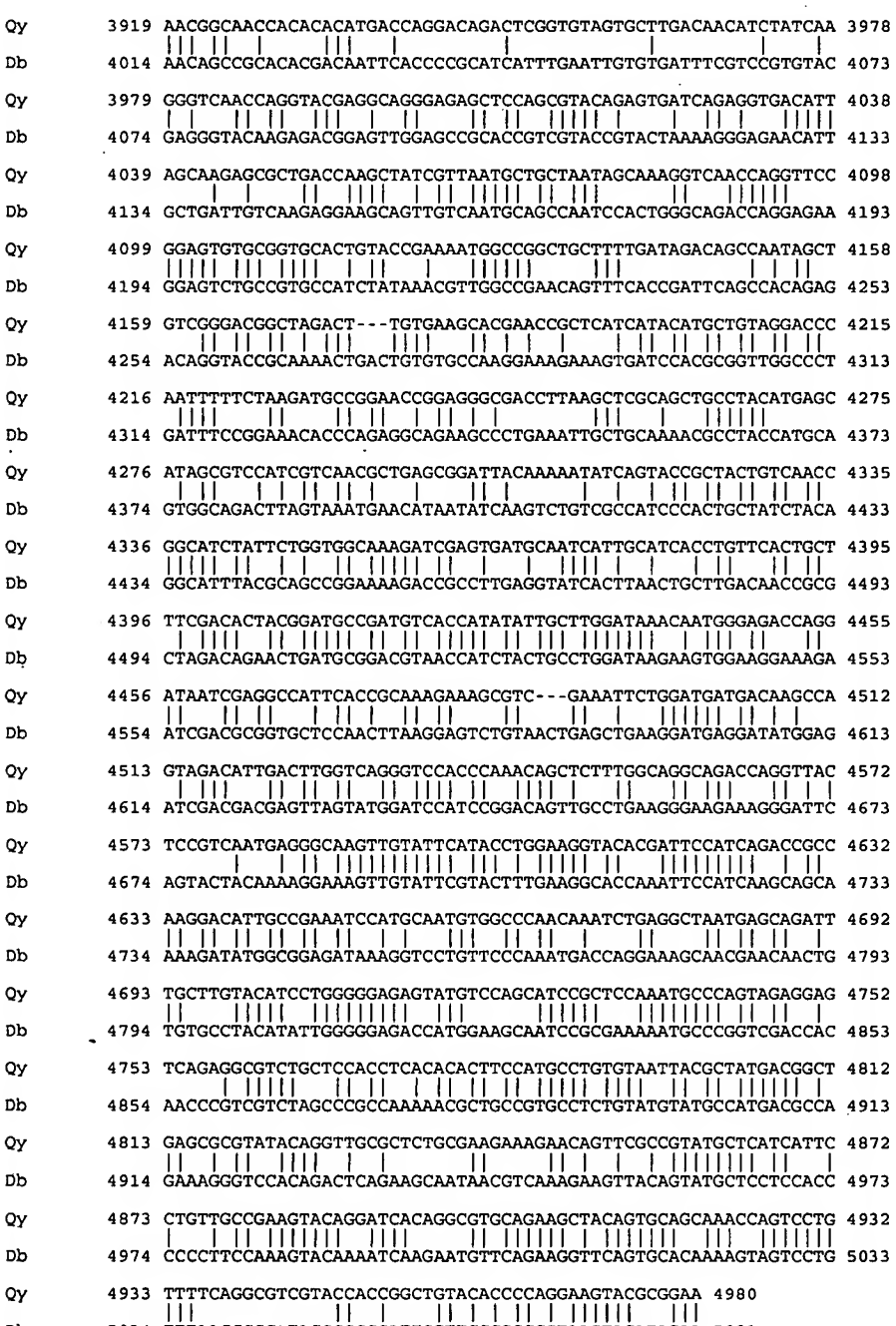

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; Sequence 7, Application US/09102248
; Patent No. 6008035
;  GENERAL INFORMATION:
;    APPLICANT:  Johnston, Robert E.
;    APPLICANT:  Davis, Nancy L.
;    APPLICANT:  Simpson, Dennis A.
;    TITLE OF INVENTION:  System for the In Vivo Delivery and
;    TITLE OF INVENTION:  Expression of Heterologous Genes in the Bone Marrow
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell Seltzer Park & Gibson, P.A.
;      STREET:  1211 East Morehead Street
;      CITY:  Charlotte
;      STATE:  No. 6008035th Carolina
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/102,248
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/801,263
;      FILING DATE:  19-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5470-147
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-420-2200
;      TELEFAX:  919-881-3175
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11663 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-102-248-7

  Query Match             26.7%;  Score 1333.2;  DB 3;  Length 11663;
  Best Local Similarity   56.1%;  Pred. No. 0;
  Matches 2820;  Conservative    0;  Mismatches 2128;  Indels   80;  Gaps   13;
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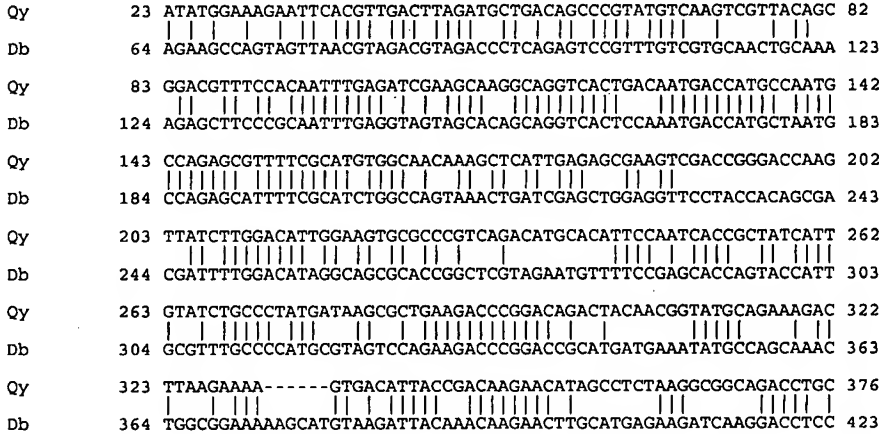

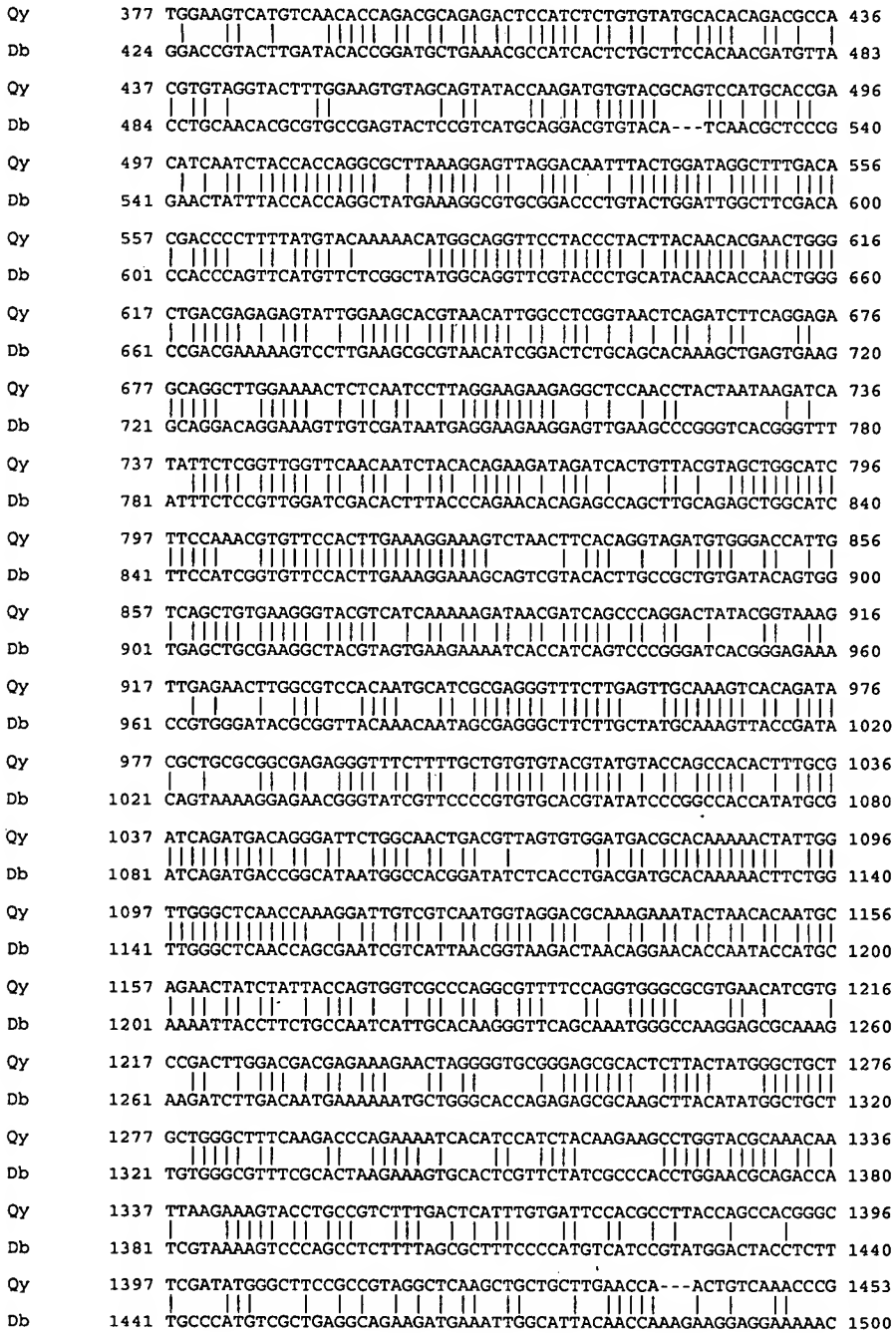
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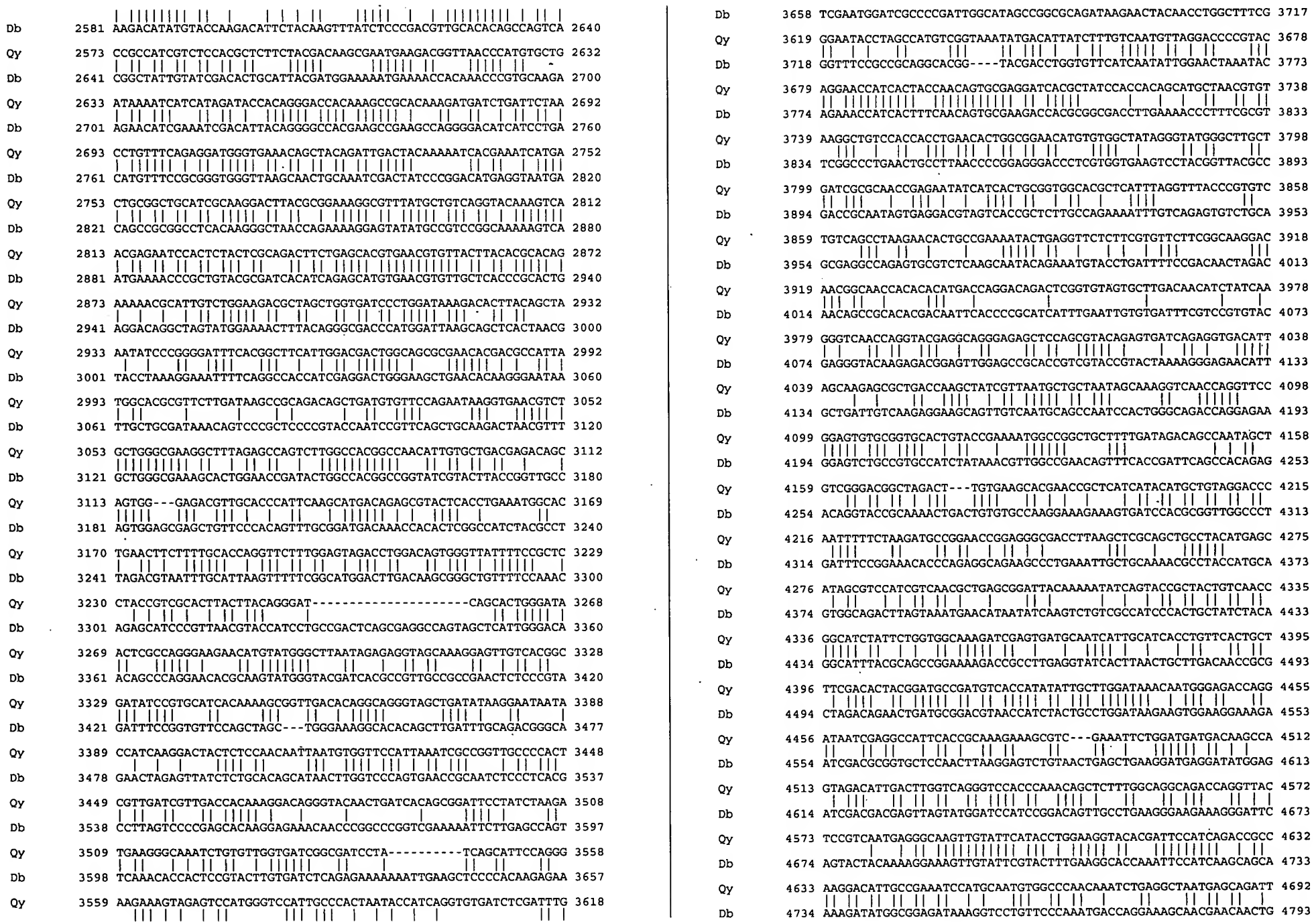

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;  GENERAL INFORMATION:
;    APPLICANT:  Johnston, Robert E.
;    APPLICANT:  Davis, Nancy L.
;    APPLICANT:  Simpson, Dennis A.
;    TITLE OF INVENTION:  System for the In Vivo Delivery and
;    TITLE OF INVENTION:  Expression of Heterologous Genes in the Bone Marrow
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell Seltzer Park & Gibson, P.A.
;      STREET:  1211 East Morehead Street
;      CITY:  Charlotte
;      STATE:  No. 6583121th Carolina
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/367,764
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/801,263
;      FILING DATE:  19-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5470-147
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-420-2200
;      TELEFAX:  919-881-3175
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11663 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
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;      LOCATION:  7608..11342
US-09-367-764-1
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  Best Local Similarity  56.1%;  Pred. No. 0;
  Matches 2820;  Conservative    0;  Mismatches 2128;  Indels   80;  Gaps   13;

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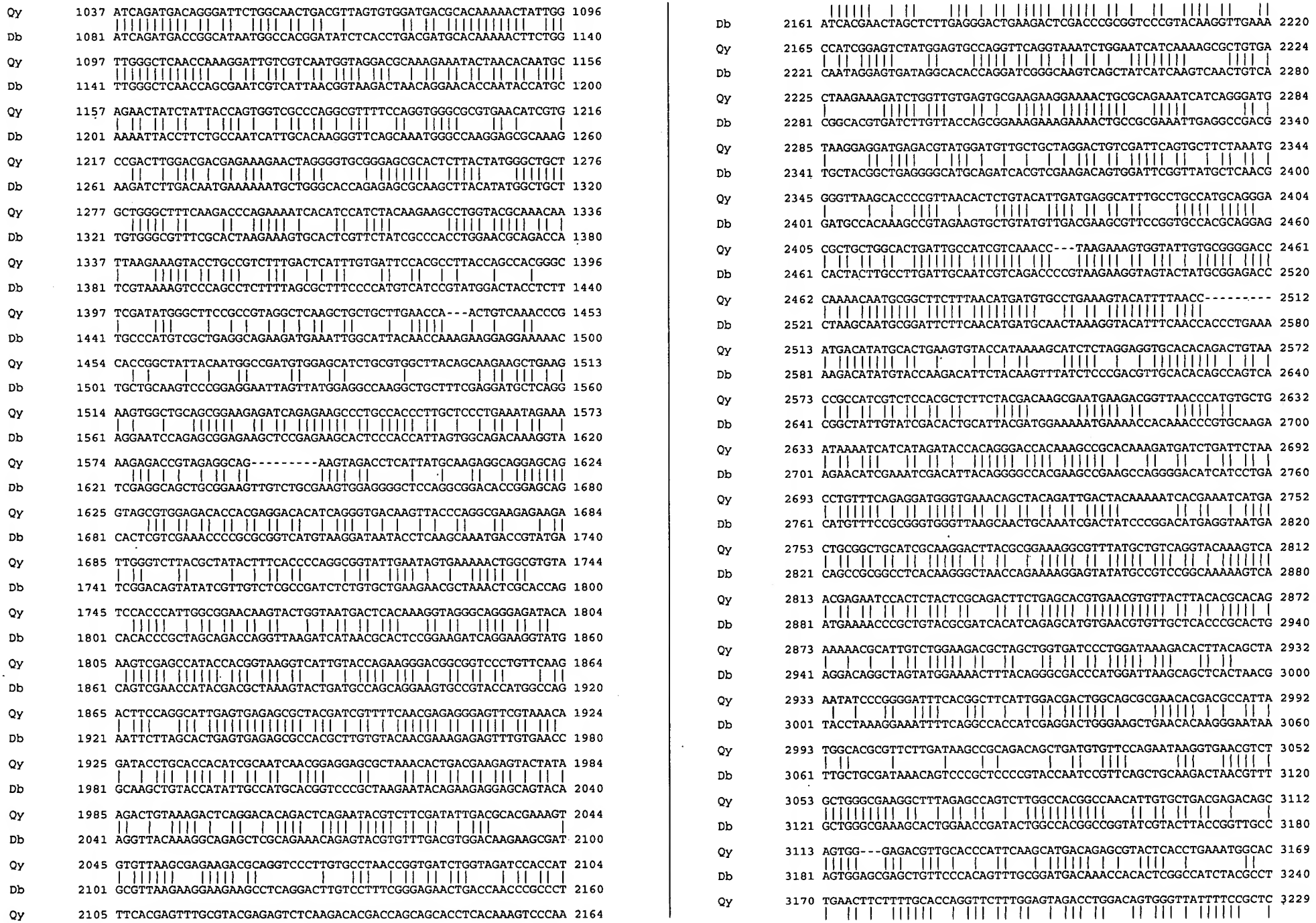

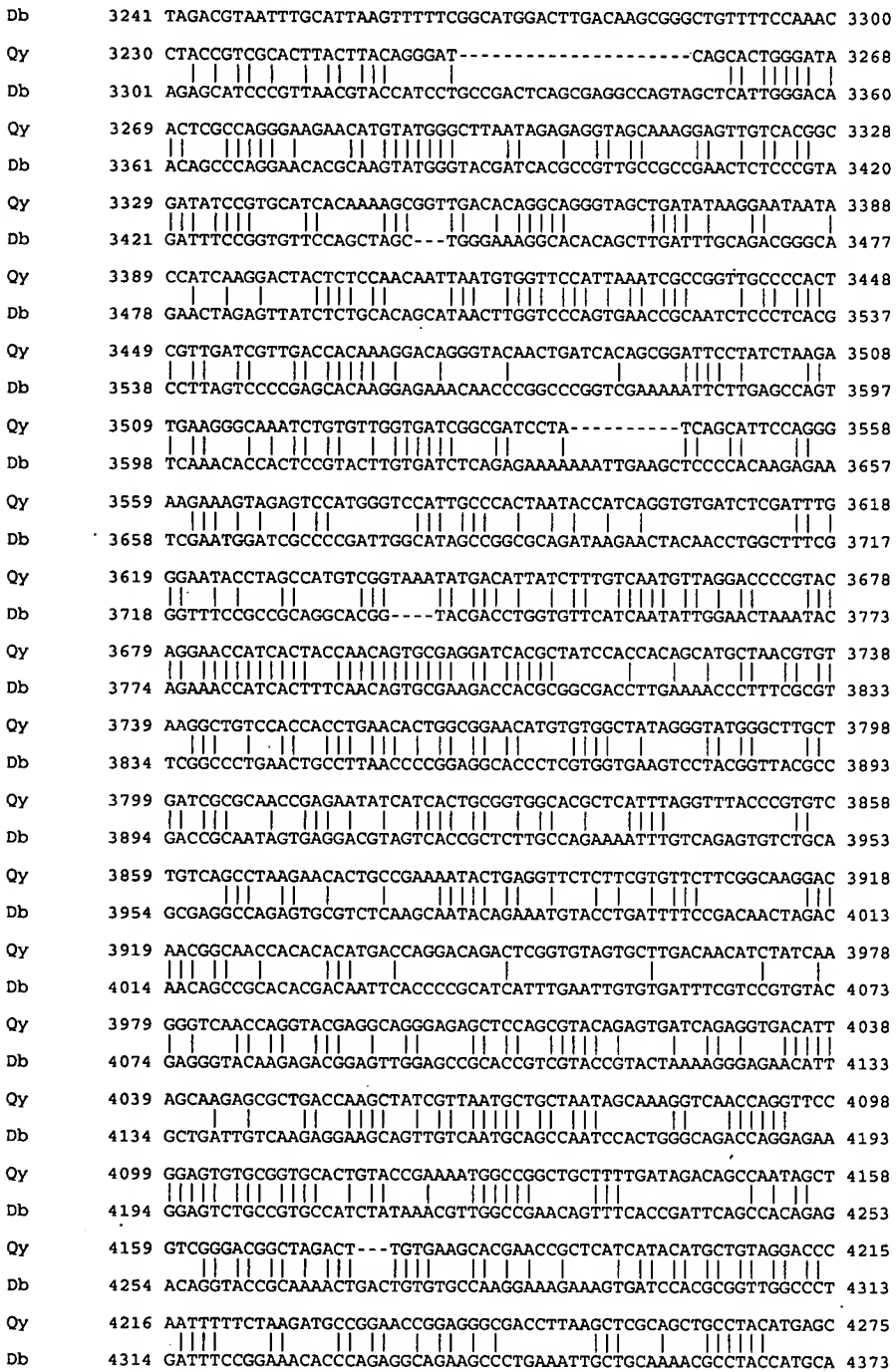


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; Sequence 7, Application US/09367764
; Patent No. 6583121
;  GENERAL INFORMATION:
;    APPLICANT:  Johnston, Robert E.
;    APPLICANT:  Davis, Nancy L.
;    APPLICANT:  Simpson, Dennis A.
;    TITLE OF INVENTION:  System for the In Vivo Delivery and
;    TITLE OF INVENTION:  Expression of Heterologous Genes in the Bone Marrow
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell Seltzer Park & Gibson, P.A.
;      STREET:  1211 East Morehead Street
;      CITY:  Charlotte
;      STATE:  No. 6583121th Carolina
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/367,764
;      FILING DATE:
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/801,263
;      FILING DATE:  19-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5470-147
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-420-2200
;      TELEFAX:  919-881-3175
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11663 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-367-764-7

  Query Match             26.7%;  Score 1333.2;  DB 4;  Length 11663;
  Best Local Similarity   56.1%;  Pred. No. 0;
  Matches 2820;  Conservative    0;  Mismatches 2128;  Indels   80;  Gaps  13;

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Qy       1574 AAGAGACCGTAGAGGCAG---------AAGTAGACCTCATTATGCAAGAGGCAGGAGCAG 1624
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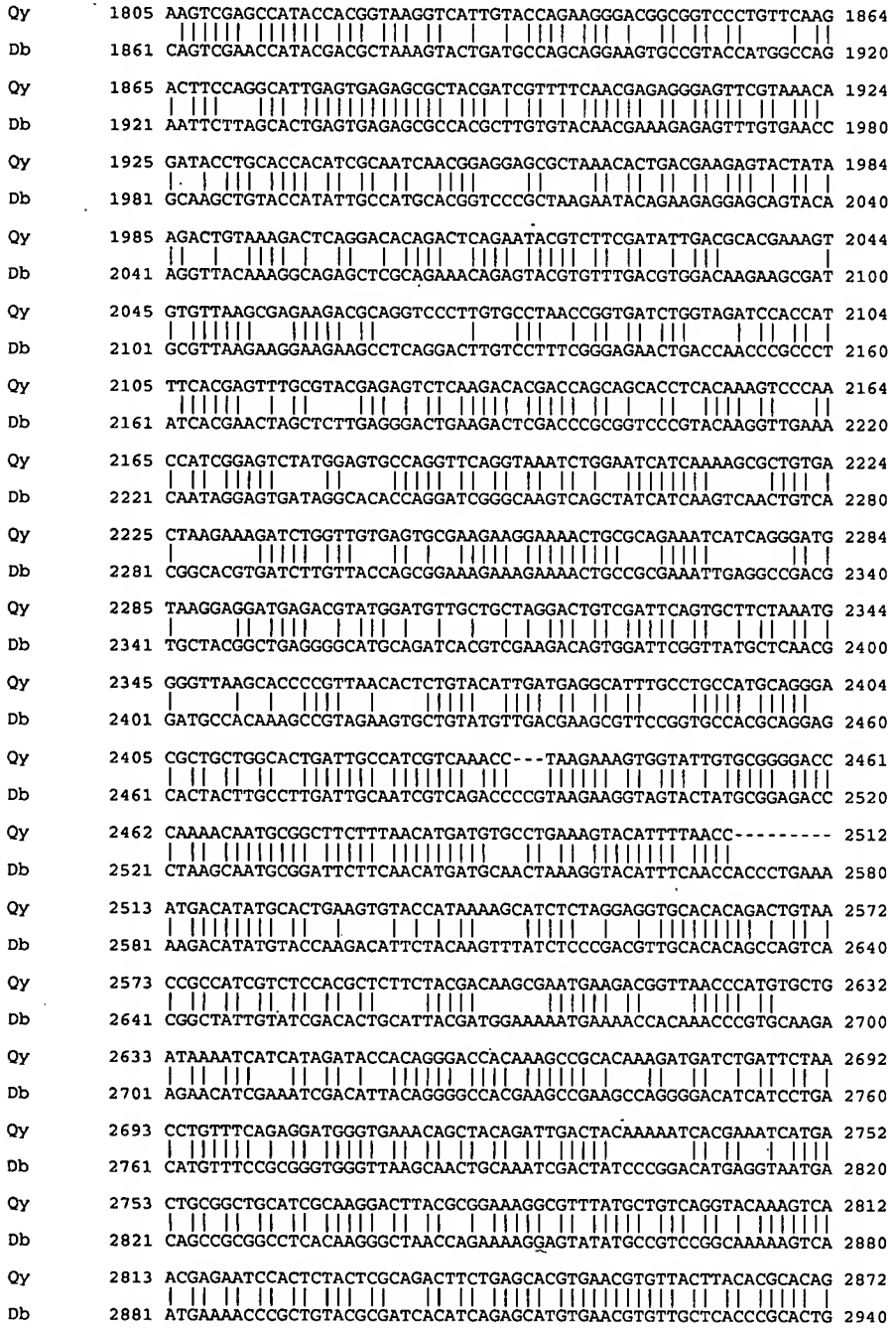

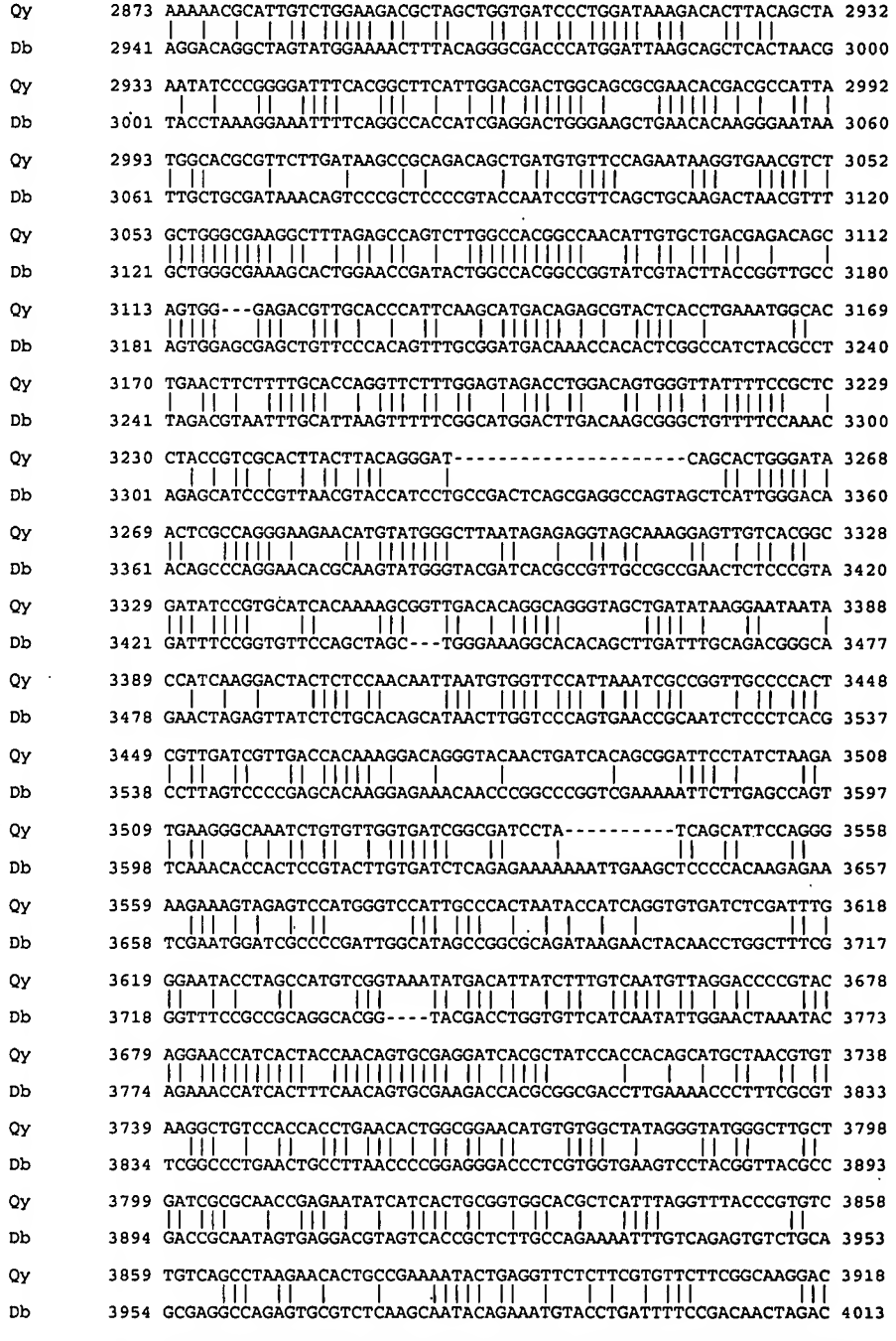

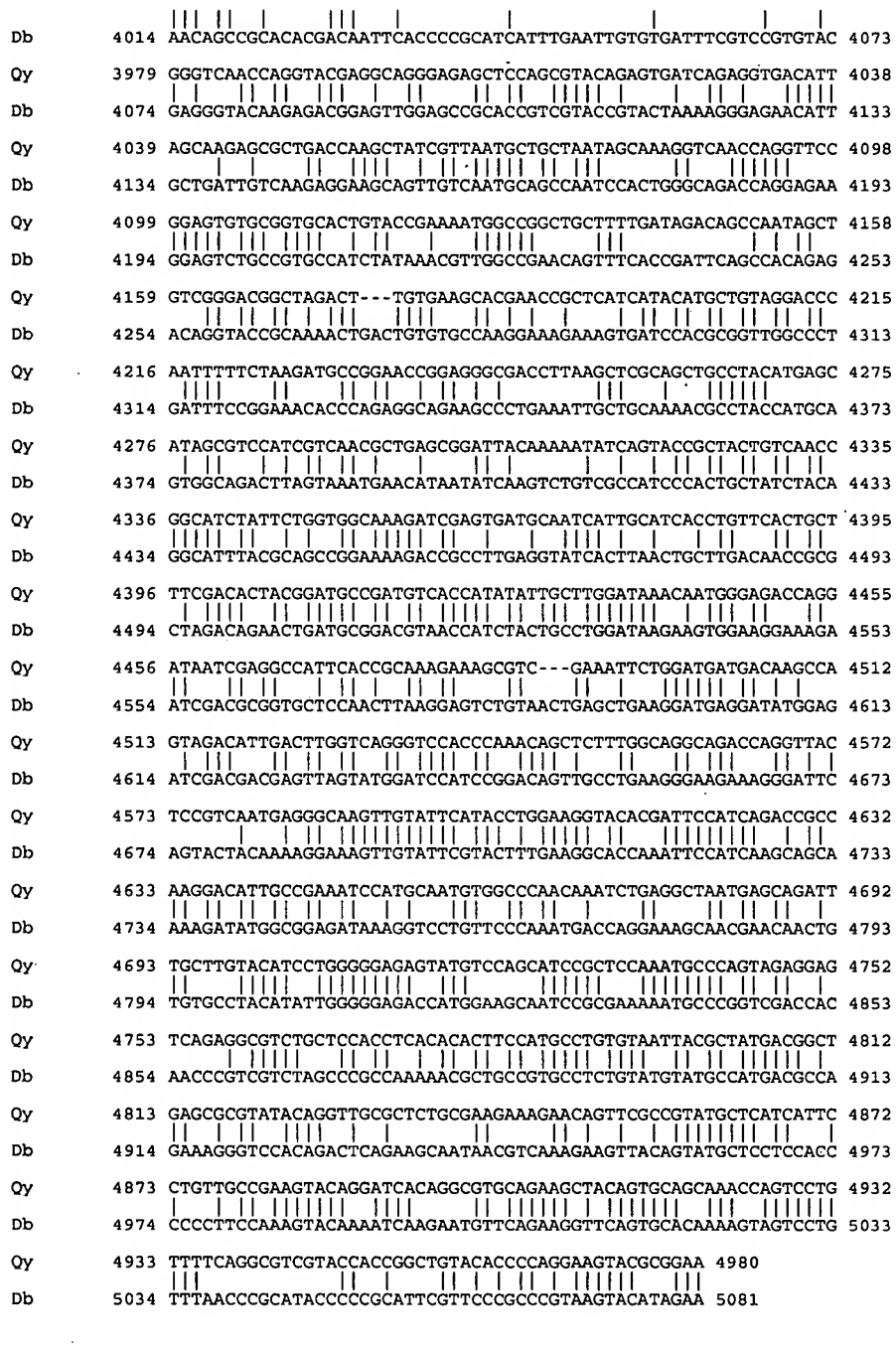

RESULT 15

US-08-801-263A-8
; Sequence 8, Application US/08801263A
; Patent No. 5811407
; GENERAL INFORMATION:
; APPLICANT: Johnston, Robert E.
; APPLICANT: Davis, Nancy L.
; APPLICANT: Simpson, Dennis A.
; TITLE OF INVENTION: System for the In Vivo Delivery and
; TITLE OF INVENTION: Expression of Heterologous Genes in the Bone Marrow
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell Seltzer Park & Gibson, P.A.
; STREET: 1211 East Morehead Street
; CITY: Charlotte
; STATE: No. 5811407th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,263A
; FILING DATE: 19-FEB-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11703 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-801-263A-8

Query Match 26.1%; Score 1303.6; DB 1; Length 11703;
Best Local Similarity 56.1%; Pred. No. 0;
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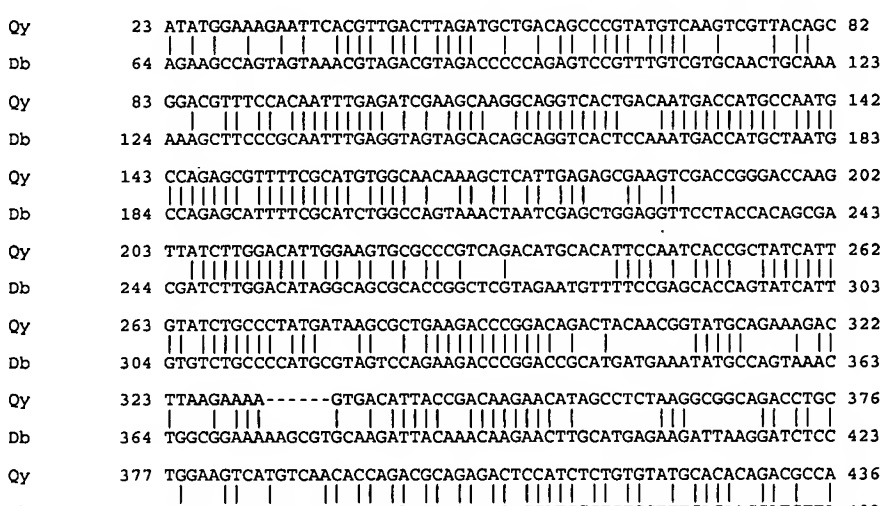

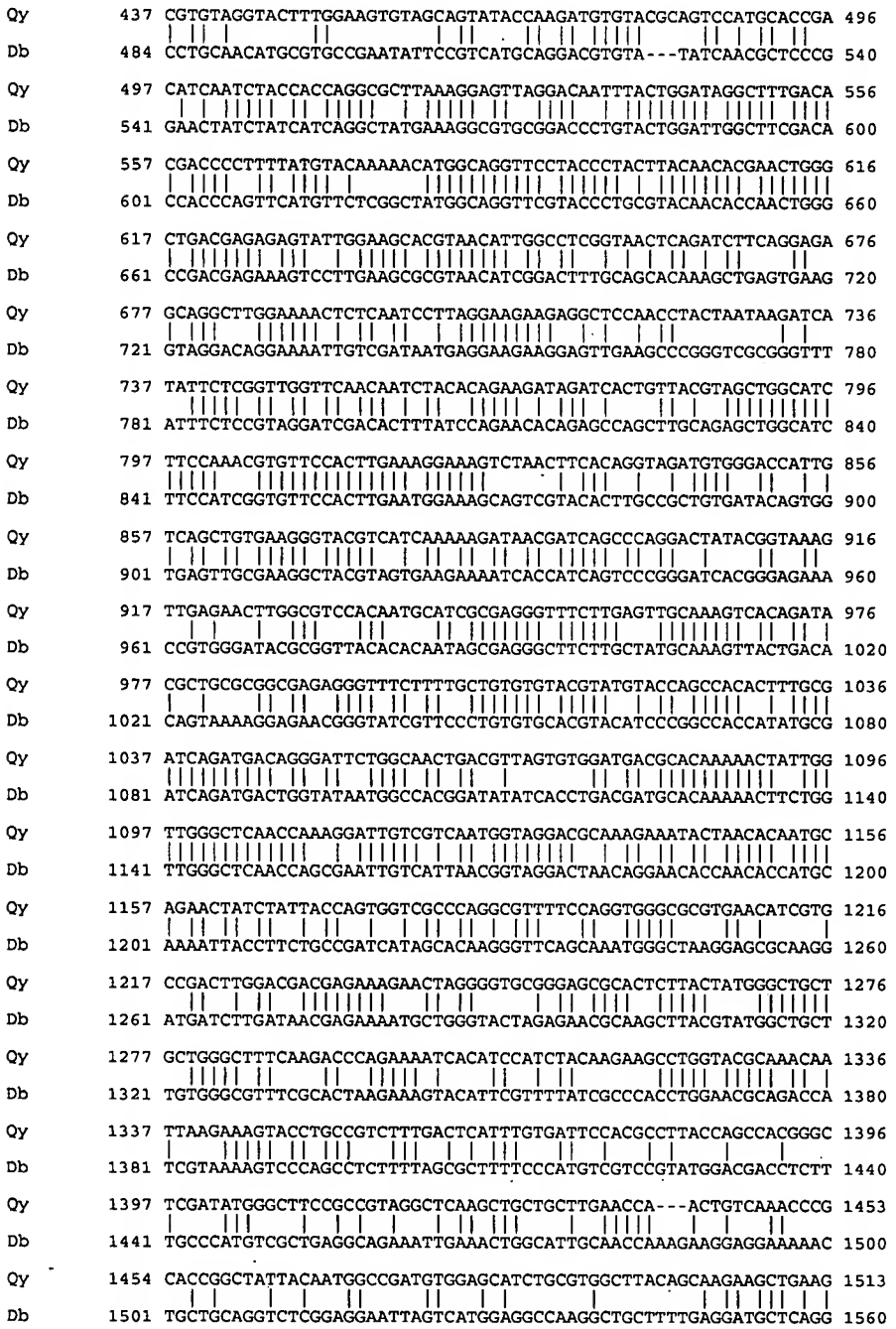

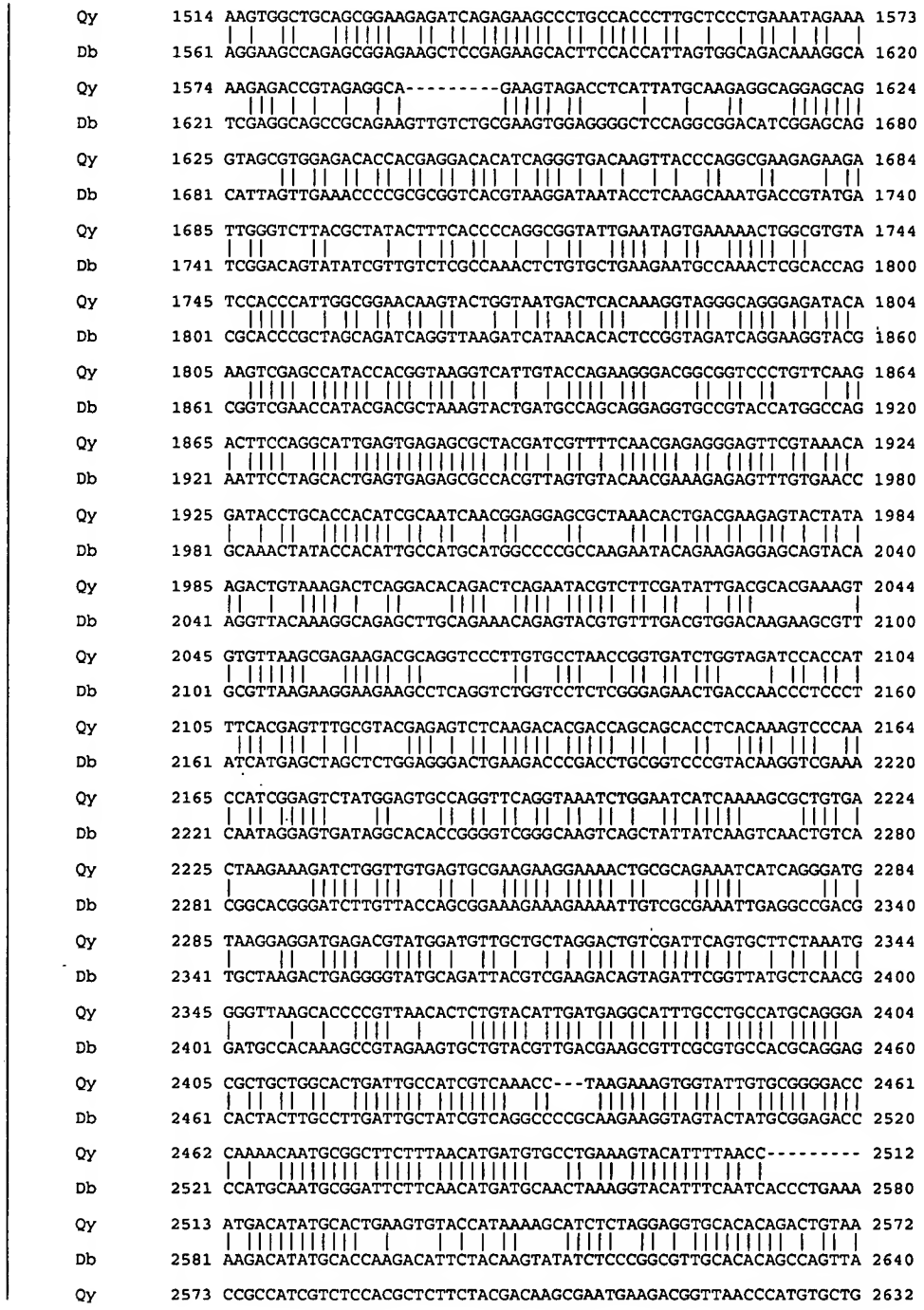

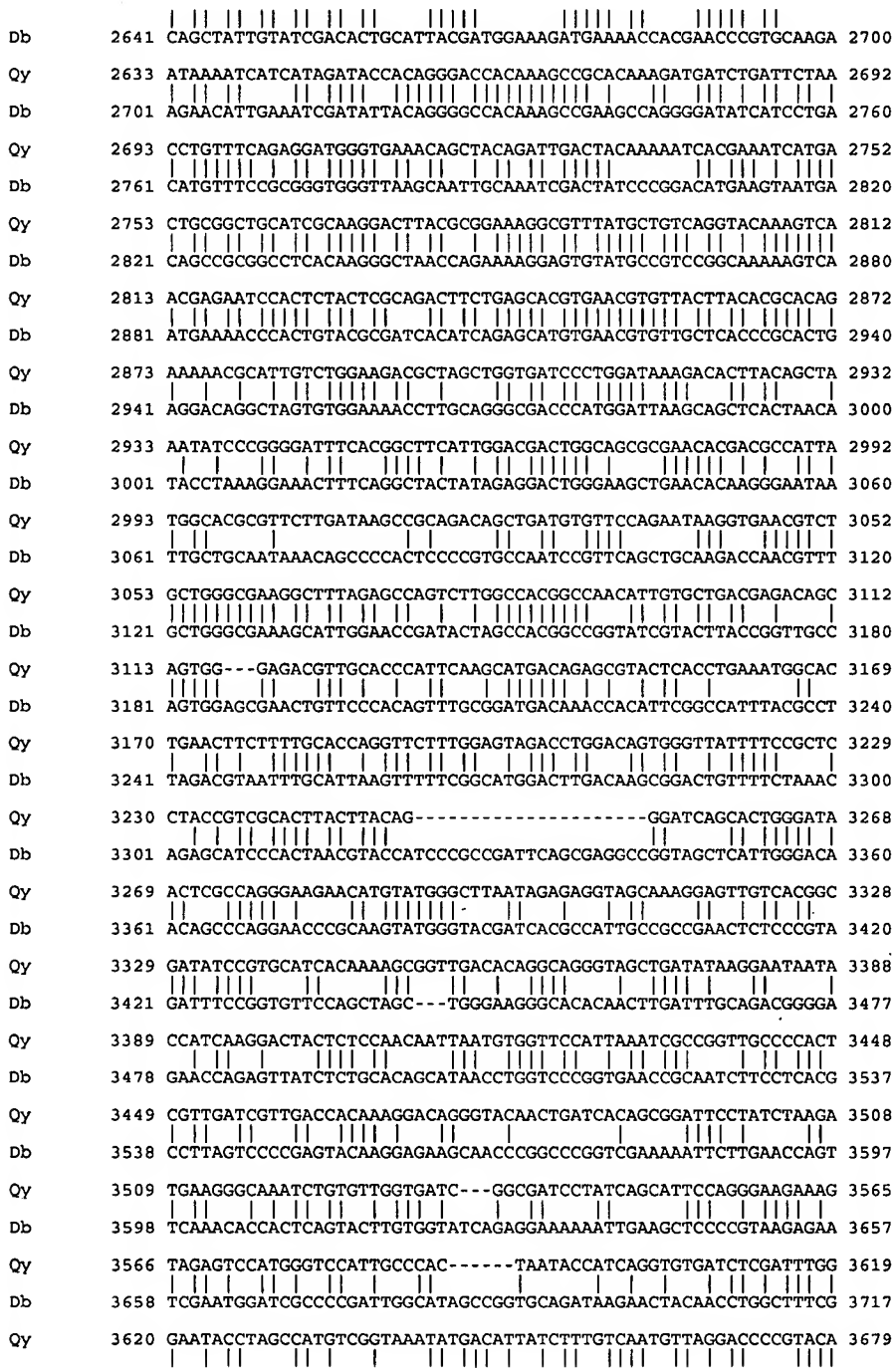

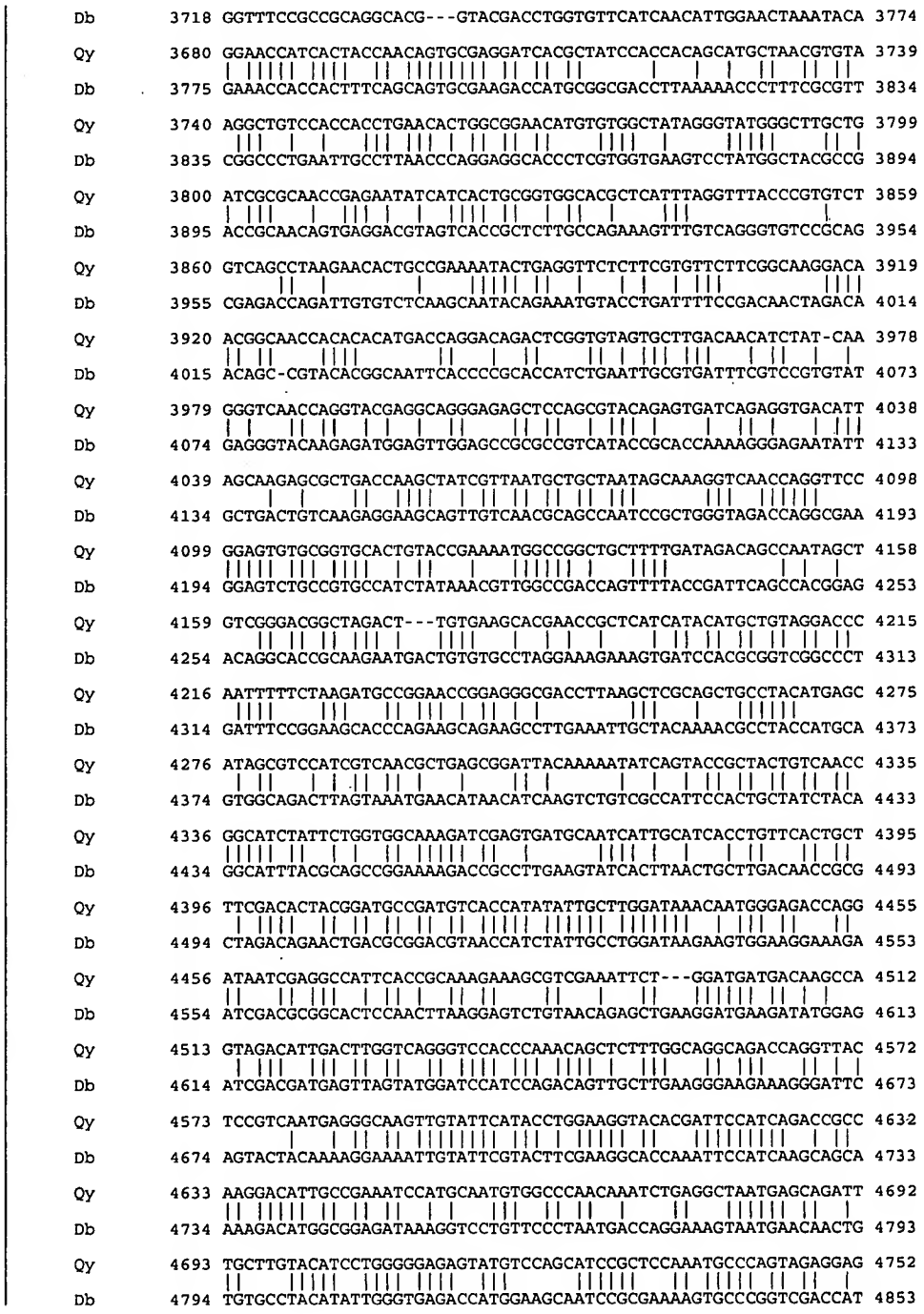

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Job time : 382 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2003, 11:11:16 ; Search time 1177 Seconds
(without alignments)
11467.451 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4492	89.8	11492	20	AAV74107	Western equine enc
2	2118	42.4	11459	21	AAA49442	Venezuelan equine
3	2116.4	42.3	12523	24	AAD29131	Venezuelan equine
4	2113.2	42.3	12379	24	AAD29139	Human immunodefici
5	2113.2	42.3	13584	24	AAD29141	Venezuelan equine
6	2111	42.2	7479	24	AAD29132	Venezuelan equine
7	2074.8	41.5	11464	20	AAV74108	Venezuelan equine
8	1565.6	31.3	11060	20	AAX78130	pSFV link DNA. Se
9	1565.6	31.3	12464	21	AAC55473	Destination vector
10	1564	31.3	7399	25	ACC45139	Alphavirus replica
11	1564	31.3	15538	20	AAX76582	Plasmid pMP44 nucl
12	1562.4	31.2	11489	24	ABN86687	Nucleotide sequenc
13	1562.4	31.2	13599	24	ABN86690	Nucleotide sequenc
14	1554.4	31.1	11517	13	AAQ26021	pSP6-SFV4 RNA tran
15	1473.8	29.5	8010	20	AAX78129	Semliki Forest vir
16	1473.8	29.5	8100	20	AAX76588	SFV EcoRV-SpeI fra
17	1333.2	26.7	11663	19	AAV33473	South African Arbo
18	1333.2	26.7	11663	19	AAV33475	South African Arbo
19	1331.6	26.6	11663	18	AAT47668	South African Arbo
20	1328.4	26.6	11717	21	AAA70577	Sindbis-like virus
21	1306.2	26.1	11626	21	AAA70607	Sindbis-like virus
22	1305.2	26.1	11703	21	AAC64506	Alphavirus SinDCCh
23	1305.2	26.1	11703	21	AAC64507	Alphavirus SinChir
24	1303.6	26.1	11703	19	AAV33476	Sindbis virus clon
25	1302.2	26.0	11717	19	AAV33474	Girdwood S.A.virus
26	1300.4	26.0	8000	25	ABX81525	Sindbis virus cDNA
27	1300.4	26.0	11740	25	ABX81526	Sindbis virus cDNA
28	1300.4	26.0	11927	20	AAX77356	Polynucleotide seq
29	1300.4	26.0	11927	21	AAA90388	Plasmid pSinRep5 h
30	1298.8	26.0	9951	20	AAX77354	Polynucleotide seq
31	1298.8	26.0	9951	21	AAA90386	Sindbis expression
32	1298.8	26.0	9951	22	AAD04742	Alphaviral vector
33	1298.8	26.0	9951	24	ABV73174	Nucleotide sequenc
34	1298.8	26.0	9951	24	ABN86686	Nucleotide sequenc
35	1298.8	26.0	12110	24	ABN86689	Nucleotide sequenc
36	1298.8	26.0	13905	20	AAX77358	Polynucleotide seq
37	1298.8	26.0	13905	21	AAA90390	Plasmid pTE5'2J DN
38	1298.8	26.0	16958	25	AAL55269	DNA of expression
39	1297.2	25.9	10524	20	AAX77355	Polynucleotide seq
40	1297.2	25.9	10524	21	AAA90387	Plasmid pSinRep5 E
41	1295.6	25.9	8000	18	AAX59321	Sindbis virus vari
42	1295.6	25.9	8000	20	AAX58571	Sindbis virus vari
43	1295.6	25.9	8000	25	ABX81524	Sindbis virus cDNA
44	1295.6	25.9	11282	20	AAZ27850	Complete cDNA sequ
45	1295.6	25.9	11282	22	AAF84024	Complete cDNA sequ

ALIGNMENTS

RESULT 1
AAV74107
ID AAV74107 standard; cDNA; 11492 BP.
XX
AC AAV74107;
XX
DT 12-APR-1999 (first entry)
XX
DE Western equine encephalitis virus cDNA.
XX
KW WEE virus; vaccine; ds.
XX
OS Western equine encephalitis virus.
XX
PN WO9853077-A1.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WO-US10645.
XX
PR 16-DEC-1997; 97US-0991840.
PR 20-MAY-1997; 97US-0047162.
PR 24-JUL-1997; 97US-0053652.
XX
PA (REED-) REED ARMY INST RES WALTER.
XX
PI Crise BJ, Oberste MS, Parker MD, Schmura SM, Smith JF;
XX
DR WPI; 1999-045316/04.
XX
PT New DNA encoding infectious Western or Venezuelan equine

PT encephalitis virus genome - useful for the production of live or
PT attenuated vaccines for human or veterinary medicine
XX
PS Example 1; Page 54-67; 112pp; English.
XX
CC This cDNA sequence codes for an infectious western equine
CC encephalitis (WEE) virus RNA transcript. DNA representing the
CC entire genome was prepared by PCR using primers (see AAV74110-21)
CC based on partial genome sequences. 5' Sequences were obtained by
CC RACE. The full-length infectious clone is useful in the production
CC of virulent WEE virus, and for introducing and testing attenuating
CC mutations. Also new are: infectious or attenuated WEE RNA
CC transcripts and WEE viral particles; cDNA (see AAV74108) encoding an
CC infectious Venezuelan equine encephalitis (VEE) variant IE viral
CC genome; infectious or attenuated VEE RNA transcripts and viral
CC particles; an attenuated chimeric virus containing non-structural
CC sequences from a first alpha-virus (aV) and structural sequences
CC from a second aV, resulting in attenuation of the second aV; a method
CC for expressing a protein (especially an antigen to protect against
CC a pathogen) by cloning its gene into an attenuated WEE or VEE IE
CC replicon so that transcription of the replicon produces RNA able to
CC infect the cells in which protein is to be produced; methods for
CC diagnosing WEE and VEE infections; and polypeptides encoded by VEE
CC variant IIIA. Attenuated WEE and VEE are used in live or inactivated
CC vaccines, for use in human or veterinary medicine. Chimeric viruses
CC are also useful as vaccines, directed against the second aV which is
CC particularly Eastern equine encephalitis (EEE) virus or some variant
CC of VEE. WEE and VEE nucleic acids are used as primers and probes to
CC diagnose virus infections and to define natural variants, also for
CC production of protein antigens which can be used as diagnostic
CC reagents, to generate antibodies, and in vaccines. The attenuated
CC viruses are highly immunogenic and provide long-lasting protection.
XX
SQ Sequence 11492 BP; 3257 A; 2854 C; 2794 G; 2570 T; 17 other;

Query Match 89.8%; Score 4492; DB 20; Length 11492;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 4826; Conservative 0; Mismatches 127; Indels 82; Gaps 18;

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Qy         61 CCGTATGTCAAGTCGTTACAGCGGACGTTTCCACAATTTGAGATCGAAGCAAGGCAGGTC 120
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Qy        121 ACTGACAATGACCATGCCAATGCCAGAGCGTTTTCGCATGTGGCAACAAAGCTCATTGAG 180
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Qy        181 AGCGAAGTCGACCGGGACCAAGTTATCTTGGACATTGGAAGTGCGCCCGTCAGACATGCA 240
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Qy        241 CATTCCAATCACCGCTATCATTGTATCTGCCCTATGATAAGCGCTGAAGACCCGGACAGA 300
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Db        265 CATTCCAACCACCGCTATCATTGTATCTGCCCCATGATAAGCGCTGAAGACCCGGACAGA 324

Qy        301 CTACAACGGTATGCAGAAAGACTTAAGAAAAGTGACAT-TACCGACAAGAACATAGCCTC 359
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Qy        478 TACGCAGTCCATGCACCGACATCAATCTACCACCAGGCGCTTAAAGGAGTTAGGACAATT 537
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Qy        598 ACTTACAACACGAACTGGGCTGACGAGAGAGTATTGGAAGCACGTAACATTGGCCTCGGT 657
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Qy        718 CAACCTACTAATAAGATCATATTCTCGGTTGGTTCAACAATCTACACAGAAGATAGATCA 777
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Qy        838 GGTAGATGTGGGACCATTGTCAGCTGTGAAGGGTACGTCATCAAAAAGATAACGATCAGC 897
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Qy        898 CCAGGACTATACGGTAAAGTTGAGAACTTGGCGTCCACAATGCATCGCGAGGGTTTCTTG 957
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Qy        958 AGTTGCAAAGTCACAGATACGCTGCGCGGCGAGAGGGTTTCTTTTGCTGTGTGTACGTAT 1017
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Qy       1078 GACGCACAAAAACTATTGGTTGGGCTCAACCAAAGGATTGTCGTCAATGGTAGGACGCAA 1137
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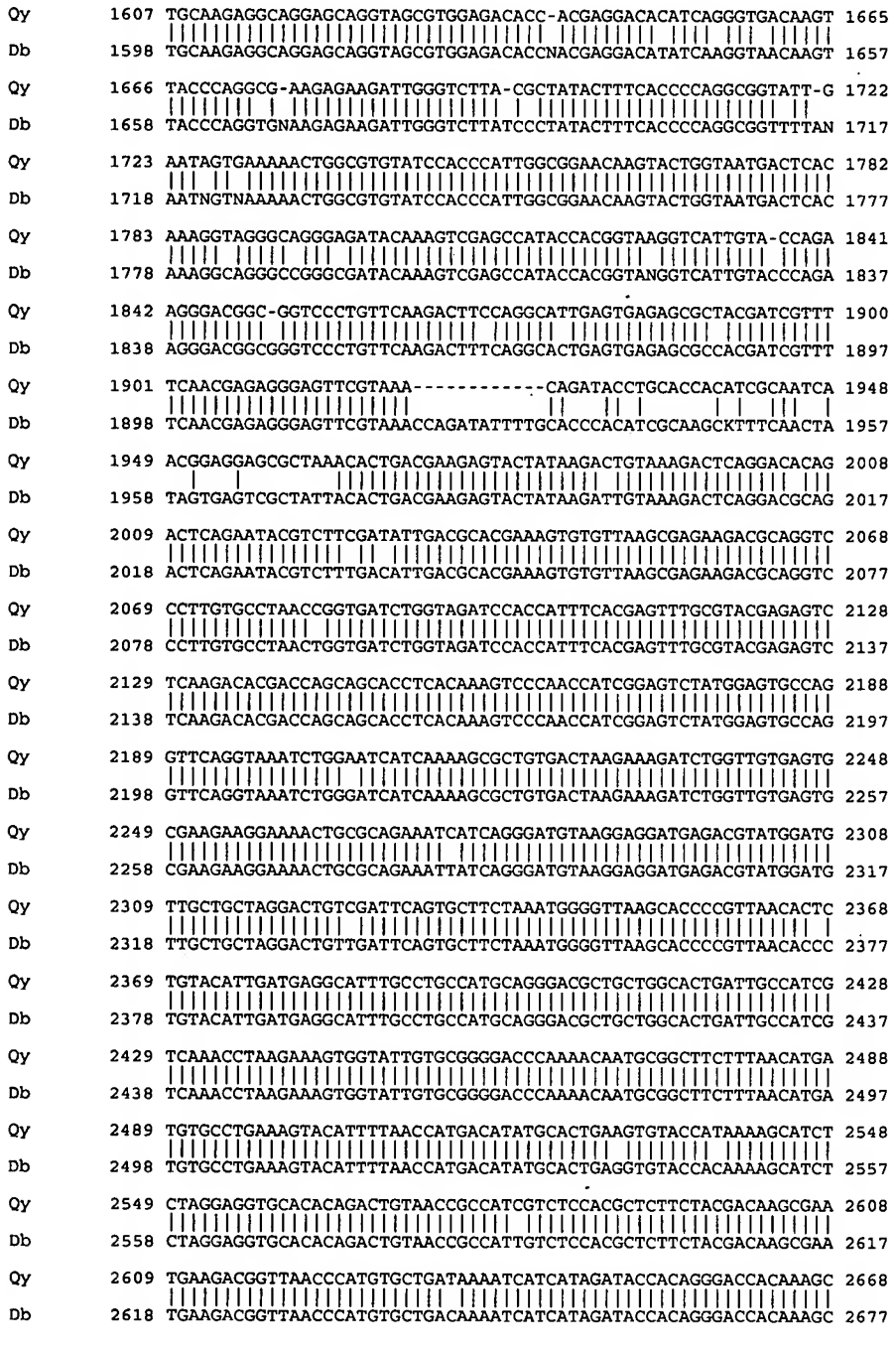
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RESULT 2
AAA49442
ID AAA49442 standard; DNA; 11459 BP.
XX
AC AAA49442;
XX
DT 25-SEP-2000 (first entry)
XX
DE Venezuelan equine encephalitis virus (VEE) wild type sequence.
XX
KW Venezuelan equine encephalitis virus; VEE; attenuation; vaccine;
KW replicon; heterologous gene expression; capsid; structural protein;
KW glycoprotein; immunogen; ds.
XX
OS Venezuelan equine encephalitis.
XX
PN WO200034445-A2.
XX
PD 15-JUN-2000.
XX
PF 07-DEC-1999; 99WO-US29041.
XX
PR 07-DEC-1998; 98US-0111330.
XX
PA (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX
PI Pushko P, Parker MD, Smith JF, Crise BJ;
XX
DR WPI; 2000-423405/36.
XX
PT Attenuated Venezuelan equine encephalitis virus useful as a vaccine
PT contains a rearrangement in genome such that its structural
PT glycoproteins precede the capsid gene
XX
PS Disclosure; Page 37-43; 43pp; English.
XX
CC An attenuated Venezuelan equine encephalitis (VEE) has been described
CC in which the virus undergoes a rearrangement of its genome such that
CC the structural glycoproteins precede the capsid gene. The resulting
CC attenuated virus is useful as a live VEE vaccine for human and
CC veterinary use. The attenuated virus can also be used in a replicon
CC expression system. The rearranged VEE replicon can be used to express
CC heterologous genes of interest in cells as well as a means for
CC expressing antigens or immunogenic proteins and peptides of interest.
CC This rearranged sequence appears in the attenuated virus designated
CC RVE1.1.1.
XX
SQ Sequence 11459 BP; 3242 A; 2804 C; 2897 G; 2516 T; 0 other;

Query Match 42.4%; Score 2118; DB 21; Length 11459;
Best Local Similarity 64.5%; Pred. No. 0;
Matches 3219; Conservative 0; Mismatches 1745; Indels 24; Gaps 3;

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Qy         70 AAGTCGTTACAGCGGACGTTTCCACAATTTGAGATCGAAGCAAGGCAGGTCACTGACAAT 129
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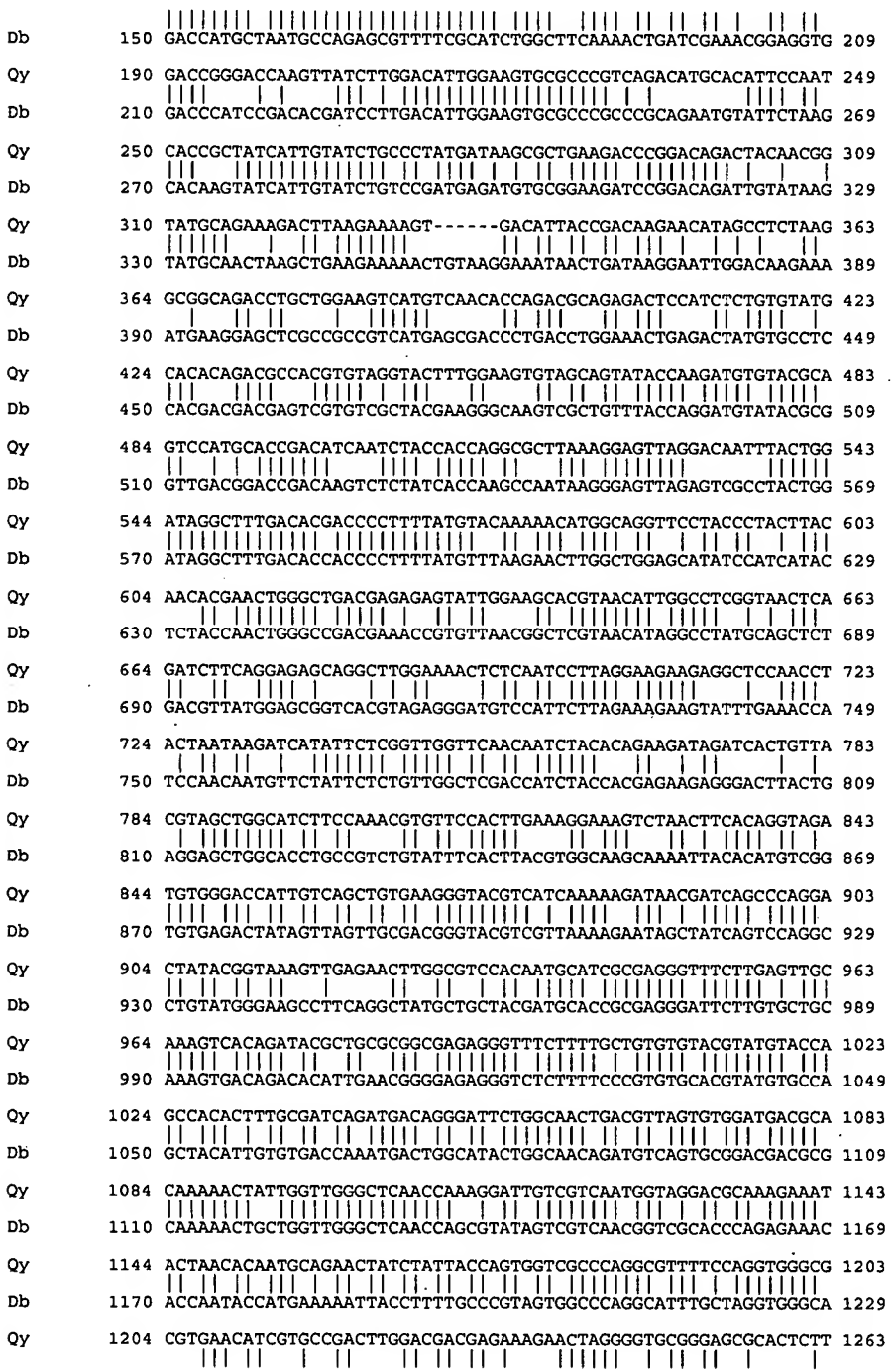
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Db 1410 GGCAGTAACACATTGGAGATCGGGCTGAGAACAAGAATCAGGAAAATGTTAGAGGAGCAC 1469
Qy 1444 GTCAAACCCGCACCGGCTATTACAATGGCCGATGTGGAGCATCTGCGTGGCTTACAGCAA 1503
Db 1470 AAGGAGCCGTCACCTCTCATTACCGCCGAGGACGTACAAGAAGCTAAGTGCGCAGCCGAT 1529
Qy 1504 GAAGCTGAAGAAGTGGCTGCAGCGGAAGAGATCAGAGAAGCCCTGCCACCCTTGCTCCCT 1563
Db 1530 GAGGCTAAGGAGGTGCGTGAAGCCGAGGAGTTGCGCGCAGCTCTACCACCTTTGGCAGCT 1589
Qy 1564 GAAATAGAAAAAGAGACCGTAGAGGCAGAAGTAGACCTCATTATGCAAGAGGCAGGAGCA 1623
Db 1590 GATGTTGAGGAGCCCACTCTGGAAGCCGATGTCGACTTGATGTTACAAGAGGCTGGGGCC 1649
Qy 1624 GGTAGCGTGGAGACACCACGAGGACACATCAGGGTGACAAGTTACCCAGGCGAAGAGAAG 1683
Db 1650 GGCTCAGTGGAGACACCTCGTGGCTTGATAAAGGTTACCAGCTACGCTGGCGAGGACAAG 1709
Qy 1684 ATTGGGTCTTACGCTATACTTTCACCCCAGGCGGTATTGAATAGTGAAAAACTGGCGTGT 1743
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Qy 1744 ATCCACCCATTGGCGGAACAAGTACTGGTAATGACTCACAAAGGTAGGGCAGGGAGATAC 1803
Db 1770 ATCCACCCTCTCGCTGAACAAGTCATAGTGATAACACACTCTGGCCGAAAAGGGCGTTAT 1829
Qy 1804 AAAGTCGAGCCATACCACGGTAAGGTCATTGTACCAGAAGGGACGGCGGTCCCTGTTCAA 1863
Db 1830 GCCGTGGAACCATACCATGGTAAAGTAGTGGTGCCAGAGGGACATGCAATACCCGTCCAG 1889
Qy 1864 GACTTCCAGGCATTGAGTGAGAGCGCTACGATCGTTTTCAACGAGAGGGAGTTCGTAAAC 1923
Db 1890 GACTTTCAAGCTCTGAGTGAAAGTGCCACCATTGTGTACAACGAACGTGAGTTCGTAAAC 1949
Qy 1924 AGATACCTGCACCACATCGCAATCAACGGAGGAGCGCTAAACACTGACGAAGAGTACTAT 1983
Db 1950 AGGTACCTGCACCATATTGCCACACATGGAGGAGCGCTGAACACTGATGAAGAATATTAC 2009
Qy 1984 AAGACTGTAAAGACTCAGGACACAGACTCAGAATACGTCTTCGATATTGACGCACGAAAG 2043
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Qy 2224 ACTAAGAAAGATCTGGTTGTGAGTGCGAAGAAGGAAAACTGCGCAGAAATCATCAGGGAT 2283
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Qy 2284 GTAAGGAGGATGAGACGTATGGATGTTGCTGCTAGGACTGTCGATTCAGTGCTTCTAAAT 2343
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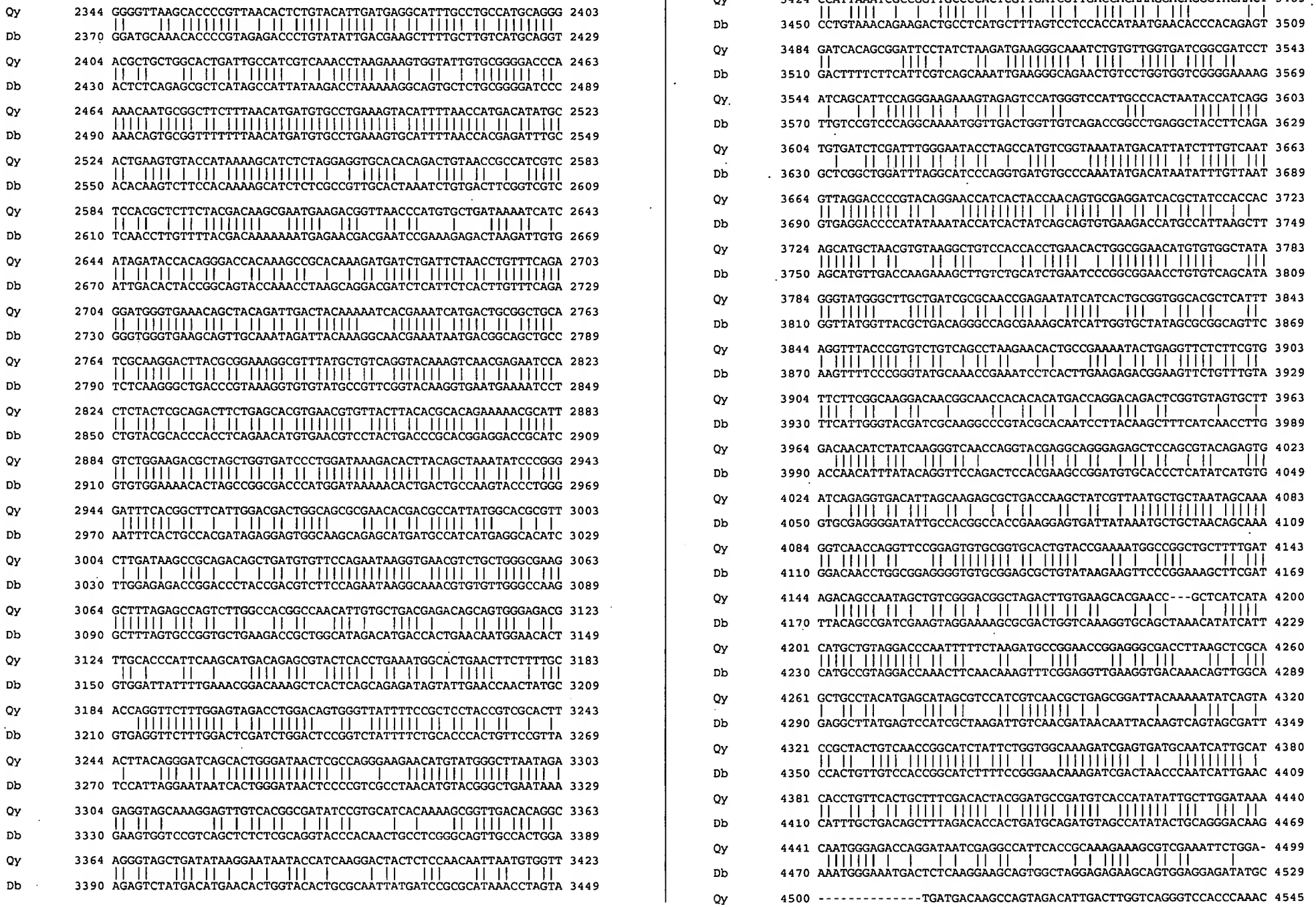

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Qy       4546 AGCTCTTTGGCAGGCAGACCAGGTTACTCCGTCAATGAGGGCAAGTTGTATTCATACCTG 4605

Db       4590 AGTTCTTTGGCTGGAAGGAAGGGCTACAGCACAAGCGATGGCAAAACTTTCTCATATTTG 4649

Qy       4606 GAAGGTACACGATTCCATCAGACCGCCAAGGACATTGCCGAAATCCATGCAATGTGGCCC 4665

Db       4650 GAAGGGACCAAGTTTCACCAGGCGGCCAAGGATATAGCAGAAATTAATGCCATGTGGCCC 4709

Qy       4666 AACAAATCTGAGGCTAATGAGCAGATTTGCTTGTACATCCTGGGGGAGAGTATGTCCAGC 4725

Db       4710 GTTGCAACGGAGGCCAATGAGCAGGTATGCATGTATATCCTCGGAGAAAGCATGAGCAGT 4769

Qy       4726 ATCCGCTCCAAATGCCCAGTAGAGGAGTCAGAGGCGTCTGCTCCACCTCACACACTTCCA 4785

Db       4770 ATTAGGTCGAAATGCCCCGTCGAAGAGTCGGAAGCCTCCACACCACCTAGCACGCTGCCT 4829

Qy       4786 TGCCTGTGTAATTACGCTATGACGGCTGAGCGCGTATACAGGTTGCGCTCTGCGAAGAAA 4845

Db       4830 TGCTTGTGCATCCATGCCATGACTCCAGAAAGAGTACAGCGCCTAAAAGCCTCACGTCCA 4889

Qy       4846 GAACAGTTCGCCGTATGCTCATCATTCCTGTTGCCGAAGTACAGGATCACAGGCGTGCAG 4905

Db       4890 GAACAAATTACTGTGTGCTCATCCTTTCCATTGCCGAAGTATAGAATCACTGGTGTGCAG 4949

Qy       4906 AAGCTACAGTGCAGCAAACCAGTCCTGTTTTCAGGCGTCGTACCACCGGCTGTACACCCC 4965

Db       4950 AAGATCCAATGCTCCCAGCCTATATTGTTCTCACCGAAAGTGCCTGCGTATATTCATCCA 5009

Qy       4966 AGGAAGTA 4973

Db       5010 AGGAAGTA 5017
```

RESULT 3
AAD29131
ID AAD29131 standard; DNA; 12523 BP.
XX
AC AAD29131;
XX
DT 07-MAY-2002 (first entry)
XX
DE Venezuelan equine encephalitis virus (VEE) replicon plasmid.
XX
KW Venezuelan equine encephalitis virus; VEE; vaccine; HIV infection;
KW human immunodeficiency virus; alpha-virus replicon; immune response;
KW therapy; ds.
XX
OS Chimeric - Venezuelan equine encephalitis virus.
OS Chimeric - Unidentified.
XX
PN WO200203917-A2.
XX
PD 17-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US21701.
XX
PR 07-JUL-2000; 2000US-216995P.
XX
PA (ALPH-) ALPHAVAX INC.
PA (UYNC-) UNIV NORTH CAROLINA.
XX
PI Olmsted R, Keith P, Dryga S, Caley I, Maughan M, Johnston R;
PI Davis N, Swanstrom R;
XX
DR WPI; 2002-171664/22.
XX
PT Composition useful for treating or preventing HIV infections, comprises
PT two or more isolated nucleic acids encoding env, gag or pol gene
PT product of HIV or immunogenic fragment of the gene products -
XX
PS Example 5; Page 141-145; 201pp; English.
XX
CC The invention relates to a composition comprising isolated nucleic acids
CC encoding env, gag or pol gene product of human immunodeficiency virus or
CC immunogenic fragment of the gene products. The gag gene product is
CC modified to inhibit formation of virus-like particles containing gag
CC gene product and their release from cells, and the pol gene product is
CC modified to inhibit reverse transcriptase activity. The invention also
CC relates to a method for producing an alpha-virus replicon particle used
CC in vaccines. The composition is useful for inducing an immune response
CC to human immunodeficiency virus (HIV) or for treating or preventing HIV
CC infection in a subject. The alpha-virus replicon particle is useful in a
CC vaccine. The composition is useful for administering a protein or peptide
CC to a subject. A composition comprising heparin affinity-purified alpha-
CC virus replicon particle is useful as a clinical trial material and as a
CC commercial product. The present sequence is Venezuelan equine
CC encephalitis virus (VEE) replicon plasmid containing the DU422 gag gene
CC (p3-40.1.6) used in the exemplification of the invention.
XX
SQ Sequence 12523 BP; 3579 A; 2959 C; 3160 G; 2825 T; 0 other;

Query Match 42.3%; Score 2116.4; DB 24; Length 12523;
Best Local Similarity 64.5%; Pred. No. 0;
Matches 3218; Conservative 0; Mismatches 1746; Indels 24; Gaps 3;

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Db         30 AATTACCTACCCAAAATGGAGAAAGTTCACGTTGACATCGAGGAAGACAGCCCATTCCTC 89

Qy         70 AAGTCGTTACAGCGGACGTTTCCACAATTTGAGATCGAAGCAAGGCAGGTCACTGACAAT 129

Db         90 AGAGCTTTGCAGCGGAGCTTCCCGCAGTTTGAGGTAGAAGCCAAGCAGGTCACTGATAAT 149

Qy        130 GACCATGCCAATGCCAGAGCGTTTTCGCATGTGGCAACAAAGCTCATTGAGAGCGAAGTC 189

Db        150 GACCATGCTAATGCCAGAGCGTTTTCGCATCTGGCTTCAAAACTGATCGAAACGGAGGTG 209

Qy        190 GACCGGGACCAAGTTATCTTGGACATTGGAAGTGCGCCCGTCAGACATGCACATTCCAAT 249

Db        210 GACCCATCCGACACGATCCTTGACATTGGAAGTGCGCCCGCCCGCAGAATGTATTCTAAG 269

Qy        250 CACCGCTATCATTGTATCTGCCCTATGATAAGCGCTGAAGACCCGGACAGACTACAACGG 309

Db        270 CACAAGTATCATTGTATCTGTCCGATGAGATGTGCGGAAGATCCGGACAGATTGTATAAG 329

Qy        310 TATGCAGAAAGACTTAAGAAAAGT------GACATTACCGACAAGAACATAGCCTCTAAG 363

Db        330 TATGCAACTAAGCTGAAGAAAAACTGTAAGGAAATAACTGATAAGGAATTGGACAAGAAA 389

Qy        364 GCGGCAGACCTGCTGGAAGTCATGTCAACACCAGACGCAGAGACTCCATCTCTGTGTATG 423

Db        390 ATGAAGGAGCTCGCCGCCGTCATGAGCGACCCTGACCTGGAAACTGAGACTATGTGCCTC 449

Qy        424 CACACAGACGCCACGTGTAGGTACTTTGGAAGTGTAGCAGTATACCAAGATGTGTACGCA 483

Db        450 CACGACGACGAGTCGTGTCGCTACGAAGGGCAAGTCGCTGTTTACCAGGATGTATACGCG 509

Qy        484 GTCCATGCACCGACATCAATCTACCACCAGGCGCTTAAAGGAGTTAGGACAATTTACTGG 543

Db        510 GTTGACGGACCGACAAGTCTCTATCACCAAGCCAATAAGGGAGTTAGAGTCGCCTACTGG 569

Qy        544 ATAGGCTTTGACACGACCCCTTTTATGTACAAAAACATGGCAGGTTCCTACCCTACTTAC 603

Db        570 ATAGGCTTTGACACCACCCCTTTTATGTTTAAGAACTTGGCTGGAGCATATCCATCATAC 629

Qy        604 AACACGAACTGGGCTGACGAGAGAGTATTGGAAGCACGTAACATTGGCCTCGGTAACTCA 663

Db        630 TCTACCAACTGGGCCGACGAAACCGTGTTAACGGCTCGTAACATAGGCCTATGCAGCTCT 689

Qy        664 GATCTTCAGGAGAGCAGGCTTGGAAAACTCTCAATCCTTAGGAAGAAGAGGCTCCAACCT 723

Db        690 GACGTTATGGAGCGGTCACGTAGAGGGATGTCCATTCTTAGAAAGAAGTATTTGAAACCA 749
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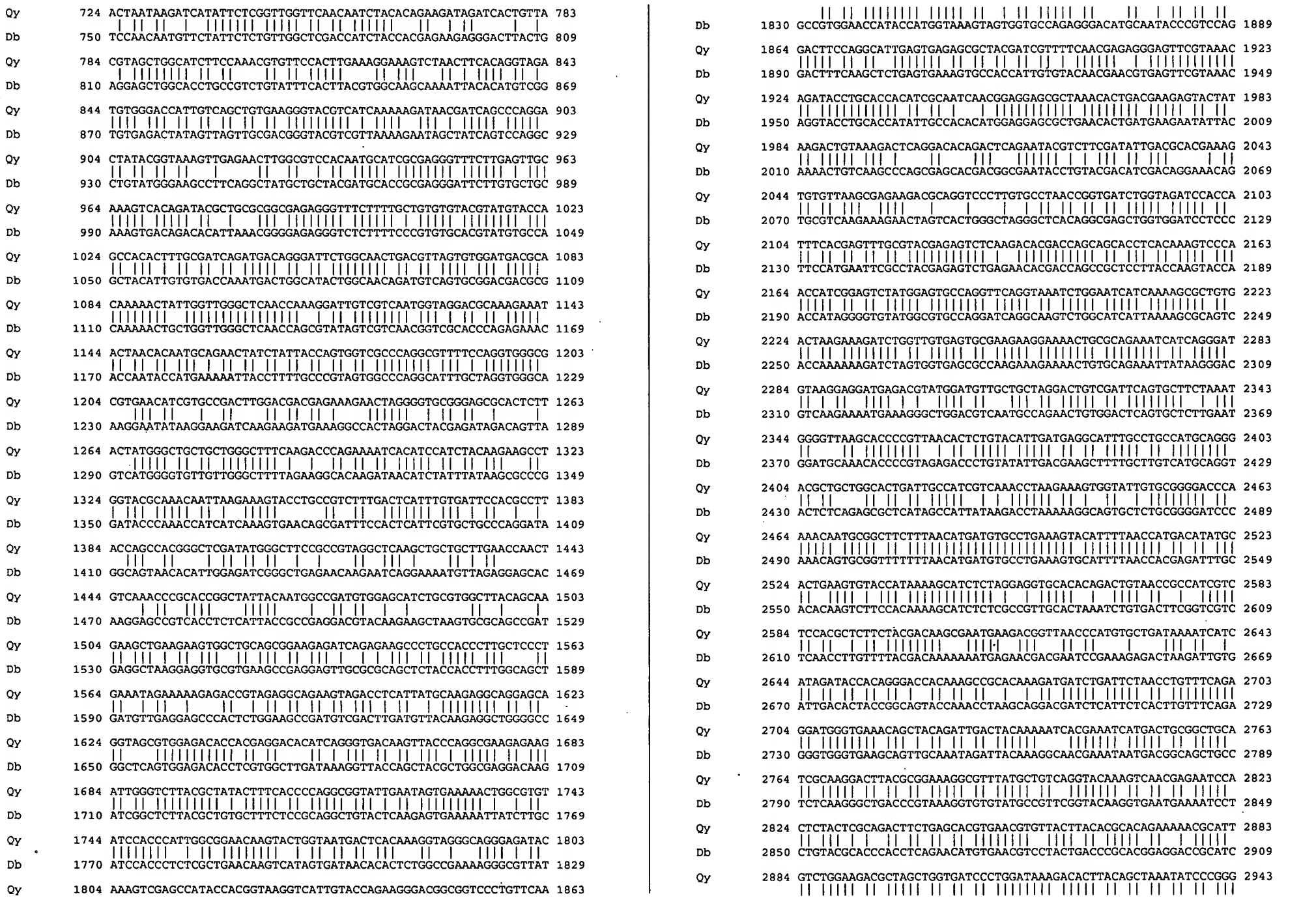

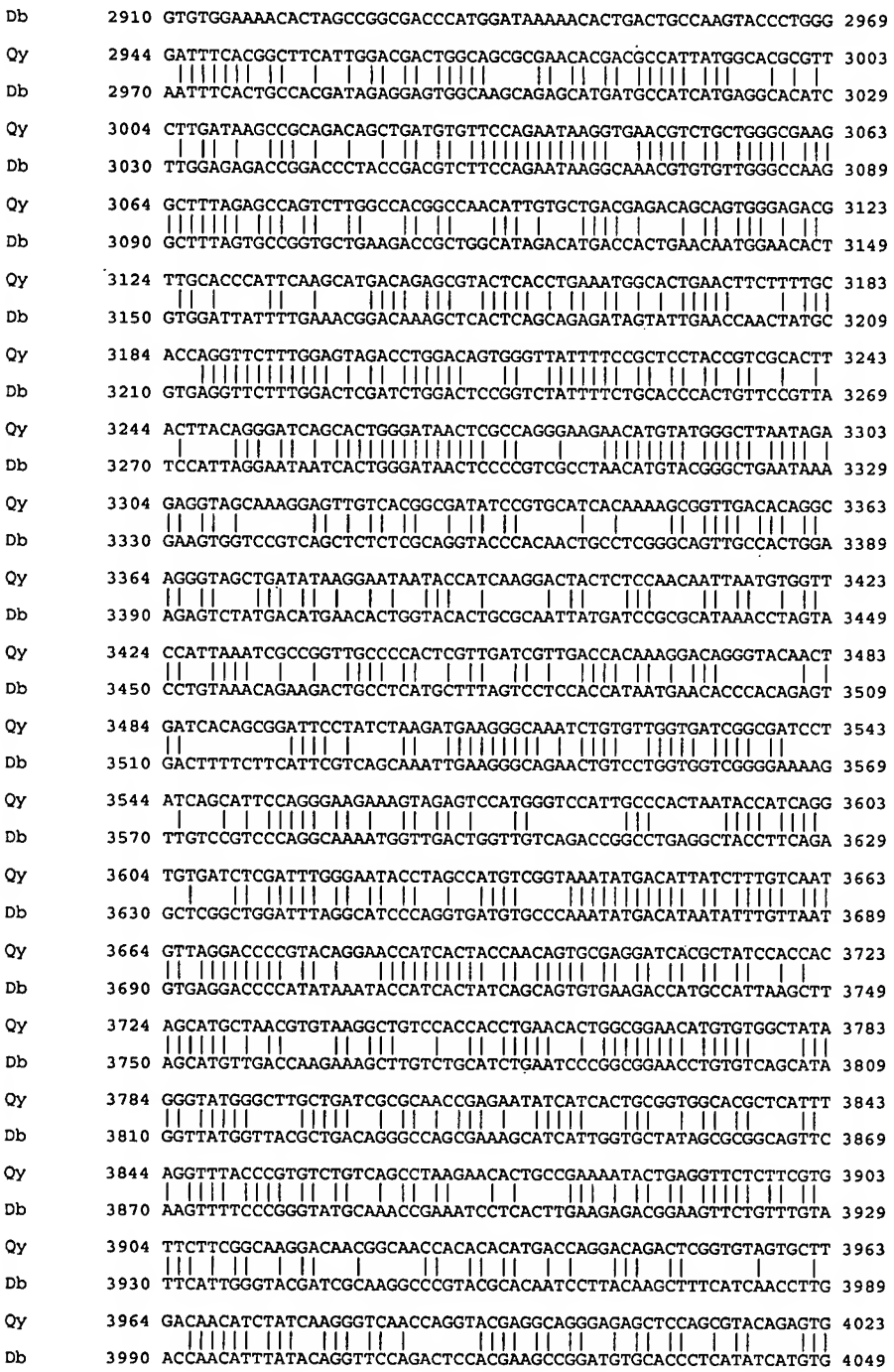

RESULT 4
AAD29139
ID AAD29139 standard; DNA; 12379 BP.

```
XX
AC   AAD29139;
XX
DT   07-MAY-2002  (first entry)
XX
DE   Human immunodeficiency virus type 1 (HIV-1) pol plasmid.
XX
KW   Human immunodeficiency virus; vaccine; HIV infection; immune response;
KW   alpha-virus replicon; therapy; pol gene; ds.
XX
OS   Chimeric - Human immunodeficiency virus type 1.
OS   Chimeric - Unidentified.
XX
PN   WO200203917-A2.
XX
PD   17-JAN-2002.
XX
PF   09-JUL-2001; 2001WO-US21701.
XX
PR   07-JUL-2000; 2000US-216995P.
XX
PA   (ALPH-) ALPHAVAX INC.
PA   (UYNC-) UNIV NORTH CAROLINA.
XX
PI   Olmsted R,  Keith P,  Dryga S,  Caley I,  Maughan M,  Johnston R;
PI   Davis N,  Swanstrom R;
XX
DR   WPI; 2002-171664/22.
XX
PT   Composition useful for treating or preventing HIV infections, comprises
PT   two or more isolated nucleic acids encoding env, gag or pol gene
PT   product of HIV or immunogenic fragment of the gene products  -
XX
PS   Example 5; Page 183-187; 201pp; English.
XX
CC   The invention relates to a composition comprising isolated nucleic acids
CC   encoding env, gag or pol gene product of human immunodeficiency virus or
CC   immunogenic fragment of the gene products. The gag gene product is
CC   modified to inhibit formation of virus-like particles containing gag
CC   gene product and their release from cells, and the pol gene product is
CC   modified to inhibit reverse transcriptase activity. The invention also
CC   relates to a method for producing an alpha-virus replicon particle used
CC   in vaccines. The composition is useful for inducing an immune response
CC   to human immunodeficiency virus (HIV) or for treating or preventing HIV
CC   infection in a subject. The alpha-virus replicon particle is useful in a
CC   vaccine. The composition is useful for administering a protein or peptide
CC   to a subject. A composition comprising heparin affinity-purified alpha-
CC   virus replicon particle is useful as a clinical trial material and as a
CC   commercial product. The present sequence is HIV-1 pol plasmid.
XX
SQ   Sequence 12379 BP; 3562 A; 2920 C; 3084 G; 2813 T; 0 other;

  Query Match             42.3%;  Score 2113.2;  DB 24;  Length 12379;
  Best Local Similarity   64.5%;  Pred. No. 0;
  Matches 3216;  Conservative    0;  Mismatches 1748;  Indels   24;  Gaps    3;

Qy         10 ACTAATCGATCCAATATGGAAAGAATTCACGTTGACTTAGATGCTGACAGCCCGTATGTC 69
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Db         30 AATTACCTACCCAAAATGGAGAAAGTTCACGTTGACATCGAGGAAGACAGCCCATTCCTC 89

Qy         70 AAGTCGTTACAGCGGACGTTTCCACAATTTGAGATCGAAGCAAGGCAGGTCACTGACAAT 129
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Db         90 AGAGCTTTGCAGCGGAGCTTCCCGCAGTTTGAGGTAGAAGCCAAGCAGGTCACTGATAAT 149

Qy        130 GACCATGCCAATGCCAGAGCGTTTTCGCATGTGGCAACAAAGCTCATTGAGAGCGAAGTC 189
              |||||||| |||||||||||||||||||||| ||||  |||| || || || |  || ||
Db        150 GACCATGCTAATGCCAGAGCGTTTTCGCATCTGGCTTCAAAACTGATCGAAACGGAGGTG 209

Qy        190 GACCGGGACCAAGTTATCTTGGACATTGGAAGTGCGCCCGTCAGACATGCACATTCCAAT 249
              ||||    | |    ||| | ||||||||||||||||||| | |         |||| ||
Db        210 GACCCATCCGACACGATCCTTGACATTGGAAGTGCGCCCGCCCGCAGAATGTATTCTAAG 269

Qy        250 CACCGCTATCATTGTATCTGCCCTATGATAAGCGCTGAAGACCCGGACAGACTACAACGG 309
              ||| |||||  || |  |||||      ||  ||  ||||||| ||| | ||  |  |
Db        270 CACAAGTATCATTGTATCTGTCCGATGAGATGTGCGGAAGATCCGGACAGATTGTATAAG 329

Qy        310 TATGCAGAAAGACTTAAGAAAAGT------GACATTACCGACAAGAACATAGCCTCTAAG 363
              ||||||    |  || |||||||         || || || || ||| |  | | |   ||
Db        330 TATGCAACTAAGCTGAAGAAAAACTGTAAGGAAATAACTGATAAGGAATTGGACAAGAAA 389

Qy        364 GCGGCAGACCTGCTGGAAGTCATGTCAACACCAGACGCAGAGACTCCATCTCTGTGTATG 423
                 |   || ||    |  ||||||      || |||   || |||    || ||||  |
Db        390 ATGAAGGAGCTCGCCGCCGTCATGAGCGACCCTGACCTGGAAACTGAGACTATGTGCCTC 449

Qy        424 CACACAGACGCCACGTGTAGGTACTTTGGAAGTGTAGCAGTATACCAAGATGTGTACGCA 483
              |||   ||||   ||||| | |||    ||    || || || ||||| ||||| |||||
Db        450 CACGACGACGAGTCGTGTCGCTACGAAGGGCAAGTCGCTGTTTACCAGGATGTATACGCG 509

Qy        484 GTCCATGCACCGACATCAATCTACCACCAGGCGCTTAAAGGAGTTAGGACAATTTACTGG 543
              ||  | | |||||||     |||| |||||  ||   ||| ||||||||        ||||||
Db        510 GTTGACGGACCGACAAGTCTCTATCACCAAGCCAATAAGGGAGTTAGAGTCGCCTACTGG 569

Qy        544 ATAGGCTTTGACACGACCCCTTTTATGTACAAAAACATGGCAGGTTCCTACCCTACTTAC 603
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Db        570 ATAGGCTTTGACACCACCCCTTTTATGTTTAAGAACTTGGCTGGAGCATATCCATCATAC 629

Qy        604 AACACGAACTGGGCTGACGAGAGAGTATTGGAAGCACGTAACATTGGCCTCGGTAACTCA 663
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Db        630 TCTACCAACTGGGCCGACGAAACCGTGTTAACGGCTCGTAACATAGGCCTATGCAGCTCT 689

Qy        664 GATCTTCAGGAGAGCAGGCTTGGAAAACTCTCAATCCTTAGGAAGAAGAGGCTCCAACCT 723
              ||  ||  |||| |     | | ||     | || || ||||| ||||||      |  ||||
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Qy        724 ACTAATAAGATCATATTCTCGGTTGGTTCAACAATCTACACAGAAGATAGATCACTGTTA 783
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Db        750 TCCAACAATGTTCTATTCTCTGTTGGCTCGACCATCTACCACGAGAAGAGGGACTTACTG 809

Qy        784 CGTAGCTGGCATCTTCCAAACGTGTTCCACTTGAAAGGAAAGTCTAACTTCACAGGTAGA 843
              | |||||||| || ||     || || |||||     || |||   || | |||| || |
Db        810 AGGAGCTGGCACCTGCCGTCTGTATTTCACTTACGTGGCAAGCAAAATTACACATGTCGG 869

Qy        844 TGTGGGACCATTGTCAGCTGTGAAGGGTACGTCATCAAAAAGATAACGATCAGCCCAGGA 903
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Qy        904 CTATACGGTAAAGTTGAGAACTTGGCGTCCACAATGCATCGCGAGGGTTTCTTGAGTTGC 963
              || || || ||    |     ||  ||  | || ||||| |||||||| |||||| | |||
Db        930 CTGTATGGGAAGCCTTCAGGCTATGCTGCTACGATGCACCGCGAGGGATTCTTGTGCTGC 989

Qy        964 AAAGTCACAGATACGCTGCGCGGCGAGAGGGTTTCTTTTGCTGTGTGTACGTATGTACCA 1023
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Qy       1024 GCCACACTTTGCGATCAGATGACAGGGATTCTGGCAACTGACGTTAGTGTGGATGACGCA 1083
              || ||| | || || || ||||| || || |||||||| || || |||| ||| |||||
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Qy       1084 CAAAAACTATTGGTTGGGCTCAACCAAAGGATTGTCGTCAATGGTAGGACGCAAAGAAAT 1143
              |||||||| |||||||||||||||  | || |||||||| ||| | || || |||||
Db       1110 CAAAAACTGCTGGTTGGGCTCAACCAGCGTATAGTCGTCAACGGTCGCACCCAGAGAAAC 1169

Qy       1144 ACTAACACAATGCAGAACTATCTATTACCAGTGGTCGCCCAGGCGTTTTCCAGGTGGGCG 1203
              || || || ||| | || || || || || || || |||||||| ||| | ||||||||
Db       1170 ACCAATACCATGAAAAATTACCTTTGCCCGTAGTGGCCCAGGCATTTGCTAGGTGGGCA 1229

Qy       1204 CGTGAACATCGTGCCGACTTGGACGACGAGAAAGAACTAGGGGTGCGGGAGCGCACTCTT 1263
              ||| ||   |  ||   || || || |    ||||||  | || ||  |      |
Db       1230 AAGGAATATAAGGAAGATCAAGAAGATGAAAGGCCACTAGGACTACGAGATAGACAGTTA 1289

Qy       1264 ACTATGGGCTGCTGCTGGGCTTTCAAGACCCAGAAAATCACATCCATCTACAAGAAGCCT 1323
              |||||  || || |||||||| |  |  || || || ||||| || || |||   ||
Db       1290 GTCATGGGGTGTTGTTGGGCTTTTAGAAGGCACAAGATAACATCTATTTATAAGCGCCCG 1349

Qy       1324 GGTACGCAAACAATTAAGAAAGTACCTGCCGTCTTTGACTCATTTGTGATTCCACGCCTT 1383
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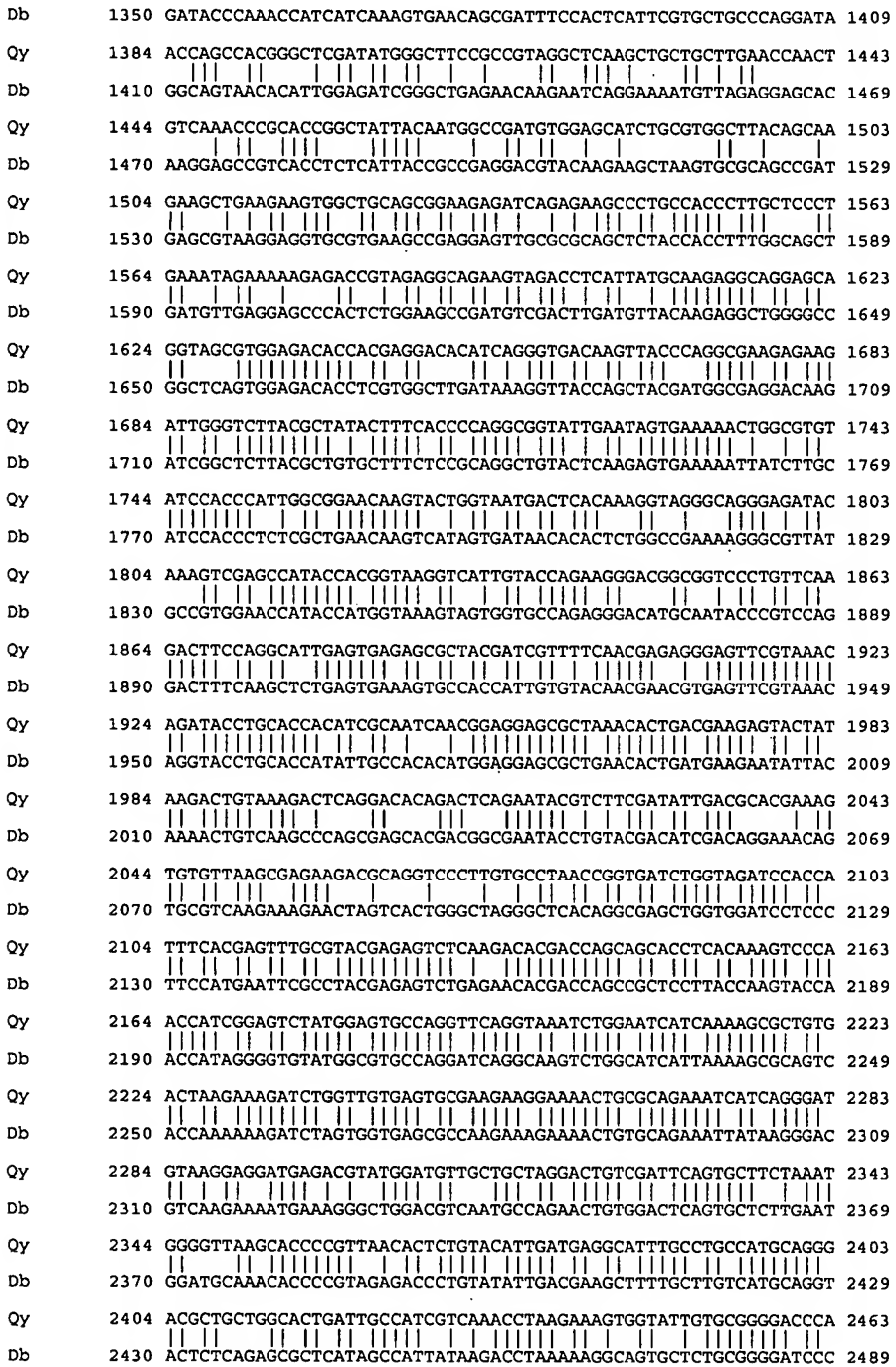
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Db 1410 GGCAGTAACACATTGGAGATCGGGCTGAGAACAAGAATCAGGAAAATGTTAGAGGAGCAC 1469
Qy 1444 GTCAAACCCGCACCGGCTATTACAATGGCCGATGTGGAGCATCTGCGTGGCTTACAGCAA 1503
Db 1470 AAGGAGCCGTCACCTCTCATTACCGCCGAGGACGTACAAGAAGCTAAGTGCGCAGCCGAT 1529
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Qy 1684 ATTGGGTCTTACGCTATACTTTCACCCCAGGCGGTATTGAATAGTGAAAAACTGGCGTGT 1743
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Qy 2164 ACCATCGGAGTCTATGGAGTGCCAGGTTCAGGTAAATCTGGAATCATCAAAAGCGCTGTG 2223
Db 2190 ACCATAGGGGTGTATGGCGTGCCAGGATCAGGCAAGTCTGGCATCATTAAAAGCGCAGTC 2249
Qy 2224 ACTAAGAAAGATCTGGTTGTGAGTGCGAAGAAGGAAAACTGCGCAGAAATCATCAGGGAT 2283
Db 2250 ACCAAAAAAAGATCTAGTGGTGAGCGCCAAGAAAGAAAACTGTGCAGAAATTATAAGGGAC 2309
Qy 2284 GTAAGGAGGATGAGACGTATGGATGTTGCTGCTAGGACTGTCGATTCAGTGCTTCTAAAT 2343
Db 2310 GTCAAGAAAATGAAAGGGCTGGACGTCAATGCCAGAACTGTGGACTCAGTGCTCTTGAAT 2369
Qy 2344 GGGGTTAAGCACCCCGTTAACACTCTGTACATTGATGAGGCATTTGCCTGCCATGCAGGG 2403
Db 2370 GGATGCAAACACCCCGTAGAGACCCTGTATATTGACGAAGCTTTTGCTTGTCATGCAGGT 2429
Qy 2404 ACGCTGCTGGCACTGATTGCCATCGTCAAACCTAAGAAAGTGGTATTGTGCGGGGACCCA 2463
Db 2430 ACTCTCAGAGCGCTCATAGCCATTATAAGACCTAAAAAGGCAGTGCTCTGCGGGGATCCC 2489
Qy 2464 AAACAATGCGGCTTCTTTAACATGATGTGCCTGAAAGTACATTTTAACCATGACATATGC 2523
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Qy 2524 ACTGAAGTGTACCATAAAAGCATCTCTAGGAGGTGCACACAGACTGTAACCGCCATCGTC 2583
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Qy 2584 TCCACGCTCTTCTACGACAAGCGAATGAAGACGGTTAACCCATGTGCTGATAAAATCATC 2643
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Qy 2644 ATAGATACCACAGGGACCACAAAGCCGCACAAAGATGATCTGATTCTAACCTGTTTCAGA 2703
Db 2670 ATTGACACTACCGGCAGTACCAAACCTAAGCAGGACGATCTCATTCTCACTTGTTTCAGA 2729
Qy 2704 GGATGGGTGAAACAGCTACAGATTGACTACAAAAATCACGAAATCATGACTGCGGCTGCA 2763
Db 2730 GGGTGGGTGAAGCAGTTGCAAATAGATTACAAAGGCAACGAAATAATGACGGCAGCTGCC 2789
Qy 2764 TCGCAAGGACTTACGCGGAAAGGCGTTTATGCTGTCAGGTACAAAGTCAACGAGAATCCA 2823
Db 2790 TCTCAAGGGCTGACCCGTAAAGGTGTGTATGCCGTTCGGTACAAGGTGAATGAAAATCCT 2849
Qy 2824 CTCTACTCGCAGACTTCTGAGCACGTGAACGTGTTACTTACACGCACAGAAAAACGCATT 2883
Db 2850 CTGTACGCACCCACCTCAGAACATGTGAACGTCCTACTGACCCGCACGGAGGACCGCATC 2909
Qy 2884 GTCTGGAAGACGCTAGCTGGTGATCCCTGGATAAAGACACTTACAGCTAAATATCCCGGG 2943
Db 2910 GTGTGGAAAACACTAGCCGGCGACCCATGGATAAAAACACTGACTGCCAAGTACCCTGGG 2969
Qy 2944 GATTTCACGGCTTCATTGGACGACTGGCAGCGCGAACACGACGCCATTATGGCACGCGTT 3003
Db 2970 AATTTCACTGCCACGATAGAGGAGTGGCAAGCAGAGCATGATGCCATCATGAGGCACATC 3029
Qy 3004 CTTGATAAGCCGCAGACAGCTGATGTGTTCCAGAATAAGGTGAACGTCTGCTGGGCGAAG 3063
Db 3030 TTGGAGAGACCGGACCCTACCGACGTCTTCCAGAATAAGGCAAACGTGTGTTGGGCCAAG 3089
Qy 3064 GCTTTAGAGCCAGTCTTGGCCACGGCCAACATTGTGCTGACGAGACAGCAGTGGGAGACG 3123
Db 3090 GCTTTAGTGCCGGTGCTGAAGACCGCTGGCATAGACATGACCACTGAACAATGGAACACT 3149
Qy 3124 TTGCACCCATTCAAGCATGACAGAGCGTACTCACCTGAAATGGCACTGAACTTCTTTTGC 3183
Db 3150 GTGGATTATTTTGAAACGGACAAAGCTCACTCAGCAGAGATAGTATTGAACCAACTATGC 3209
Qy 3184 ACCAGGTTCTTTGGAGTAGACCTGGACAGTGGGTTATTTTCCGCTCCTACCGTCGCACTT 3243
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Qy       3664 GTTAGGACCCCGTACAGGAACCATCACTACCAACAGTGCGAGGATCACGCTATCCACCAC 3723
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Qy       3784 GGGTATGGGCTTGCTGATCGCGCAACCGAGAATATCATCACTGCGGTGGCACGCTCATTT 3843
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Qy       3844 AGGTTTACCCGTGTCTGTCAGCCTAAGAACACTGCCGAAAATACTGAGGTTCTCTTCGTG 3903
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Qy       4024 ATCAGAGGTGACATTAGCAAGAGCGCTGACCAAGCTATCGTTAATGCTGCTAATAGCAAA 4083
Db       4050 GTGCGAGGGGATATTGCCACGGCCACCGAAGGAGTGATTATAAATGCTGCTAACAGCAAA 4109

Qy       4084 GGTCAACCAGGTTCCGGAGTGTGCGGTGCACTGTACCGAAAATGGCCGGCTGCTTTTGAT 4143
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Qy       4144 AGACAGCCAATAGCTGTCGGGACGGCTAGACTTGTGAAGCACGAACC---GCTCATCATA 4200
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Qy       4201 CATGCTGTAGGACCCAATTTTTCTAAGATGCCGGAACCGGAGGGCGACCTTAAGCTCGCA 4260
Db       4230 CATGCCGTAGGACCAAACTTCAACAAAGTTTCGGAGGTTGAAGGTGACAAACAGTTGGCA 4289

Qy       4261 GCTGCCTACATGAGCATAGCGTCCATCGTCAACGCTGAGCGGATTACAAAAATATCAGTA 4320
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Qy       4321 CCGCTACTGTCAACCGGCATCTATTCTGGTGGCAAAGATCGAGTGATGCAATCATTGCAT 4380
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Qy       4381 CACCTGTTCACTGCTTTCGACACTACGGATGCCGATGTCACCATATATTGCTTGGATAAA 4440
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Qy       4441 CAATGGGAGACCAGGATAATCGAGGCCATTCACCGCAAAGAAAGCGTCGAAATTCTGGA- 4499
Db       4470 AAATGGGAAATGACTCTCAAGGAAGCAGTGGCTAGGAGAGAAGCAGTGGAGGAGATATGC 4529

Qy       4500 --------------TGATGACAAGCCAGTAGACATTGACTTGGTCAGGGTCCACCCAAAC 4545
Db       4530 ATATCCGACGACTCTTCAGTGACAGAACCTGATGCAGAGCTGGTGAGGGTGCATCCGAAG 4589

Qy       4546 AGCTCTTTGGCAGGCAGACCAGGTTACTCCGTCAATGAGGGCAAGTTGTATTCATACCTG 4605
Db       4590 AGTTCTTTGGCTGGAAGGAAGGGCTACAGCACAAGCGATGGCAAAACTTTCTCATATTTG 4649

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Qy       4786 TGCCTGTGTAATTACGCTATGACGGCTGAGCGCGTATACAGGTTGCGCTCTGCGAAGAAA 4845
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Qy       4846 GAACAGTTCGCCGTATGCTCATCATTCCTGTTGCCGAAGTACAGGATCACAGGCGTGCAG 4905
Db       4890 GAACAAATTACTGTGTGCTCATCCTTTCCATTGCCGAAGTATAGAATCACTGGTGTGCAG 4949

Qy       4906 AAGCTACAGTGCAGCAAACCAGTCCTGTTTTCAGGCGTCGTACCACCGGCTGTACACCCC 4965
Db       4950 AAGATCCAATGCTCCCAGCCTATATTGTTCTCACCGAAAGTGCCTGCGTATATTCATCCA 5009

Qy       4966 AGGAAGTA 4973
Db       5010 AGGAAGTA 5017
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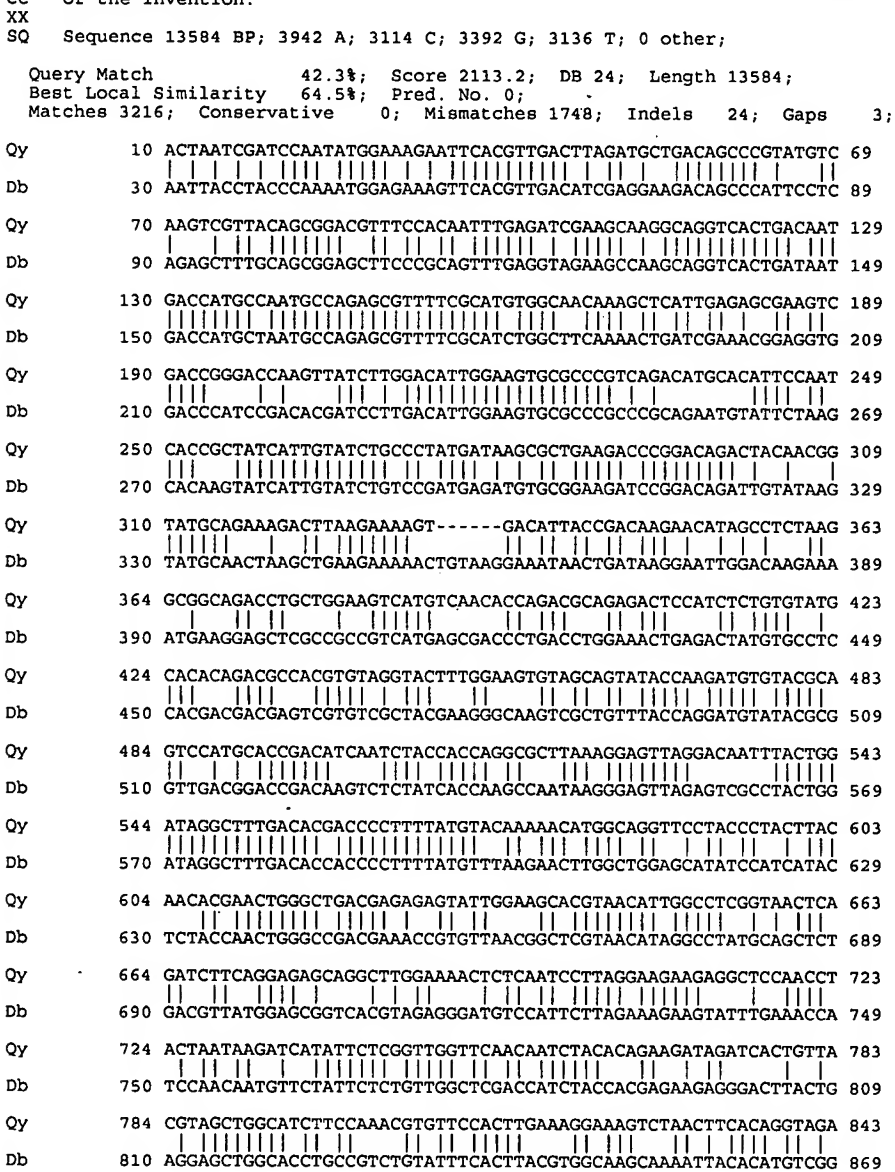
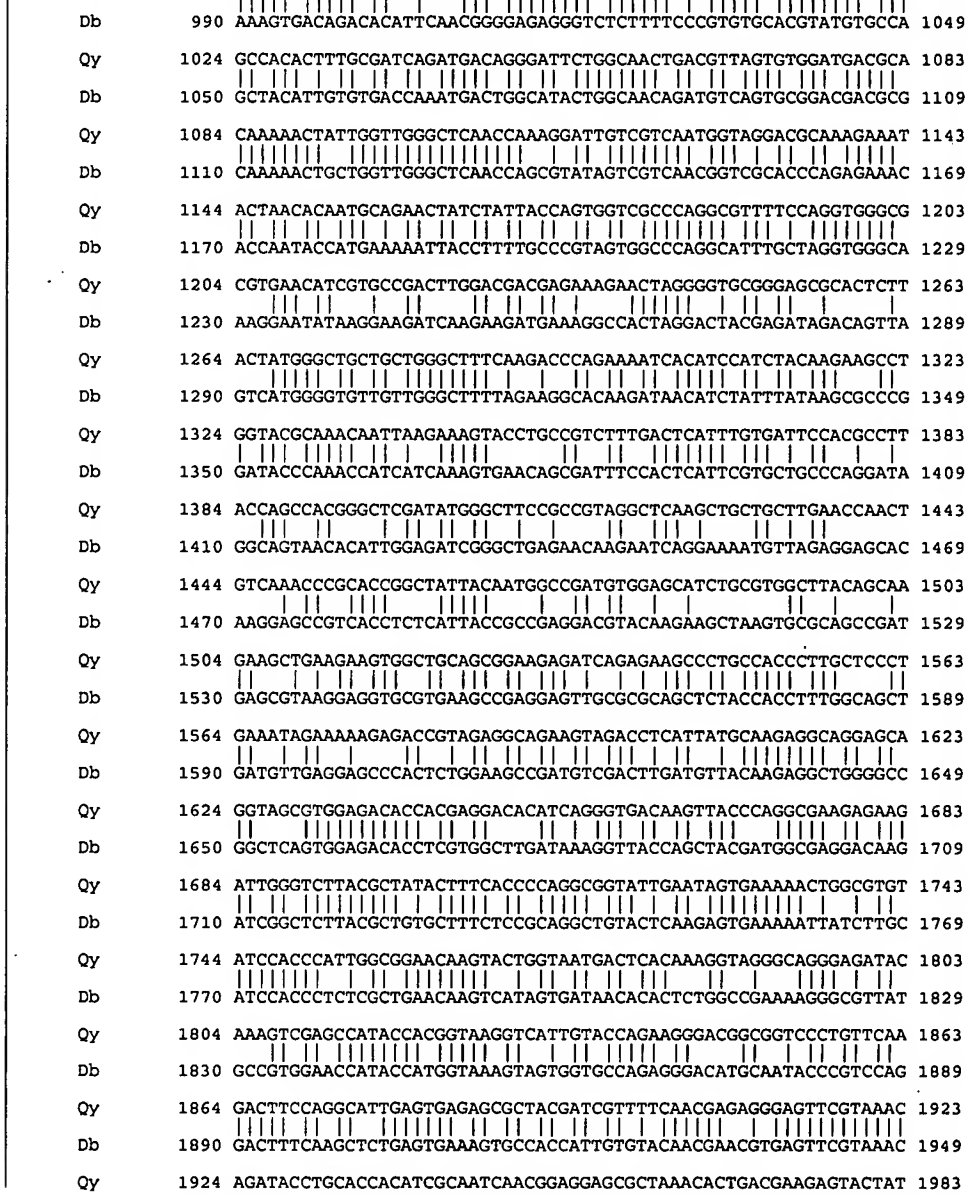
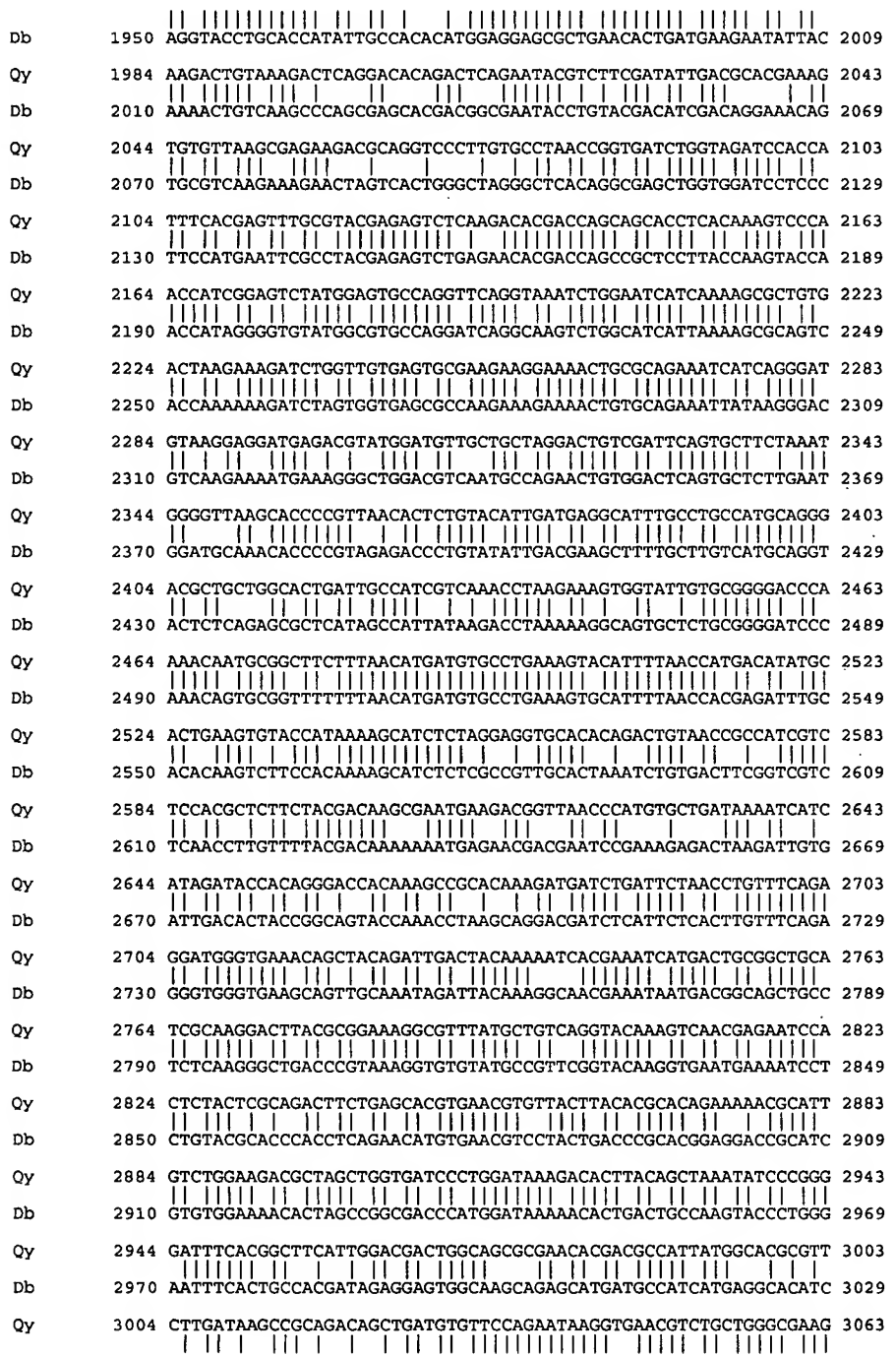
RESULT 5
AAD29141
ID AAD29141 standard; DNA; 13584 BP.
XX
AC AAD29141;
XX
DT 07-MAY-2002 (first entry)
XX
DE Venezuelan equine encephalitis virus (VEE) RNA replicon plasmid.
XX
KW Venezuelan equine encephalitis virus; VEE; vaccine; HIV infection;
KW human immunodeficiency virus; alpha-virus replicon; immune response;
KW therapy; ds.
XX
OS Chimeric - Venezuelan equine encephalitis virus.
OS Chimeric - Unidentified.
XX
PN WO200203917-A2.
XX
PD 17-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US21701.
XX
PR 07-JUL-2000; 2000US-216995P.
XX
PA (ALPH-) ALPHAVAX INC.
PA (UYNC-) UNIV NORTH CAROLINA.
XX
PI Olmsted R, Keith P, Dryga S, Caley I, Maughan M, Johnston R;
PI Davis N, Swanstrom R;
XX
DR WPI; 2002-171664/22.
XX
PT Composition useful for treating or preventing HIV infections, comprises
PT two or more isolated nucleic acids encoding env, gag or pol gene
PT product of HIV or immunogenic fragment of the gene products -
XX
PS Example 5; Page 190-195; 201pp; English.
XX
CC The invention relates to a composition comprising isolated nucleic acids
CC encoding env, gag or pol gene product of human immunodeficiency virus or
CC immunogenic fragment of the gene products. The gag gene product is
CC modified to inhibit formation of virus-like particles containing gag
CC gene product and their release from cells, and the pol gene product is
CC modified to inhibit reverse transcriptase activity. The invention also

CC relates to a method for producing an alpha-virus replicon particle used
CC in vaccines. The composition is useful for inducing an immune response
CC to human immunodeficiency virus (HIV) or for treating or preventing HIV
CC infection in a subject. The alpha-virus replicon particle is useful in a
CC vaccine. The composition is useful for administering a protein or peptide
CC to a subject. A composition comprising heparin affinity-purified alpha-
CC virus replicon particle is useful as a clinical trial material and as a
CC commercial product. The present sequence is Venezuelan equine
CC encephalitis virus (VEE) RNA replicon plasmid used in the exemplification
CC of the invention.
XX
SQ Sequence 13584 BP; 3942 A; 3114 C; 3392 G; 3136 T; 0 other;

Query Match 42.3%; Score 2113.2; DB 24; Length 13584;
Best Local Similarity 64.5%; Pred. No. 0;
Matches 3216; Conservative 0; Mismatches 1748; Indels 24; Gaps 3;



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Db 2010 AAAACTGTCAAGCCCAGCGAGCACGACGGCGAATACCTGTACGACATCGACAGGAAACAG 2069
Qy 2044 TGTGTTAAGCGAGAAGACGCAGGTCCCTTGTGCCTAACCGGTGATCTGGTAGATCCACCA 2103
Db 2070 TGCGTCAAGAAAGAACTAGTCACTGGGCTAGGGCTCACAGGCGAGCTGGTGGATCCTCCC 2129
Qy 2104 TTTCACGAGTTTGCGTACGAGAGTCTCAAGACACGACCAGCAGCACCTCACAAAGTCCCA 2163
Db 2130 TTCCATGAATTCGCCTACGAGAGTCTGAGAACACGACCAGCCGCTCCTTACCAAGTACCA 2189
Qy 2164 ACCATCGGAGTCTATGGAGTGCCAGGTTCAGGTAAATCTGGAATCATCAAAAGCGCTGTG 2223
Db 2190 ACCATAGGGGTGTATGGCGTGCCAGGATCAGGCAAGTCTGGCATCATTAAAAGCGCAGTC 2249
Qy 2224 ACTAAGAAAGATCTGGTTGTGAGTGCGAAGAAGGAAAACTGCGCAGAAATCATCAGGGAT 2283
Db 2250 ACCAAAAAAGATCTAGTGGTGAGCGCCAAGAAAGAAAACTGTGCAGAAATTATAAGGGAC 2309
Qy 2284 GTAAGGAGGATGAGACGTATGGATGTTGCTGCTAGGACTGTCGATTCAGTGCTTCTAAAT 2343
Db 2310 GTCAAGAAAATGAAAGGGCTGGACGTCAATGCCAGAACTGTGGACTCAGTGCTCTTGAAT 2369
Qy 2344 GGGGTTAAGCACCCCGTTAACACTCTGTACATTGATGAGGCATTTGCCTGCCATGCAGGG 2403
Db 2370 GGATGCAAACACCCCGTAGAGACCCTGTATATTGACGAAGCTTTTGCTTGTCATGCAGGT 2429
Qy 2404 ACGCTGCTGGCACTGATTGCCATCGTCAAACCTAAGAAAGTGGTATTGTGCGGGGACCCA 2463
Db 2430 ACTCTCAGAGCGCTCATAGCCATTATAAGACCTAAAAAGGCAGTGCTCTGCGGGGATCCC 2489
Qy 2464 AAACAATGCGGCTTCTTTAACATGATGTGCCTGAAAGTACATTTTAACCATGACATATGC 2523
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Qy 2524 ACTGAAGTGTACCATAAAAGCATCTCTAGGAGGTGCACACAGACTGTAACCGCCATCGTC 2583
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Qy 2884 GTCTGGAAGACGCTAGCTGGTGATCCCTGGATAAAGACACTTACAGCTAAATATCCCGGG 2943
Db 2910 GTGTGGAAAACACTAGCCGGCGACCCATGGATAAAAACACTGACTGCCAAGTACCCTGGG 2969
Qy 2944 GATTTCACGGCTTCATTGGACGACTGGCAGCGCGAACACGACGCCATTATGGCACGCGTT 3003
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Qy 3004 CTTGATAAGCCGCAGACAGCTGATGTGTTCCAGAATAAGGTGAACGTCTGCTGGGCGAAG 3063
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Qy 3064 GCTTTAGAGCCAGTCTTGGCCACGGCCAACATTGTGCTGACGAGACAGCAGTGGGAGACG 3123
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Db 3210 GTGAGGTTCTTTGGACTCGATCTGGACTCCGGTCTATTTTCTGCACCCACTGTTCCGTTA 3269
Qy 3244 ACTTACAGGGATCAGCACTGGGATAACTCGCCAGGGAAGAACATGTATGGGCTTAATAGA 3303
Db 3270 TCCATTAGGAATAATCACTGGGATAACTCCCCGTCGCCTAACATGTACGGGCTGAATAAA 3329
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Db 3630 GCTCGGCTGGATTTAGGCATCCCAGGTGATGTGCCCAAATATGACATAATATTTGTTAAT 3689
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Qy 3784 GGGTATGGGCTTGCTGATCGCGCAACCGAGAATATCATCACTGCGGTGGCACGCTCATTT 3843
Db 3810 GGTTATGGTTACGCTGACAGGGCCAGCGAAAGCATCATTGGTGCTATAGCGCGGCAGTTC 3869
Qy 3844 AGGTTTACCCGTGTCTGTCAGCCTAAGAACACTGCCGAAAATACTGAGGTTCTCTTCGTG 3903
Db 3870 AAGTTTTCCCGGGTATGCAAACCGAAATCCTCACTTGAAGAGACGGAAGTTCTGTTTGTA 3929
Qy 3904 TTCTTCGGCAAGGACAACGGCAACCACACACATGACCAGGACAGACTCGGTGTAGTGCTT 3963
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Qy 3964 GACAACATCTATCAAGGGTCAACCAGGTACGAGGCAGGGAGAGCTCCAGCGTACAGAGTG 4023
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Qy 4084 GGTCAACCAGGTTCCGGAGTGTGCGGTGCACTGTACCGAAAATGGCCGGCTGCTTTTGAT 4143
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Qy       4441 CAATGGGAGACCAGGATAATCGAGGCCATTCACCGCAAAGAAAGCGTCGAAATTCTGGA- 4499
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Qy       4500 --------------TGATGACAAGCCAGTAGACATTGACTTGGTCAGGGTCCACCCAAAC 4545
Db       4530 ATATCCGACGACTCTTCAGTGACAGAACCTGATGCAGAGCTGGTGAGGGTGCATCCGAAG 4589

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Qy       4606 GAAGGTACACGATTCCATCAGACCGCCAAGGACATTGCCGAAATCCATGCAATGTGGCCC 4665
Db       4650 GAAGGGACCAAGTTTCACCAGGCGGCCAAGGATATAGCAGAAATTAATGCCATGTGGCCC 4709

Qy       4666 AACAAATCTGAGGCTAATGAGCAGATTTGCTTGTACATCCTGGGGGAGAGTATGTCCAGC 4725
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Qy       4726 ATCCGCTCCAAATGCCCAGTAGAGGAGTCAGAGGCGTCTGCTCCACCTCACACACTTCCA 4785
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Qy       4786 TGCCTGTGTAATTACGCTATGACGGCTGAGCGCGTATACAGGTTGCGCTCTGCGAAGAAA 4845
Db       4830 TGCTTGTGCATCCATGCCATGACTCCAGAAAGAGTACAGCGCCTAAAAGCCTCACGTCCA 4889

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Qy       4906 AAGCTACAGTGCAGCAAACCAGTCCTGTTTTCAGGCGTCGTACCACCGGCTGTACACCCC 4965
Db       4950 AAGATCCAATGCTCCCAGCCTATATTGTTCTCACCGAAAGTGCCTGCGTATATTCATCCA 5009

Qy       4966 AGGAAGTA 4973
Db       5010 AGGAAGTA 5017
```

RESULT 6
AAD29132
ID AAD29132 standard; DNA; 7479 BP.
XX
AC AAD29132;
XX
DT 07-MAY-2002 (first entry)
XX
DE Venezuelan equine encephalitis virus (VEE) non-structural gene.
XX
KW Venezuelan equine encephalitis virus; VEE; vaccine; HIV infection;
KW human immunodeficiency virus; alpha-virus replicon; immune response;
KW therapy; non-structural gene; ds.
XX
OS Venezuelan equine encephalitis virus.
XX
FH Key Location/Qualifiers
FT CDS 1..7479
FT /*tag= a
FT /product= "VEE non-structural protein"
FT /transl_except= (pos:5635..5643, aa:Gln-Arg)
FT /note= "Insertion of 3 bases alters the reading frame;
FT CDS does not include stop codon"
FT /partial
XX
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XX
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XX
PF 09-JUL-2001; 2001WO-US21701.
XX
PR 07-JUL-2000; 2000US-216995P.
XX
PA (ALPH-) ALPHAVAX INC.
PA (UYNC-) UNIV NORTH CAROLINA.
XX
PI Olmsted R, Keith P, Dryga S, Caley I, Maughan M, Johnston R;
PI Davis N, Swanstrom R;
XX
DR WPI; 2002-171664/22.
DR P-PSDB; AAE18302.
XX
PT Composition useful for treating or preventing HIV infections, comprises
PT two or more isolated nucleic acids encoding env, gag or pol gene
PT product of HIV or immunogenic fragment of the gene products -
XX
PS Example 2; Page 145-156; 201pp; English.
XX
CC The invention relates to a composition comprising isolated nucleic acids
CC encoding env, gag or pol gene product of human immunodeficiency virus or
CC immunogenic fragment of the gene products. The gag gene product is
CC modified to inhibit formation of virus-like particles containing gag
CC gene product and their release from cells, and the pol gene product is
CC modified to inhibit reverse transcriptase activity. The invention also
CC relates to a method for producing an alpha-virus replicon particle used
CC in vaccines. The composition is useful for inducing an immune response
CC to human immunodeficiency virus (HIV) or for treating or preventing HIV
CC infection in a subject. The alpha-virus replicon particle is useful in a
CC vaccine. The composition is useful for administering a protein or peptide
CC to a subject. A composition comprising heparin affinity-purified alpha-
CC virus replicon particle is useful as a clinical trial material and as a
CC commercial product. The present sequence is a non-structural gene from
CC Venezuelan equine encephalitis virus (VEE) used in the exemplification
CC of the invention.
XX
SQ Sequence 7479 BP; 2141 A; 1774 C; 1900 G; 1664 T; 0 other;

Query Match 42.2%; Score 2111; DB 24; Length 7479;
Best Local Similarity 64.5%; Pred. No. 0;
Matches 3209; Conservative 0; Mismatches 1740; Indels 24; Gaps 3;

```
Qy         25 ATGGAAAGAATTCACGTTGACTTAGATGCTGACAGCCCGTATGTCAAGTCGTTACAGCGG 84
Db          1 ATGGAGAAAGTTCACGTTGACATCGAGGAAGACAGCCCATTCCTCAGAGCTTTGCAGCGG 60

Qy         85 ACGTTTCCACAATTTGAGATCGAAGCAAGGCAGGTCACTGACAATGACCATGCCAATGCC 144
Db         61 AGCTTCCCGCAGTTTGAGGTAGAAGCCAAGCAGGTCACTGATAATGACCATGCTAATGCC 120

Qy        145 AGAGCGTTTTCGCATGTGGCAACAAAGCTCATTGAGAGCGAAGTCGACCGGGACCAAGTT 204
Db        121 AGAGCGTTTTCGCATCTGGCTTCAAAACTGATCGAAACGGAGGTGGACCCATCCGACACG 180

Qy        205 ATCTTGGACATTGGAAGTGCGCCCGTCAGACATGCACATTCCAATCACCGCTATCATTGT 264
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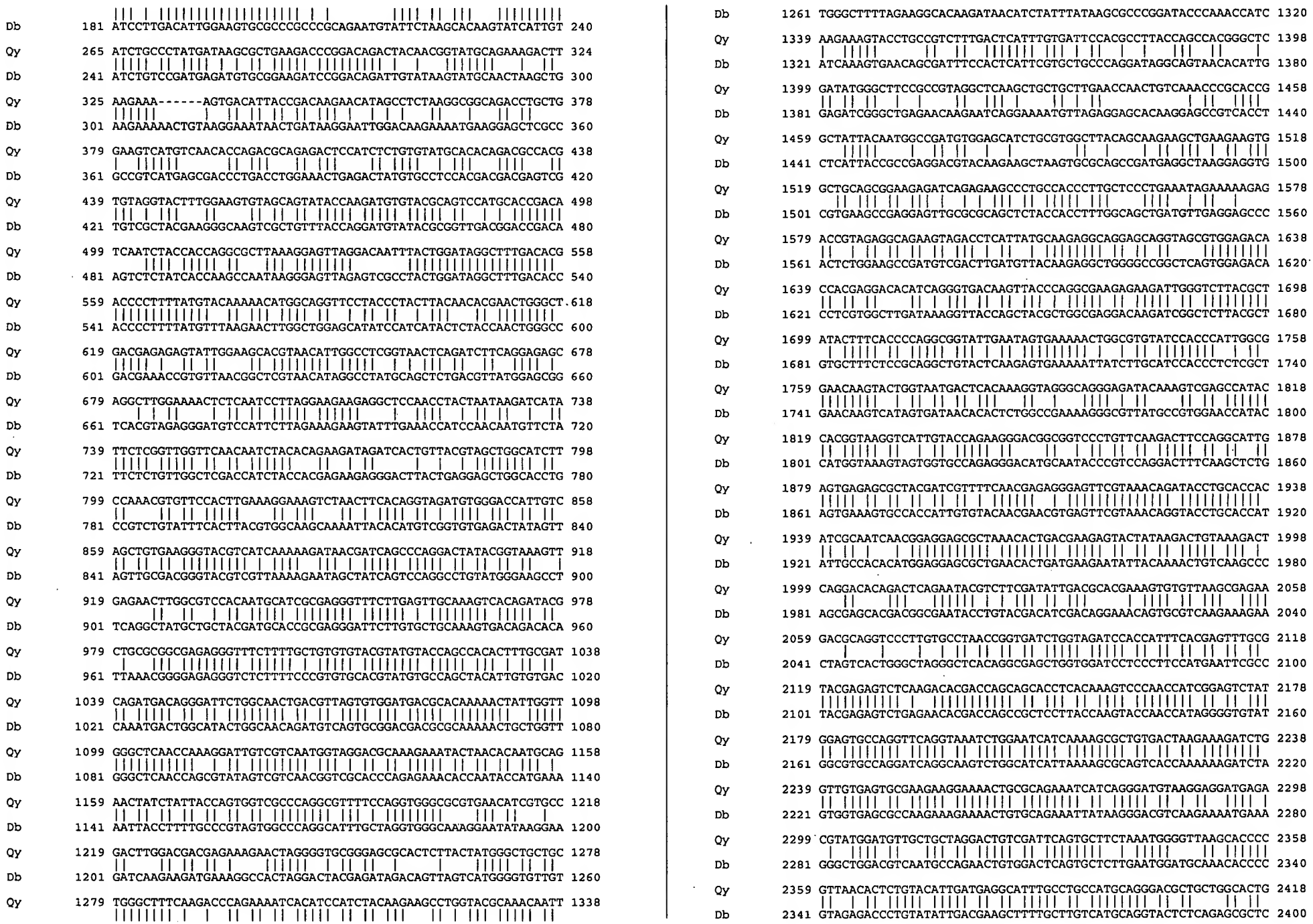

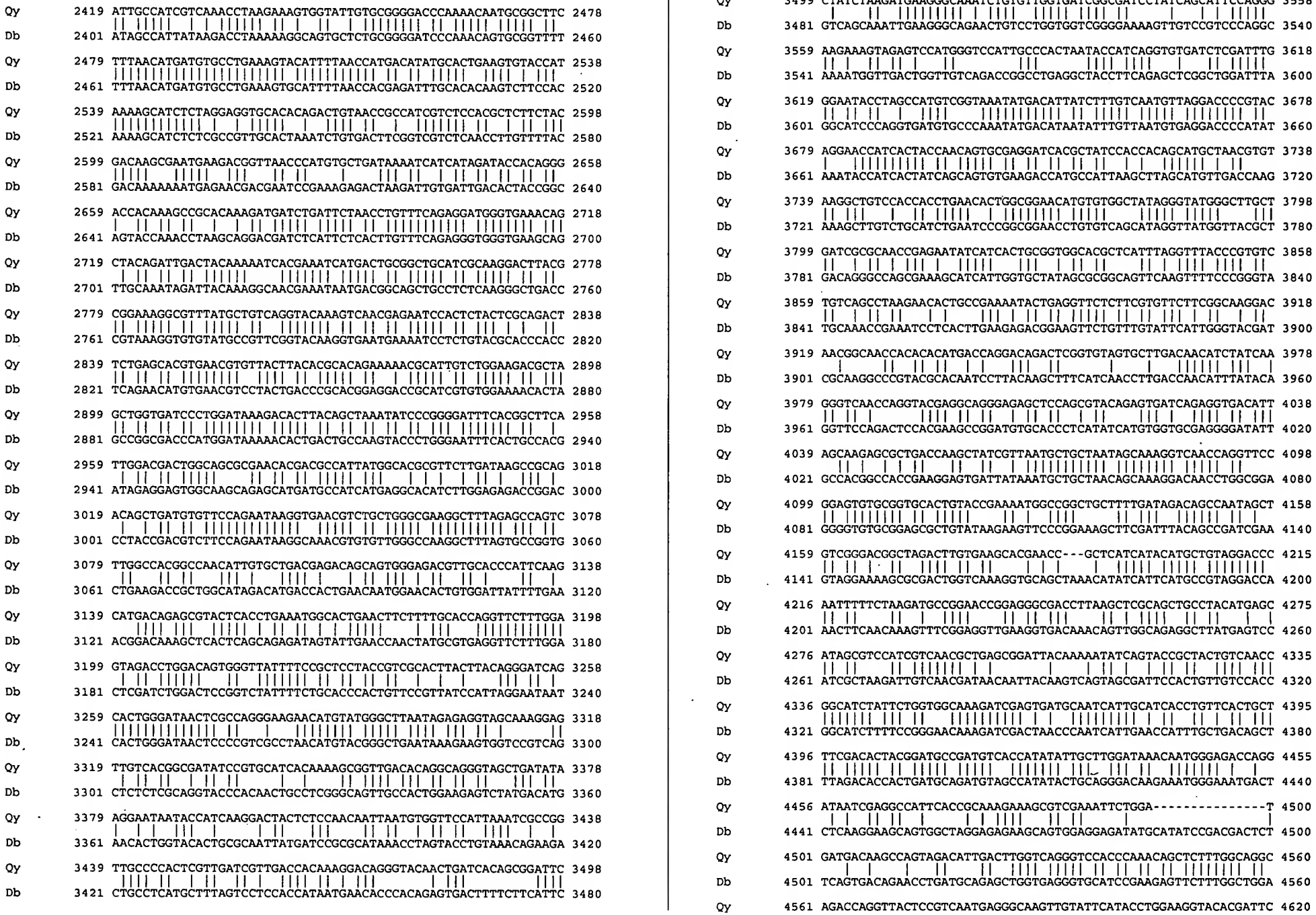

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Db       4561 AGGAAGGGCTACAGCACAAGCGATGGCAAAACTTTCTCATATTTGGAAGGGACCAAGTTT 4620

Qy       4621 CATCAGACCGCCAAGGACATTGCCGAAATCCATGCAATGTGGCCCAACAAATCTGAGGCT 4680

Db       4621 CACCAGGCGGCCAAGGATATAGCAGAAATTAATGCCATGTGGCCCGTTGCAACGGAGGCC 4680

Qy       4681 AATGAGCAGATTTGCTTGTACATCCTGGGGGAGAGTATGTCCAGCATCCGCTCCAAATGC 4740

Db       4681 AATGAGCAGGTATGCATGTATATCCTCGGAGAAAGCATGAGCAGTATTAGGTCGAAATGC 4740

Qy       4741 CCAGTAGAGGAGTCAGAGGCGTCTGCTCCACCTCACACACTTCCATGCCTGTGTAATTAC 4800

Db       4741 CCCGTCGAAGAGTCGGAAGCCTCCACACCACCTAGCACGCTGCCTTGCTTGTGCATCCAT 4800

Qy       4801 GCTATGACGGCTGAGCGCGTATACAGGTTGCGCTCTGCGAAGAAAGAACAGTTCGCCGTA 4860

Db       4801 GCCATGACTCCAGAAAGAGTACAGCGCCTAAAAGCCTCACGTCCAGAACAAATTACTGTG 4860

Qy       4861 TGCTCATCATTCCTGTTGCCGAAGTACAGGATCACAGGCGTGCAGAAGCTACAGTGCAGC 4920

Db       4861 TGCTCATCCTTTCCATTGCCGAAGTATAGAATCACTGGTGTGCAGAAGATCCAATGCTCC 4920

Qy       4921 AAACCAGTCCTGTTTTCAGGCGTCGTACCACCGGCTGTACACCCCAGGAAGTA 4973

Db       4921 CAGCCTATATTGTTCTCACCGAAAGTGCCTGCGTATATTCATCCAAGGAAGTA 4973


RESULT 7
AAV74108
ID   AAV74108 standard; cDNA; 11464 BP.
XX
AC   AAV74108;
XX
DT   12-APR-1999  (first entry)
XX
DE   Venezuelan equine encephalitis virus IE variant cDNA.
XX
KW   VEE IE virus; vaccine; ds.
XX
OS   Venezuelan equine encephalitis virus.
XX
PN   WO9853077-A1.
XX
PD   26-NOV-1998.
XX
PF   20-MAY-1998;   98WO-US10645.
XX
PR   16-DEC-1997;   97US-0991840.
PR   20-MAY-1997;   97US-0047162.
PR   24-JUL-1997;   97US-0053652.
XX
PA   (REED-) REED ARMY INST RES WALTER.
XX
PI   Crise BJ,  Oberste MS,  Parker MD,  Schmura SM,  Smith JF;
XX
DR   WPI; 1999-045316/04.
XX
PT   New DNA encoding infectious Western or Venezuelan equine
PT   encephalitis virus genome - useful for the production of live or
PT   attenuated vaccines for human or veterinary medicine
XX
PS   Claim 24; Page 68-79; 112pp; English.
XX
CC   This cDNA sequence codes for an infectious Venezuelan equine
CC   encephalitis virus IE variant (VEE IE) RNA transcript.  Using
CC   primers (see AAV74122-29) specific to genomic RNA of VEE IE, RT-PCR
CC   was used to generate cDNA fragments which were subsequently cloned
CC   and used to assemble the full-length cDNA.  The full-length
CC   infectious clone is useful in the production of virulent VEE IE
CC   virus, and for introducing and testing attenuating mutations.  Also
CC   new are: infectious or attenuated VEE IE RNA transcripts and viral
CC   particles; cDNA (see AAV74107) encoding an infectious Western equine
CC   encephalitis (WEE) viral genome; infectious or attenuated WEE RNA
CC   transcripts and viral particles; an attenuated chimeric virus
CC   containing non-structural sequences from a first alpha-virus (aV)
CC   and structural sequences from a second aV, resulting in attenuation
CC   of the second aV; a method for expressing a protein (especially an
CC   antigen to protect against a pathogen) by cloning its gene into an
CC   attenuated WEE or VEE IE replicon so that transcription of the
CC   replicon produces RNA able to infect the cells in which protein is
CC   to be produced; methods for diagnosing WEE and VEE infections; and
CC   polypeptides encoded by VEE variant IIIA (see AAV74109).  Attenuated
CC   WEE and VEE are used in live or inactivated vaccines, for use in
CC   human or veterinary medicine.  Chimeric viruses are also useful as
CC   vaccines, directed against the second aV which is particularly
CC   Eastern equine encephalitis (EEE) virus or some variant of VEE.
CC   WEE and VEE nucleic acids are used as primers and probes to
CC   diagnose virus infections and to define natural variants, also for
CC   production of protein antigens which can be used as diagnostic
CC   reagents, to generate antibodies, and in vaccines.  The attenuated
CC   viruses are highly immunogenic and provide long-lasting protection.
XX
SQ   Sequence 11464 BP; 3259 A; 2734 C; 2900 G; 2571 T; 0 other;

  Query Match             41.5%;  Score 2074.8;  DB 20;  Length 11464;
  Best Local Similarity   64.1%;  Pred. No. 0;
  Matches 3202;  Conservative    0;  Mismatches 1772;  Indels   24;  Gaps    4;

Qy          1 ACCCTACAAACTAATCGATCCAATATGGAAAGAATTCACGTTGACTTAGATGCTGACAGC 60

Db         20 AGCCCAAACCAATAACTACCCAAAATGGAGAAAGTTCACGTTGACATCGAGGAAGATAGT 79

Qy         61 CCGTATGTCAAGTCGTTACAGCGGACGTTTCCACAATTTGAGATCGAAGCAAGGCAGGTC 120

Db         80 CCCTTCCTCAGAGCATTACAACGGAGCTTCCCGCAGTTTGAGGTAGAAGCCAAGCAGGTC 139

Qy        121 ACTGACAATGACCATGCCAATGCCAGAGCGTTTTCGCATGTGGCAACAAAGCTCATTGAG 180

Db        140 ACAGATAATGACCATGCTAACGCCAGAGCGTTTTCGCATTTGGCATCGAAATTGATCGAG 199

Qy        181 AGCGAAGTCGACCGGGACCAAGTTATCTTGGACATTGGAAGTGCGCCCGTCAGACATGCA 240

Db        200 ACGGAGGTGGAACCATCCGATACGATCCTAGACATTGGAAGTGCGCCTGCCCGCAGAATG 259

Qy        241 CATTCCAATCACCGCTATCATTGTATCTGCCCTATGATAAGCGCTGAAGACCCGGACAGA 300

Db        260 TATTCCAAGCATAAGTACCATTGCATCTGTCCGATGAAATGTGCAGAAGATCCGGACAGA 319

Qy        301 CTACAACGGTATGCAGAAAGACTTAAGAAAAGT------GACATTACCGACAAGAACATA 354

Db        320 CTGTTTAAGTATGCAGCCAAGCTGAAGAAGAACTGTAAAGAGATTACAGATAAGGAACTG 379

Qy        355 GCCTCTAAGGCGGCAGACCTGCTGGAAGTCATGTCAACACCAGACGCAGAGACTCCATCT 414

Db        380 GACAAGAAGATGAAGGAGCTTGCGGAAGTCATGAGCGACCCTGATCTCGAAACTGAAACG 439

Qy        415 CTGTGTATGCACACAGACGCCACGTGTAGGTACTTTGGAAGTGTAGCAGTATACCAAGAT 474

Db        440 ATTTGCCTTCACGACGATGAAACCTGTCGATTTGAGGGTCAAGTCGCAGTGTATCAGGAT 499

Qy        475 GTGTACGCAGTCCATGCACCGACATCAATCTACCACCAGGCGCTTAAAGGAGTTAGGACA 534

Db        500 GTGTACGCGGTTGACGGACCGACGAGCCTTTACCATCAGGCCAACAAAGGGGTCAGAGTC 559

Qy        535 ATTTACTGGATAGGCTTTGACACGACCCCTTTTATGTACAAAAACATGGCAGGTTCCTAC 594

Db        560 GCCTATTGGATAGGATTCGACACTACCCCTTTTATGTTTAAGAACCTGGCTGGAGCATAT 619

Qy        595 CCTACTTACAACACGAACTGGGCTGACGAGAGAGTATTGGAAGCACGTAACATTGGCCTC 654

Db        620 CCCTCCTATTCGACCAACTGGGCCGACGAGACCGTGTTAACGGCTCGTAATATAGGCTTG 679

Qy        655 GGTAACTCAGATCTTCAGGAGAGCAGGCTTGGAAAACTCTCAATCCTTAGGAAGAAGAGG 714

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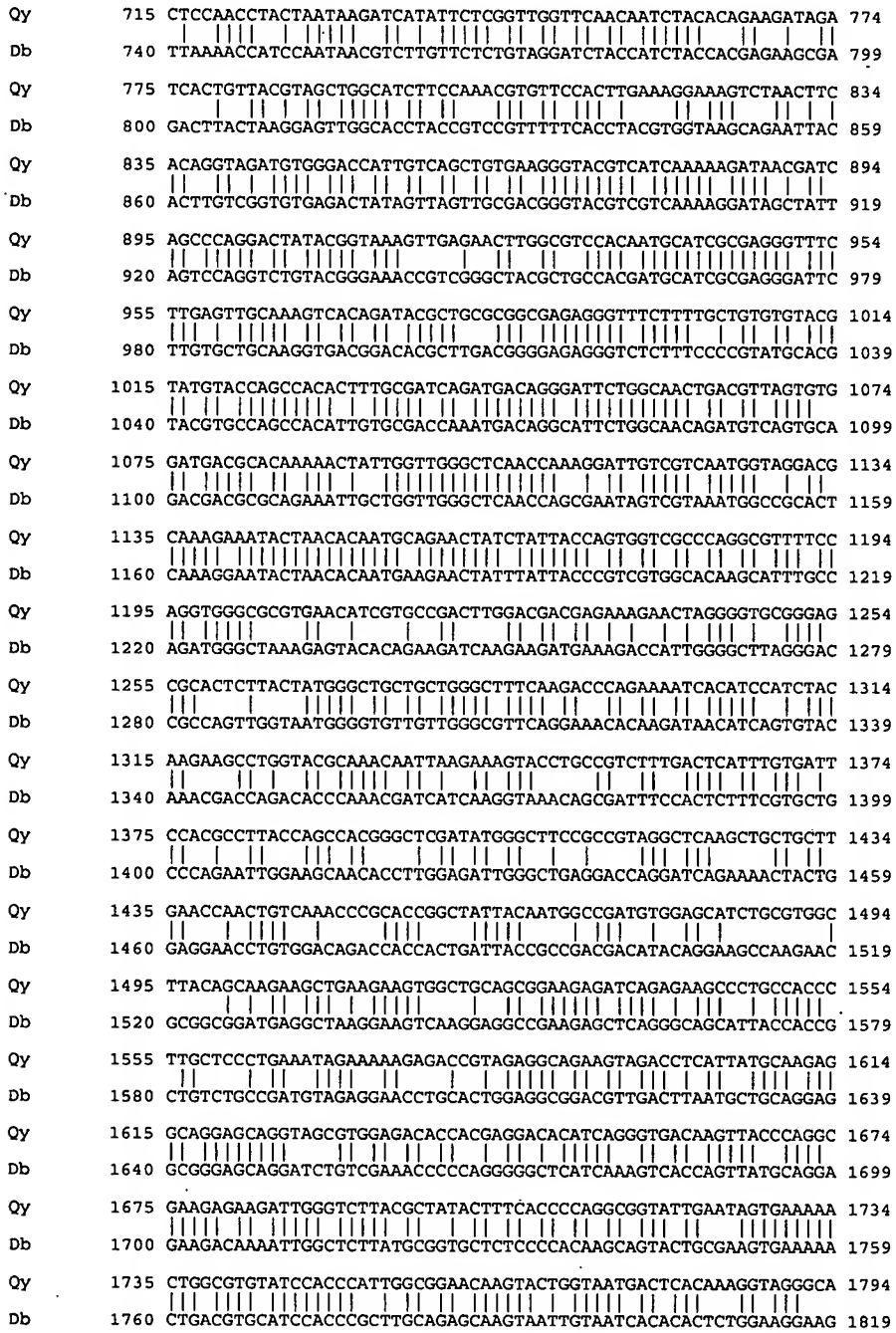
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Qy 1675 GAAGAGAAGATTGGGTCTTACGCTATACTTTCACCCCAGGCGGTATTGAATAGTGAAAAA 1734
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Qy 1735 CTGGCGTGTATCCACCCATTGGCGGAACAAGTACTGGTAATGACTCACAAAGGTAGGGCA 1794
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Qy 1855 CCTGTTCAAGACTTCCAGGCATTGAGTGAGAGCGCTACGATCGTTTTCAACGAGAGGGAG 1914
Db 1880 CCTGTCCAAGACTTCCAAGCACTCAGTGAGAGCGCCACAATTGTGTACAACGAACGTGAG 1939
Qy 1915 TTCGTAAACAGATACCTGCACCACATCGCAATCAACGGAGGAGCGCTAAACACTGACGAA 1974
Db 1940 TTCGTGAATAGGTATTTACACCACATTGCCACGCACGGTGGAGCTCTGAACACAGACGAG 1999
Qy 1975 GAGTACTATAAGACTGTAAAGACTCAGGACACAGACTCAGAATACGTCTTCGATATTGAC 2034
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Qy 2095 GATCCACCATTTCACGAGTTTGCGTACGAGAGTCTCAAGACACGACCAGCAGCACCTCAC 2154
Db 2120 GATCCCCCCTTCCATGAATTTGCATATGAAAGCTTGAGGACACGTCCGCCCGCACCTTAT 2179
Qy 2155 AAAGTCCCAACCATCGGAGTCTATGGAGTGCCAGGTTCAGGTAAATCTGGAATCATCAAA 2214
Db 2180 CAAGTACCAACTATAGGTGTGTATGGCGTTCCCGGGTCCGGGAAGTCTGGAATTATTAAG 2239
Qy 2215 AGCGCTGTGACTAAGAAAGATCTGGTTGTGAGTGCGAAGAAGGAAAACTGCGCAGAAATC 2274
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Qy 2455 GGGGACCCAAAACAATGCGGCTTCTTTAACATGATGTGCCTGAAAGTACATTTTAACCAT 2514
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Qy 2575 GCCATCGTCTCCACGCTCTTCTACGACAAGCGAATGAAGACGGTTAACCCATGTGCTGAT 2634
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Qy 2635 AAAATCATCATAGATACCACAGGGACCACAAAGCCGCACAAAGATGATCTGATTCTAACC 2694
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Qy 2695 TGTTTCAGAGGATGGGTGAAACAGCTACAGATTGACTACAAAAATCACGAAATCATGACT 2754
Db 2720 TGTTTTAGGGGATGGGTTAAGCAACTGCAAATAGACTACAAAGGAAATGAAATAATGACC 2779
Qy 2755 GCGGCTGCATCGCAAGGACTTACGCGGAAAGGCGTTTATGCTGTCAGGTACAAAGTCAAC 2814
Db 2780 GCGGCTGCCTCACAGGGATTGACGCGGAAAGGTGTCTATGCAGTTAGGTACAAAGTTAAC 2839
Qy 2815 GAGAATCCACTCTACTCGCAGACTTCTGAGCACGTGAACGTGTTACTTACACGCACAGAA 2874
Db 2840 GAGAACCCATTGTACGCACCCACCTCAGAGCATGTAAATGTGCTGTTGACCCGGACGGAA 2899
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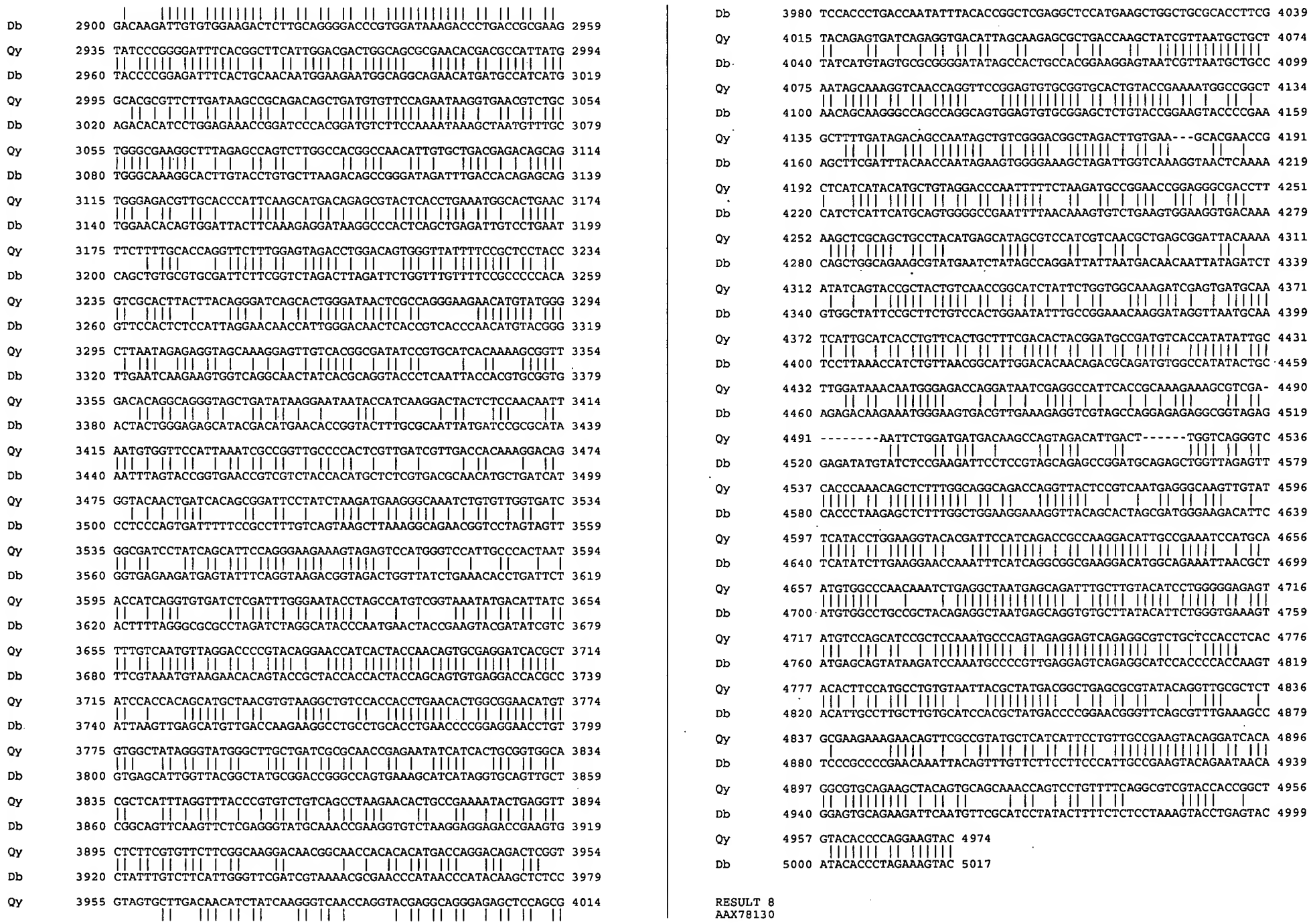

RESULT 8
AAX78130

```
ID   AAX78130 standard; DNA; 11060 BP.
XX
AC   AAX78130;
XX
DT   20-AUG-1999  (first entry)
XX
DE   pSFV link DNA.
XX
KW   Alphavirus; replicon; expression vector; heterologous splice site;
KW   RNA splicing; viral RNA replication; antigen; vaccination; therapy; ss.
XX
OS   Semliki forest virus.
OS   Synthetic.
XX
PN   WO9925859-A1.
XX
PD   27-MAY-1999.
XX
PF   13-NOV-1998;   98WO-CA01065.
XX
PR   14-NOV-1997;   97US-0065793.
XX
PA   (CONN-) CONNAUGHT LAB LTD.
XX
PI   Parrington M;
XX
DR   WPI; 1999-385140/32.
XX
PT   New vector (EV) used to express an antigen for vaccination, e.g.
PT   against human immune deficiency virus
XX
PS   Disclosure; Fig 4A-H; 60pp; English.
XX
CC   This invention describes the construction of a novel expression vector
CC   (EV) containing an alphavirus replicon having a heterologous splice site.
CC   The expression vector contains (i) a DNA molecule (I) complementary to
CC   at least part of an alphavirus RNA genome, and (ii) inserted into a
CC   region of (I) that is not essential for its replication, a heterologous
CC   DNA (II), under control of a promoter. (I) includes at least one
CC   heterologous splice site (HSS) to prevent aberrant RNA splicing of the
CC   alphavirus and is the complement of the complete alphavirus genomic
CC   region essential for replication of viral RNA. The expression vector is
CC   used to express (II) in humans or animals, e.g. to express an antigen
CC   for vaccination (against human immune deficiency virus) or to produce a
CC   therapeutically active protein or peptide. Introducing an HSS: (1) makes
CC   it more likely that any splicing will occur at this site, rather than at
CC   a cryptic splice site; (2) restores function of the alphavirus when
CC   eliminated, and (3) may improve transport of RNA from the nucleus.
XX
SQ   Sequence 11060 BP; 2978 A; 2826 C; 2926 G; 2330 T; 0 other;

  Query Match             31.3%;  Score 1565.6;  DB 20;  Length 11060;
  Best Local Similarity   58.3%;  Pred. No. 0;
  Matches 2905;  Conservative    0;  Mismatches 2039;  Indels   36;  Gaps    8;

Qy         31 AGAATTCACGTTGACTTAGATGCTGACAGCCCGTATGTCAAGTCGTTACAGCGGACGTTT 90
              | | | || |||||  | || ||||||||||| |   ||||||| || |||  | | |||
Db         96 AAAGTGCATGTTGATATTGAGGCTGACAGCCCATTCATCAAGTCTTTGCAGAAGGCATTT 155

Qy         91 CCACAATTTGAGATCGAAGCAAGGCAGGTCACTGACAATGACCATGCCAATGCCAGAGCG 150
              ||    || ||| | ||  ||  |||||||||    ||||||||||| ||||||||||
Db        156 CCGTCGTTCGAGGTGGAGTCATTGCAGGTCACACCAAATGACCATGCAAATGCCAGAGCA 215

Qy        151 TTTTCGCATGTGGCAACAAAGCTCATTGAGAGCGAAGTCGACCGGGACCAAGTTATCTTG 210
              ||||||||  |||| || ||  | || |||   ||    |||  ||| | | ||||||
Db        216 TTTTCGCACCTGGCTACCAAATTGATCGAGCAGGAGACTGACAAAGACACACTCATCTTG 275

Qy        211 GACATTGGAAGTGCGCCCGTCAGACATGCACATTCCAATCACCGCTATCATTGTATCTGC 270
              || || || ||||||||   |||          || |  |||   || || ||  | |||
Db        276 GATATCGGCAGTGCGCCTTCCAGGAGAATGATGTCTACGCACAAATACCACTGCGTATGC 335

Qy        271 CCTATGATAAGCGCTGAAGACCCGGACAGACTACAACGGTATGCAGAAAGACT------T 324
              ||||||   ||||| |||||||| || || ||  |  | || ||| | | |||

Db        336 CCTATGCGCAGCGCAGAAGACCCCGAAAGGCTCGATAGCTACGCAAAGAAACTGGCAGCG 395

Qy        325 AAGAAAAGTGACATTACCGACAAGAACATAGCCTCTAAGGCGGCAGACCTGCTGGAAGTC 384
                 | |  |    || |   | || ||    ||     | |||||||  |   |||
Db        396 GCCTCCGGGAAGGTGCTGGATAGAGAGATCGCAGGAAAAATCACCGACCTGCAGACCGTC 455

Qy        385 ATGTCAACACCAGACGCAGAGACTCCATCTCTGTGTATGCACACAGACGCCACGTGTAGG 444
              ||| | || |||||||| ||  |||||  |  | ||  |||| |||||||  |||||||  |
Db        456 ATGGCTACGCCAGACGCTGAATCTCCAACCTTTTGCCTGCATACAGACGTCACGTGTCGT 515

Qy        445 TACTTTGGAAGTGTAGCAGTATACCAAGATGTGTACGCAGTCCATGCACCGACATCAATC 504
                  |     || || |||||||| || |||||  || || ||||||||  |||||  |
Db        516 ACGGCAGCCGAAGTGGCCGTATACCAGGACGTGTATGCTGTACATGCACCAACATCGCTG 575

Qy        505 TACCACCAGGCGCTTAAAGGAGTTAGGACAATTTACTGGATAGGCTTTGACACGACCCCT 564
              |||||  ||||||  | |||||  || || ||    || |||||  || ||||||||  |||||
Db        576 TACCATCAGGCGATGAAAGGTGTCAGAACGGCGTATTGGATTGGGTTTGACACCACCCCG 635

Qy        565 TTTATGTACAAAAACATGGCAGGTTCCTACCCTACTTACAACACGAACTGGGCTGACGAG 624
              |||||||    |      | |||||  | || || || |||  ||| ||||||||  ||||||
Db        636 TTTATGTTTGACGCGCTAGCAGGCGCGTATCCAACCTACGCCACAAACTGGGCCGACGAG 695

Qy        625 AGAGTATTGGAAGCACGTAACATTGGCCTCGGTAACTCAGATCTTCAGGAGAGCAGGCTT 684
                 || ||  | ||  | |||||  || ||  ||     ||     |    ||| | || ||
Db        696 CAGGTGTTACAGGCCAGGAACATAGGACTGTGTGCAGCATCCTTGACTGAGGGAAGACTC 755

Qy        685 GGAAAACTCTCAATCCTTAGGAAGAAGAGGCTCCAACCTACTAATAAGATCATATTCTCG 744
              || ||||| || || ||  | ||||||     |  |||||    | |   |||| ||||||
Db        756 GGCAAACTGTCCATTCTCCGCAAGAAGCAATTGAAACCTTGCGACACAGTCATGTTCTCG 815

Qy        745 GTTGGTTCAACAATCTACACAGAAGATAGATCACTGTTACGTAGCTGGCATCTTCCAAAC 804
              || || || ||| | ||||| ||     |||   ||  |  | |||||||| | ||   |
Db        816 GTAGGATCTACATTGTACACTGAGAGCAGAAAGCTACTGAGGAGCTGGCACTTACCCTCC 875

Qy        805 GTGTTCCACTTGAAAGGAAAGTCTAACTTCACAGGTAGATGTGGGACCATTGTCAGCTGT 864
              || |||||| ||||||| ||      ||| ||  |||| || |  ||||| ||    |||
Db        876 GTATTCCACCTGAAAGGTAAACAATCCTTTACCTGTAGGTGCGATACCATCGTATCATGT 935

Qy        865 GAAGGGTACGTCATCAAAAAGATAACGATCAGCCCAGGACTATACGGTAAAGTTGAGAAC 924
              ||||||||||  | || || || || ||  |||| || || |||||||||    |
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              |  ||    ||    ||  |||||  |||  |    |||||    ||||||  || |
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              || || || || || || ||||| |    ||| |||||||| ||  | || || ||  |
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              || || ||||| || || || || || || ||  |||| |||||||| ||| ||||||||
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              ||  | ||  | || |||   || |||  || ||||||| | ||| |    || ||| |
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              || || || |||   || || || || ||| |  | ||||||    ||||||  |||||
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              || || ||   ||| ||     |||| |||||||| || |  || || |||||   |||
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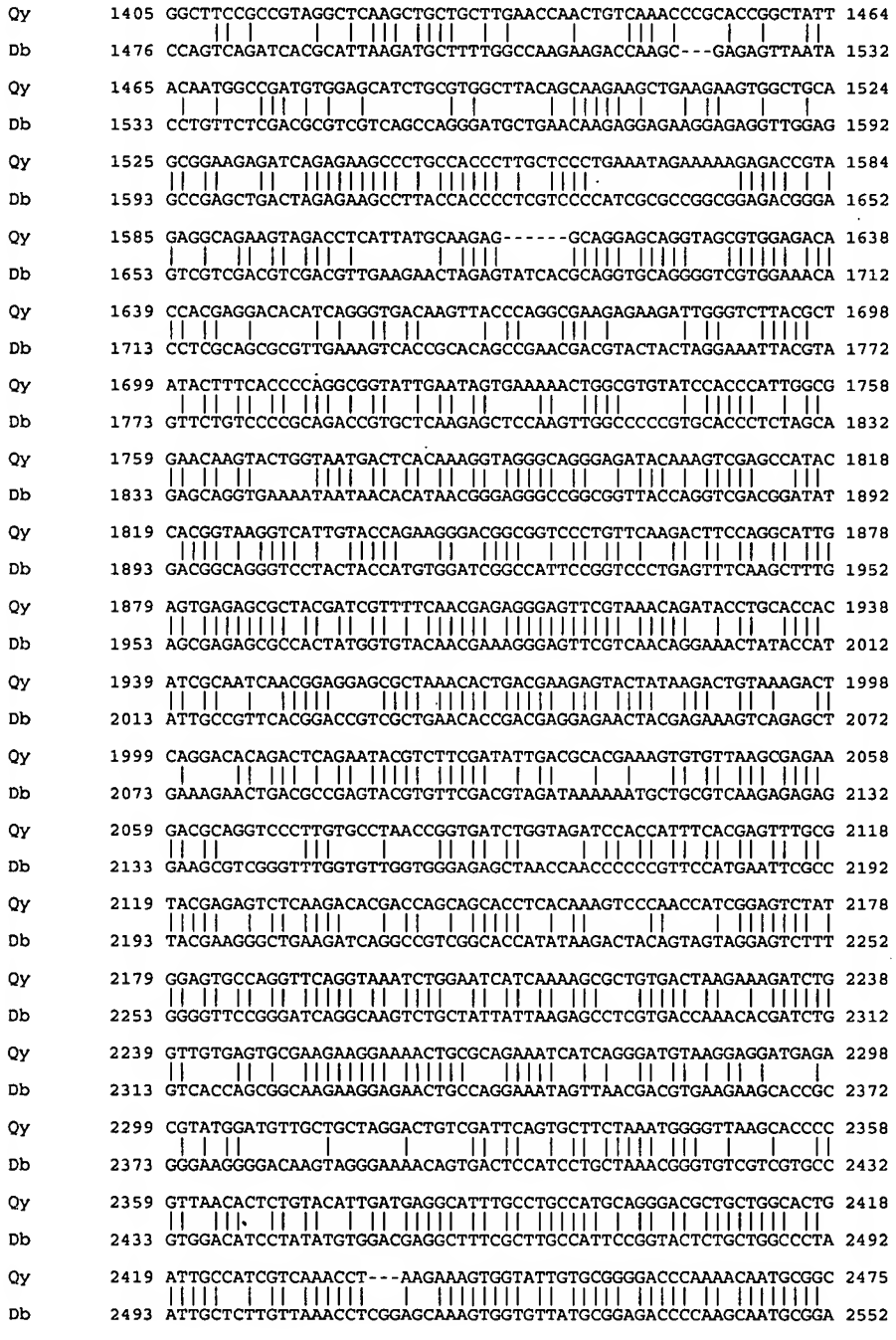
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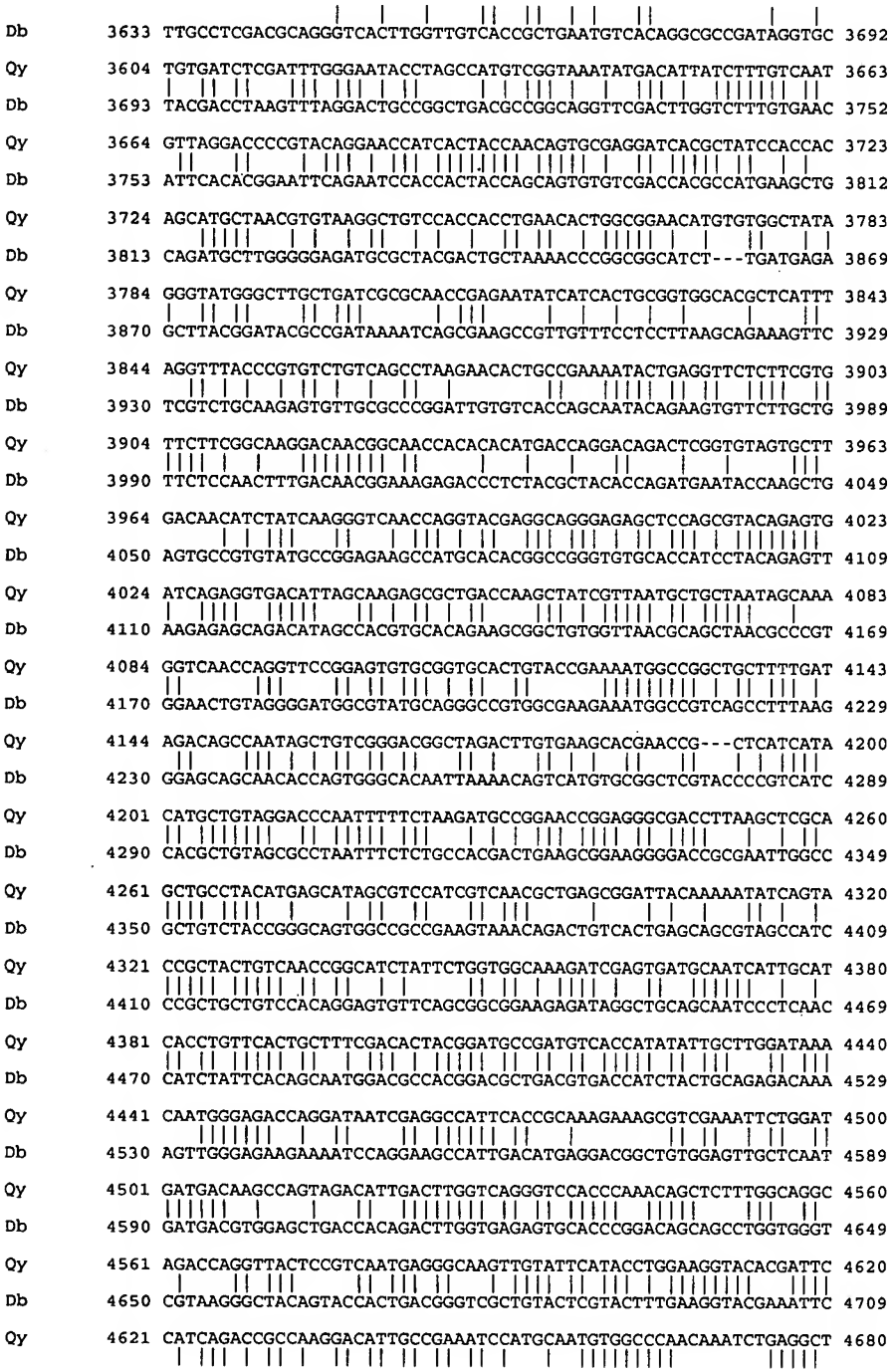

RESULT 9
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AC AAC55473;
XX
DT 11-JAN-2001 (first entry)
XX
DE Destination vector pDEST9 nucleotide sequence.
XX
KW Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
KW mutant; recombinational cloning; entry vector; destination vector;
KW gene product targeting; fusion tag cleavage; ds.
XX
OS Bacteriophage lambda.
OS Synthetic.
XX
PN WO200052027-A1.
XX
PD 08-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US05432.
XX
PR 02-MAR-1999; 99US-0122389.
PR 23-MAR-1999; 99US-0126049.
PR 28-MAY-1999; 99US-0136744.
XX
PA (LIFE-) LIFE TECHNOLOGIES INC.
XX
PI Hartley JL, Brasch MA, Temple GF, Cheo D;
XX
DR WPI; 2000-543948/49.
XX
PT Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides -
XX
PS Disclosure; Fig 29; 459pp; English.
XX
CC The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule

CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is
CC used in the exemplification of the present invention.
XX
SQ Sequence 12464 BP; 3328 A; 3120 C; 3257 G; 2759 T; 0 other;

Query Match 31.3%; Score 1565.6; DB 21; Length 12464;
Best Local Similarity 58.3%; Pred. No. 0;
Matches 2905; Conservative 0; Mismatches 2039; Indels 36; Gaps 8;

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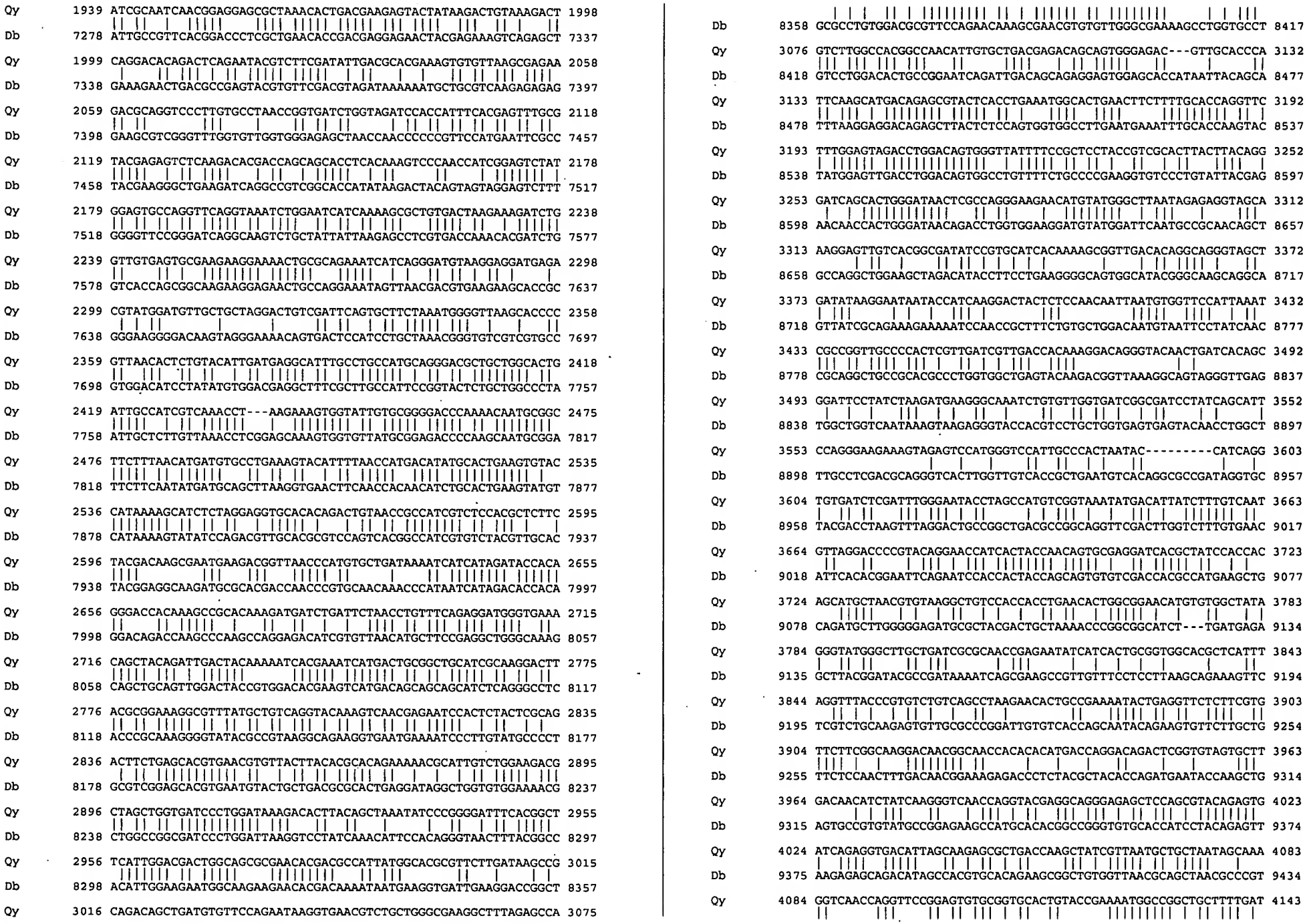

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RESULT 10
ACC45139
ID ACC45139 standard; DNA; 7399 BP.
XX
AC ACC45139;
XX
DT 11-JUN-2003 (first entry)
XX
DE Alphavirus replication unit NS1-NS4 gene related sequence.
XX
KW Vaccine; alpha virus replication unit; NS1-NS4; gene; ds.
XX
OS Alphavirus.
XX
PN CN1367020-A.
XX
PD 04-SEP-2002.
XX
PF 19-OCT-2001; 2001CN-0128979.
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PI Zhao L, Qin S;
XX
DR WPI; 2003-168348/17.
XX
PT Nucleic acid vaccine capable of being high-effectively and safely
PT expressed comprises a conventional nucleic acid vaccine plasmid and
PT alpha virus replication unit NS1-NS4 -
XX
PS Example; Fig 1; 14pp; Chinese.
XX
CC The present invention describes a nucleic acid vaccine which can be
CC effectively safely expressed. The nucleic acid vaccine plasmid forming
CC the nucleic acid vaccine is formed from a conventional nucleic acid
CC vaccine plasmid and an alphavirus replication unit NS1-NS4 gene
CC recombination. After having been injected into body, under the action
CC of a CMV promoter, the nucleic acid vaccine can transcribe the NS1-NS4
CC replication unit and RNA of its downstream target gene with high
CC replication, and it possess high expression efficiency of its target
CC antigen, and after its transcription in the cell and expression level
CC has reach a certain high level, it can induce the cell transfected by
CC performing a death process to form a self-destroying mechanism so as to
CC effectively solve the safety problem of nucleic acid vaccines. The
CC present sequence represents an alphavirus replication unit NS1-NS4 gene
CC related nucleotide sequence, which is used in an example from the
CC present invention.
XX
SQ Sequence 7399 BP; 1966 A; 1915 C; 2025 G; 1493 T; 0 other;

Query Match 31.3%; Score 1564; DB 25; Length 7399;
Best Local Similarity 58.3%; Pred. No. 0;
Matches 2904; Conservative 0; Mismatches 2040; Indels 36; Gaps 8;

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Qy         91 CCACAATTTGAGATCGAAGCAAGGCAGGTCACTGACAATGACCATGCCAATGCCAGAGCG 150

Db        155 CCGTCGTTCGAGGTGGAGTCATTGCAGGTCACACCAAATGACCATGCAAATGCCAGAGCA 214

Qy        151 TTTTCGCATGTGGCAACAAAGCTCATTGAGAGCGAAGTCGACCGGGACCAAGTTATCTTG 210

Db        215 TTTTCGCACCTGGCTACCAAATTGATCGAGCAGGAGACTGACAAAGACACACTCATCTTG 274

Qy        211 GACATTGGAAGTGCGCCCGTCAGACATGCACATTCCAATCACCGCTATCATTGTATCTGC 270

Db        275 GATATCGGCAGTGCGCCTTCCAGGAGAATGATGTCTACGCACAAATACCACTGCGTATGC 334

Qy        271 CCTATGATAAGCGCTGAAGACCCGGACAGACTACAACGGTATGCAGAAAGACT------T 324

Db        335 CCTATGCGCAGCGCAGAAGACCCCGAAAGGCTCGATAGCTACGCAAAGAAACTGGCAGCG 394

Qy        325 AAGAAAAGTGACATTACCGACAAGAACATAGCCTCTAAGGCGGCAGACCTGCTGGAAGTC 384

Db        395 GCCTCCGGGAAGGTGCTGGATAGAGAGATCGCAGGAAAAATCACCGACCTGCAGACCGTC 454

Qy        385 ATGTCAACACCAGACGCAGAGACTCCATCTCTGTGTATGCACACAGACGCCACGTGTAGG 444

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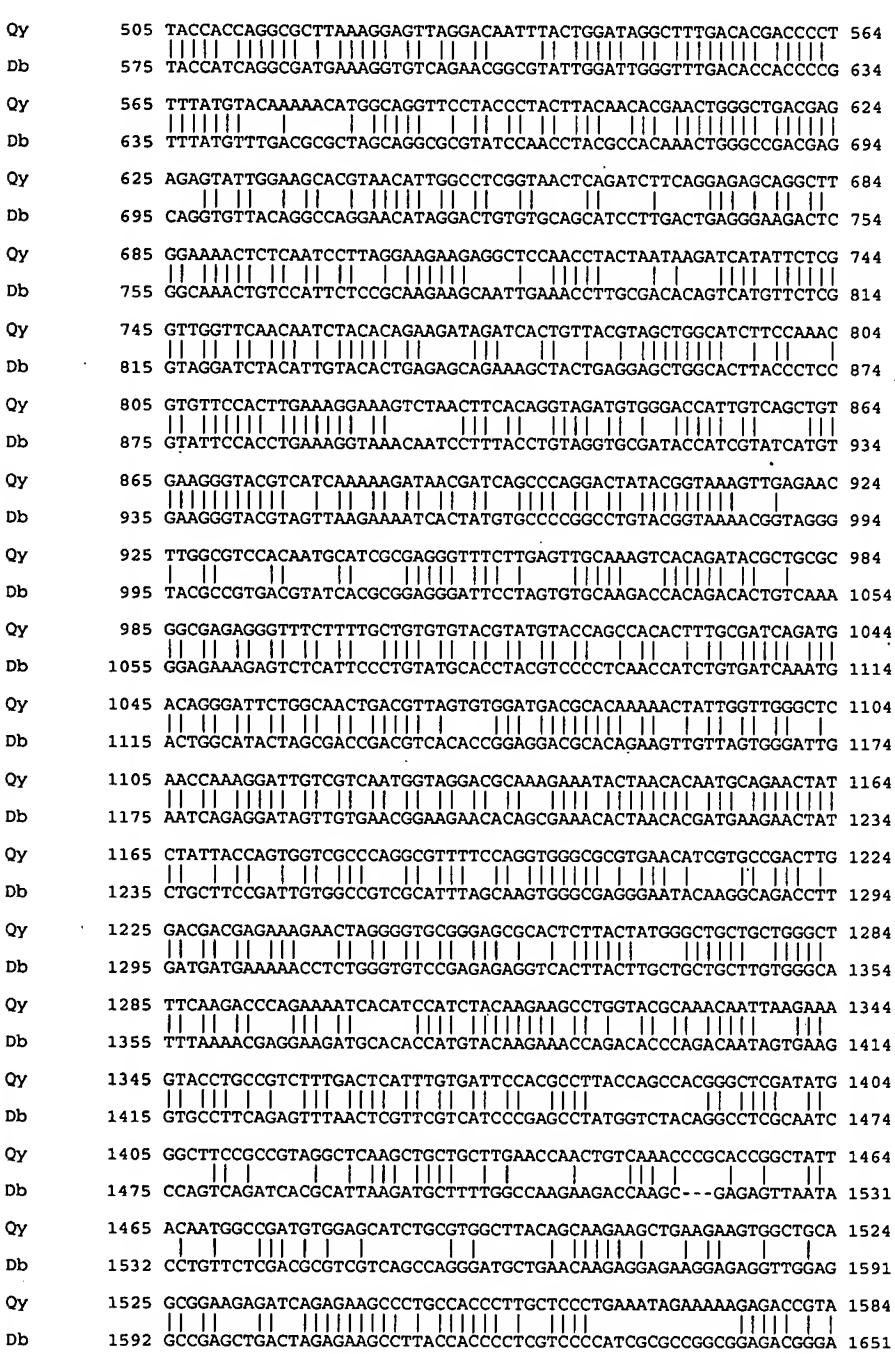
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Qy 565 TTTATGTACAAAAACATGGCAGGTTCCTACCCTACTTACAACACGAACTGGGCTGACGAG 624
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Qy 625 AGAGTATTGGAAGCACGTAACATTGGCCTCGGTAACTCAGATCTTCAGGAGAGCAGGCTT 684
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Qy 805 GTGTTCCACTTGAAAGGAAAGTCTAACTTCACAGGTAGATGTGGGACCATTGTCAGCTGT 864
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Qy 1585 GAGGCAGAAGTAGACCTCATTATGCAAGAG------GCAGGAGCAGGTAGCGTGGAGACA 1638
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Qy 1879 AGTGAGAGCGCTACGATCGTTTTCAACGAGAGGGAGTTCGTAAACAGATACCTGCACCAC 1938
Db 1952 AGCGAGAGCGCCACTATGGTGTACAACGAAAGGGAGTTCGTCAACAGGAAACTATACCAT 2011
Qy 1939 ATCGCAATCAACGGAGGAGCGCTAAACACTGACGAAGAGTACTATAAGACTGTAAAGACT 1998
Db 2012 ATTGCCGTTCACGGACCGTCGCTGAACACCGACGAGGAGAACTACGAGAAAGTCAGAGCT 2071
Qy 1999 CAGGACACAGACTCAGAATACGTCTTCGATATTGACGCACGAAAGTGTGTTAAGCGAGAA 2058
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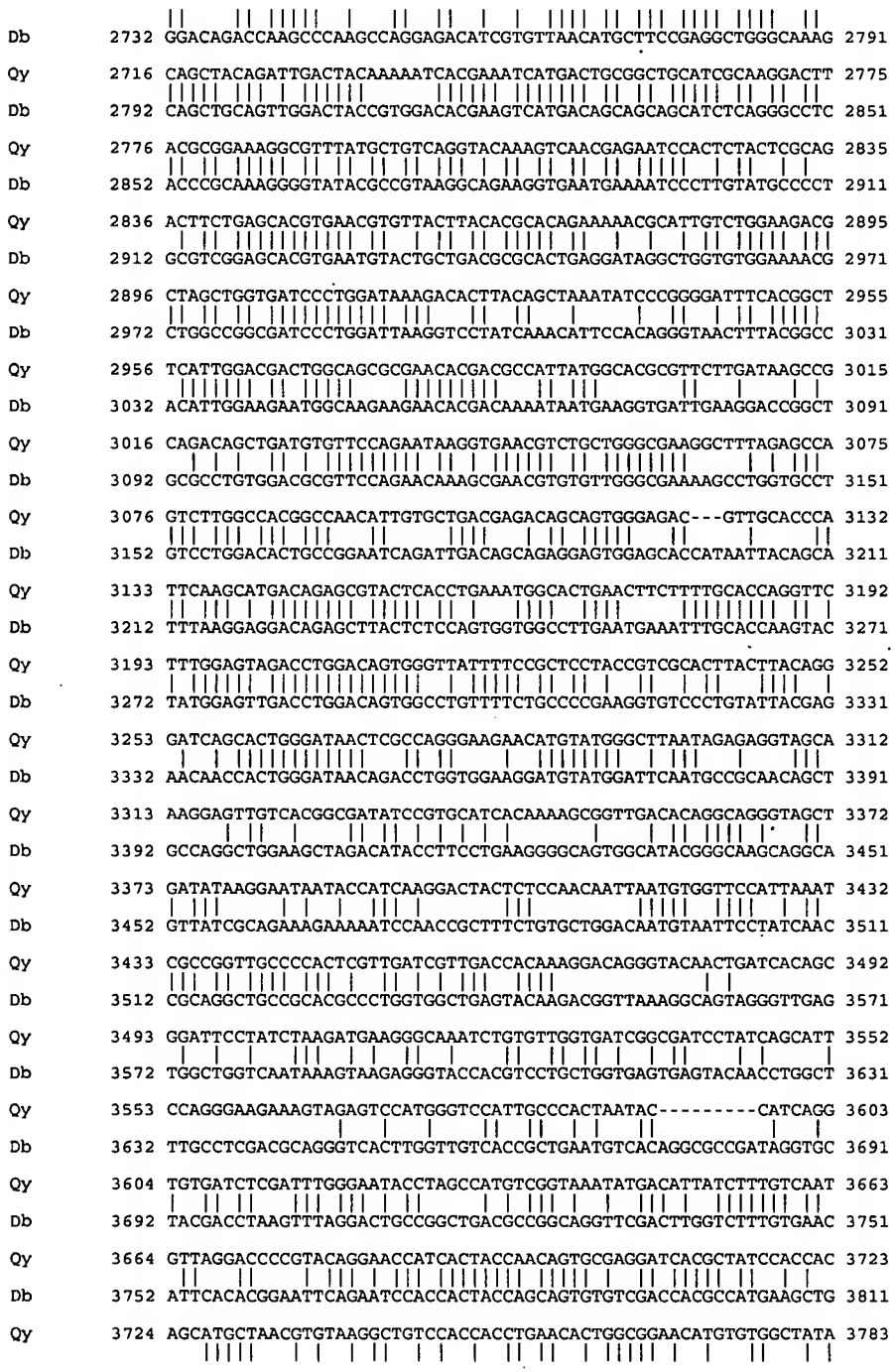
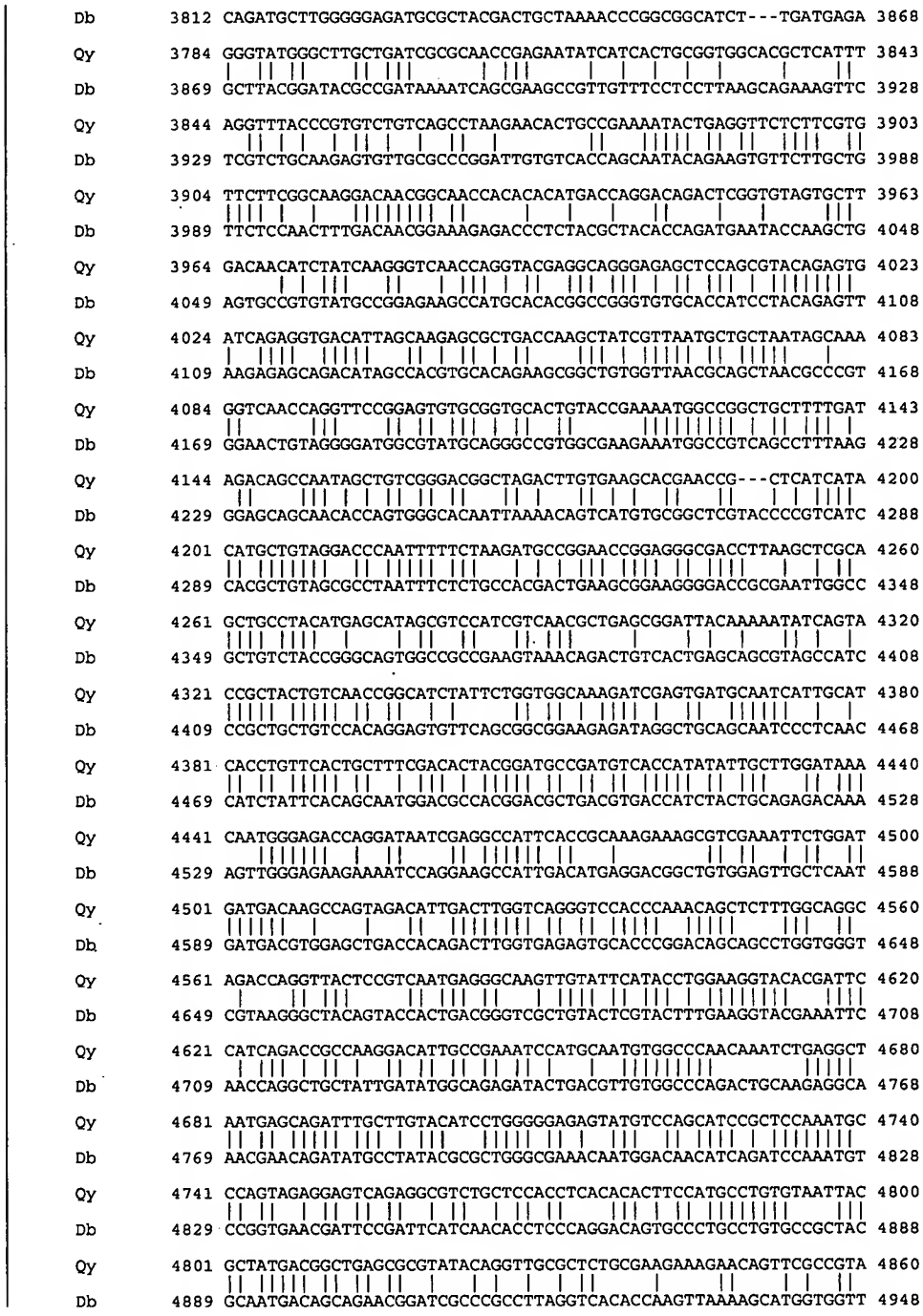
Db 2612 CATAAAAGTATATCCAGACGTTGCACGCGTCCAGTCACGGCCATCGTGTCTACGTTGCAC 2671
Qy 2596 TACGACAAGCGAATGAAGACGGTTAACCCATGTGCTGATAAAATCATCATAGATACCACA 2655
Db 2672 TACGGAGGCAAGATGCGCACGACCAACCCGTGCAACAAACCCATAATCATAGACACCACA 2731
Qy 2656 GGGACCACAAAGCCGCACAAAGATGATCTGATTCTAACCTGTTTCAGAGGATGGGTGAAA 2715





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Qy       4861 TGCTCATCATTCCTGTTGCCGAAGTACAGGATCACAGGCGTGCAGAAGCTACAGTGCAGC 4920
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Db       4949 TGCTCATCTTTTCCCCTCCCGAAATACCATGTAGATGGGGTGCAGAAGGTAAAGTGCGAG 5008

Qy       4921 AAACCAGTCCTGTTTTCAGGCGTCGTACCACCGGCTGTACACCCCAGGAAGTACGCGGAA 4980
              ||      |||||||           |||||  | |  ||    ||  ||||||| || | |
Db       5009 AAGGTTCTCCTGTTCGACCCGACGGTACCTTCAGTGGTTAGTCCGCGGAAGTATGCCGCA 5068
```

RESULT 11
AAX76582
ID AAX76582 standard; DNA; 15538 BP.
XX
AC AAX76582;
XX
DT 11-AUG-1999 (first entry)
XX
DE Plasmid pMP44 nucleotide sequence.
XX
KW Plasmid pMP44; hepatitis delta ribozyme; alphavirus vector; vaccine;
KW paramyxovirus; respiratory syncytial virus fusion protein; RSV F;
KW detection; infection; immune response; immunisation; ss.
XX
OS Synthetic.
XX
PN WO9925858-A1.
XX
PD 27-MAY-1999.
XX
PF 13-NOV-1998; 98WO-CA01064.
XX
PR 14-NOV-1997; 97US-0065791.
XX
PA (CONN-) CONNAUGHT LAB LTD.
XX
PI Li X, Parrington M;
XX
DR WPI; 1999-370764/31.
XX
PT Improved alphavirus vector containing DNA encoding a paramyxovirus
PT protein
XX
PS Claim 19; Fig 3; 61pp; English.
XX
CC The present invention describes an improved alphavirus vector containing
CC DNA encoding an immunogenic paramyxovirus protein and DNA to enhance the
CC immunoprotective ability of the paramyxovirus protein in vivo. The vector
CC comprises: (1) a first DNA sequence which is complementary to at least
CC part of an alphavirus RNA genome and including the complement of the
CC complete alphavirus RNA genome replication regions to permit in vivo
CC replication; and (2) a second DNA sequence encoding a paramyxovirus
CC protein or protein fragment that generates antibodies that specifically
CC react with the paramyxovirus protein; where the second DNA sequence is
CC inserted into a region of the first DNA sequence which is non-essential
CC for replication, the first and second DNA sequences being under
CC transcriptional control of a promoter. The vector is used to immunize a
CC host against disease caused by infection with paramyxovirus, especially
CC respiratory syncytial virus. Human RSV is a major pathogen responsible
CC for severe respiratory tract infections in infants, young children and
CC the institutionalized elderly. The vector provides a protective immune
CC response using a lower dose and less time than vectors in US8476397 and
CC US8896500. Additionally the vectors using native RSV F produce
CC protective immune responses in the absence of pretreatment of the animal
CC model with cardiotoxin, a material known to increase the uptake of DNA
CC and enhance the immune response. The present sequence represents a
CC specifically claimed plasmid pMP44 nucleotide sequence from the present
CC invention.
XX
SQ Sequence 15538 BP; 4313 A; 3774 C; 3837 G; 3614 T; 0 other;

Query Match 31.3%; Score 1564; DB 20; Length 15538;
Best Local Similarity 58.3%; Pred. No. 0;

Matches 2904; Conservative 0; Mismatches 2040; Indels 36; Gaps 8;

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Qy         31 AGAATTCACGTTGACTTAGATGCTGACAGCCCGTATGTCAAGTCGTTACAGCGGACGTTT 90
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Db       2642 AAAGTGCATGTTGATATTGAGGCTGACAGCCCATTCATCAAGTCTTTGCAGAAGGCATTT 2701

Qy         91 CCACAATTTGAGATCGAAGCAAGGCAGGTCACTGACAATGACCATGCCAATGCCAGAGCG 150
              ||     || ||| | ||  ||  |||||||||     |||||||||| ||||||||||
Db       2702 CCGTCGTTCGAGGTGGAGTCATTGCAGGTCACACCAAATGACCATGCAAATGCCAGAGCA 2761

Qy        151 TTTTCGCATGTGGCAACAAAGCTCATTGAGAGCGAAGTCGACCGGGACCAAGTTATCTTG 210
              ||||||||  |||| || ||  | || |||   ||     |||   |||  | | ||||||
Db       2762 TTTTCGCACCTGGCTACCAAATTGATCGAGCAGGAGACTGACAAAGACACACTCATCTTG 2821

Qy        211 GACATTGGAAGTGCGCCCGTCAGACATGCACATTCCAATCACCGCTATCATTGTATCTGC 270
              || || || ||||||||   |||          || |  |||   || || ||  | |||
Db       2822 GATATCGGCAGTGCGCCTTCCAGGAGAATGATGTCTACGCACAAATACCACTGCGTATGC 2881

Qy        271 CCTATGATAAGCGCTGAAGACCCGGACAGACTACAACGGTATGCAGAAAGACT------T 324
              ||||||   ||||| |||||||| || || ||  |  | || ||| | | |||      |
Db       2882 CCTATGCGCAGCGCAGAAGACCCCGAAAGGCTCGATAGCTACGCAAAGAAACTGGCAGCG 2941

Qy        325 AAGAAAAGTGACATTACCGACAAGAACATAGCCTCTAAGGCGGCAGACCTGCTGGAAGTC 384
                  |  |  |   || |  | || ||   ||    | |||||| |  |||
Db       2942 GCCTCCGGGAAGGTGCTGGATAGAGAGATCGCAGGAAAAATCACCGACCTGCAGACCGTC 3001

Qy        385 ATGTCAACACCAGACGCAGAGACTCCATCTCTGTGTATGCACACAGACGCCACGTGTAGG 444
              ||| | || |||||||| ||  ||||  |  | ||  |||| |||||| |||||| |
Db       3002 ATGGCTACGCCAGACGCTGAATCTCCTACCTTTGCCTGCATACAGACGTCACGTGTCGT 3061

Qy        445 TACTTTGGAAGTGTAGCAGTATACCAAGATGTGTACGCAGTCCATGCACCGACATCAATC 504
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Db       3122 TACCATCAGGCGATGAAAGGTGTCAGAACGGCGTATTGGATTGGGTTTGACACCACCCCG 3181

Qy        565 TTTATGTACAAAAACATGGCAGGTTCCTACCCTACTTACAACACGAACTGGGCTGACGAG 624
              |||||||   |     | |||||  | || || || |||  ||| |||||||| ||||||
Db       3182 TTTATGTTTGACGCGCTAGCAGGCGCGTATCCAACCTACGCCACAAACTGGGCCGACGAG 3241

Qy        625 AGAGTATTGGAAGCACGTAACATTGGCCTCGGTAACTCAGATCTTCAGGAGAGCAGGCTT 684
              || ||  | ||  | |||||| || ||  ||     ||     |   ||| | || ||
Db       3242 CAGGTGTTACAGGCCAGGAACATAGGACTGTGTGCAGCATCCTTGACTGAGGGAAGACTC 3301

Qy        685 GGAAAACTCTCAATCCTTAGGAAGAAGAGGCTCCAACCTACTAATAAGATCATATTCTCG 744
              || ||||| || || ||  | ||||||   |  |||||   | |   |||| ||||||
Db       3302 GGCAAACTGTCCATTCTCCGCAAGAAGCAATTGAAACCTTGCGACACAGTCATGTTCTCG 3361

Qy        745 GTTGGTTCAACAATCTACACAGAAGATAGATCACTGTTACGTAGCTGGCATCTTCCAAAC 804
              || || || ||| | ||||| ||    |||   ||  |  | ||||||||  | ||   |
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Qy        805 GTGTTCCACTTGAAAGGAAAGTCTAACTTCACAGGTAGATGTGGGACCATTGTCAGCTGT 864
              || |||||| |||||||  ||       ||| ||  |||| || |  ||||| ||    |||
Db       3422 GTATTCCACCTGAAAGGTAAACAATCCTTTACCTGTAGGTGCGATACCATCGTATCATGT 3481

Qy        865 GAAGGGTACGTCATCAAAAAGATAACGATCAGCCCAGGACTATACGGTAAAGTTGAGAAC 924
              ||||||||||  | || || || || ||  |||| || || |||||||||  |
Db       3482 GAAGGGTACGTAGTTAAGAAAATCACTATGTGCCCCGGCCTGTACGGTAAAACGGTAGGG 3541

Qy        925 TTGGCGTCCACAATGCATCGCGAGGGTTTCTTGAGTTGCAAAGTCACAGATACGCTGCGC 984
              |  ||    ||    ||    ||||| ||| |    |||||  ||||||  || |
Db       3542 TACGCCGTGACGTATCACGCGGAGGGATTCCTAGTGTGCAAGACCACAGACACTGTCAAA 3601

Qy        985 GGCGAGAGGGTTTCTTTTGCTGTGTGTACGTATGTACCAGCCACACTTTGCGATCAGATG 1044
              || || || || || ||  |||| || || || || || ||  | || | || ||||| |||
Db       3602 GGAGAAAGAGTCTCATTCCCTGTATGCACCTACGTCCCCTCAACCATCTGTGATCAAATG 3661

Qy       1045 ACAGGGATTCTGGCAACTGACGTTAGTGTGGATGACGCACAAAAACTATTGGTTGGGCTC 1104
              || || || || || || ||||| |    ||| |||||||| ||  | || || ||  |
Db       3662 ACTGGCATACTAGCGACCGACGTCACACCGGAGGACGCACAGAAGTTGTTAGTGGGATTG 3721
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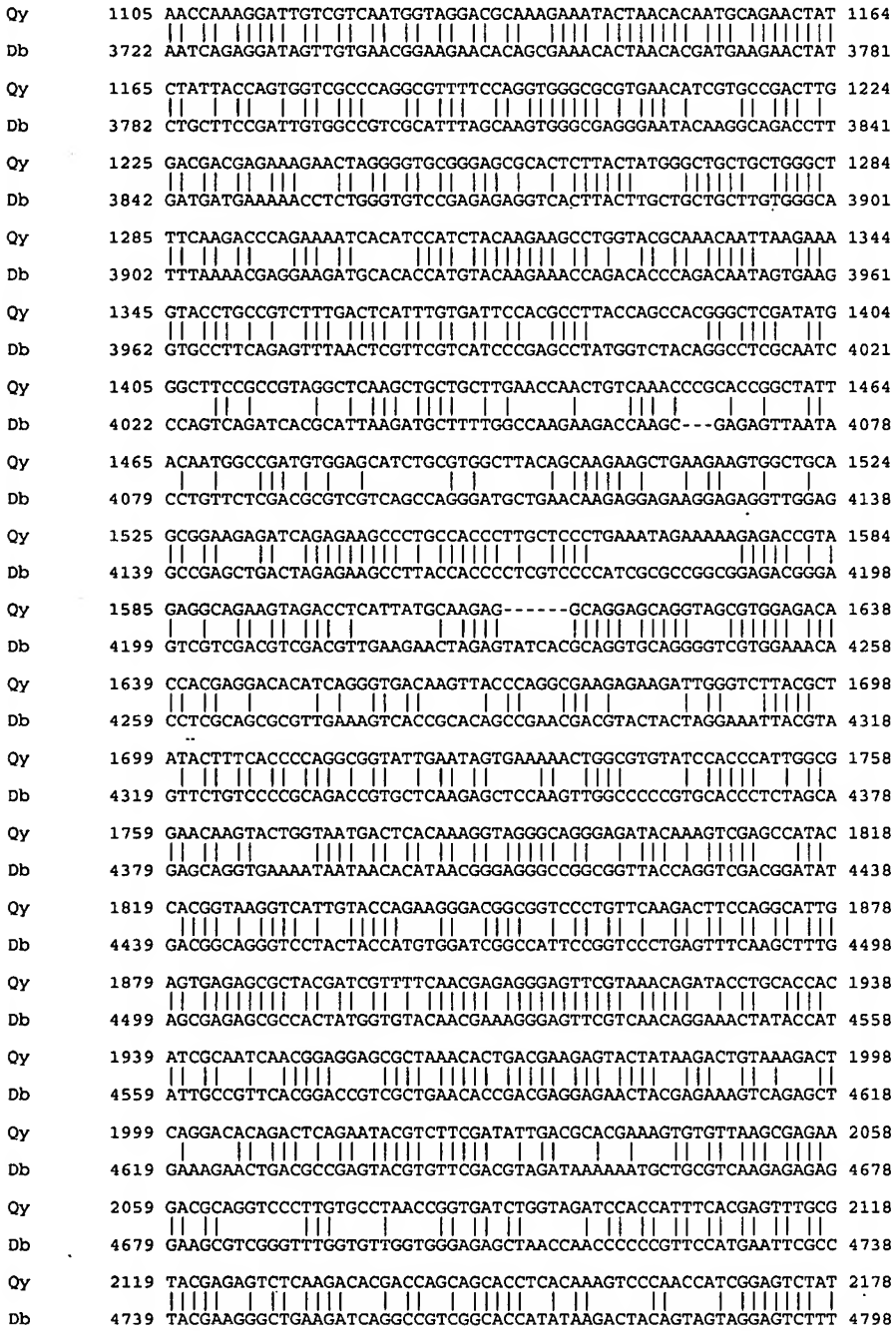
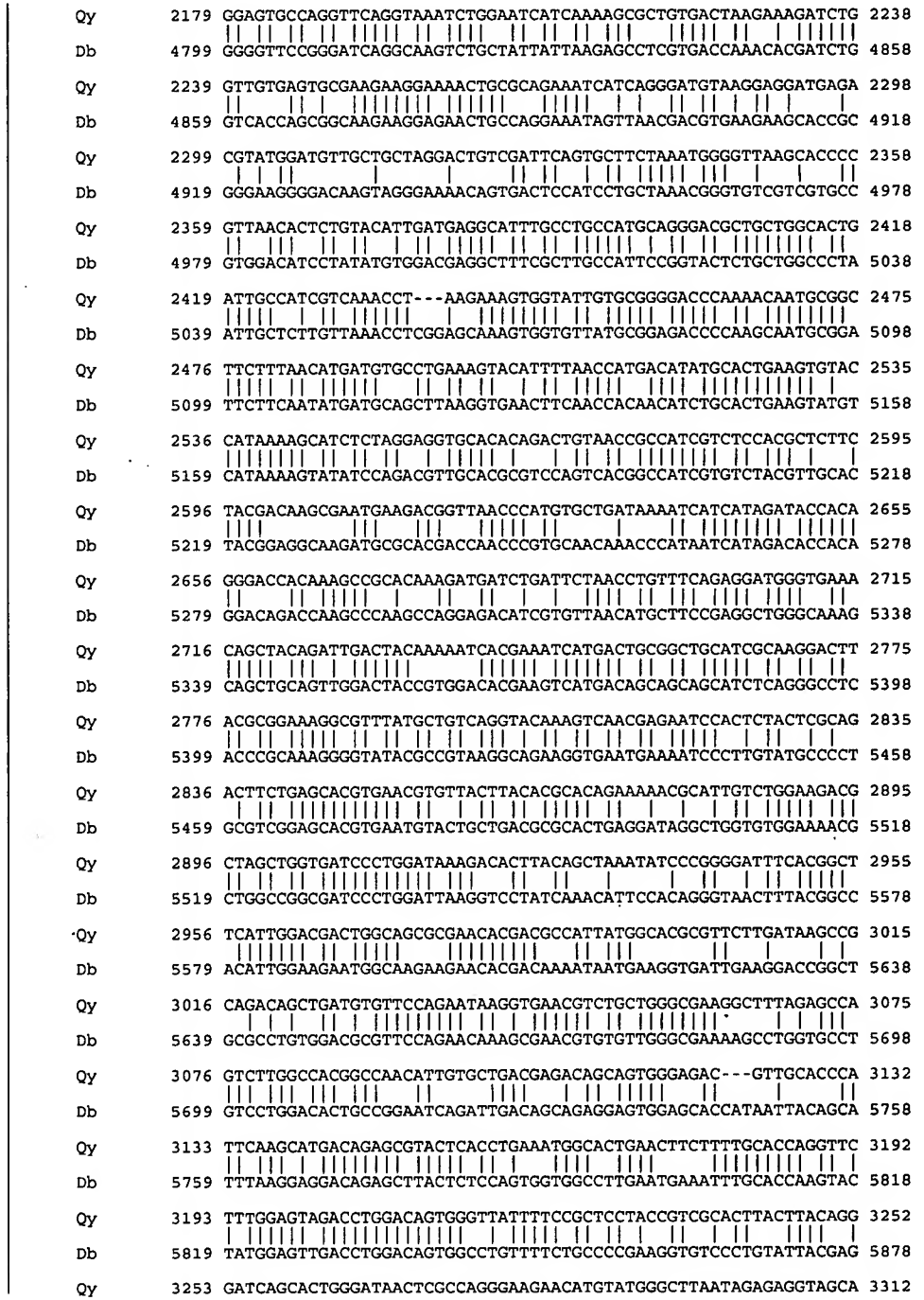
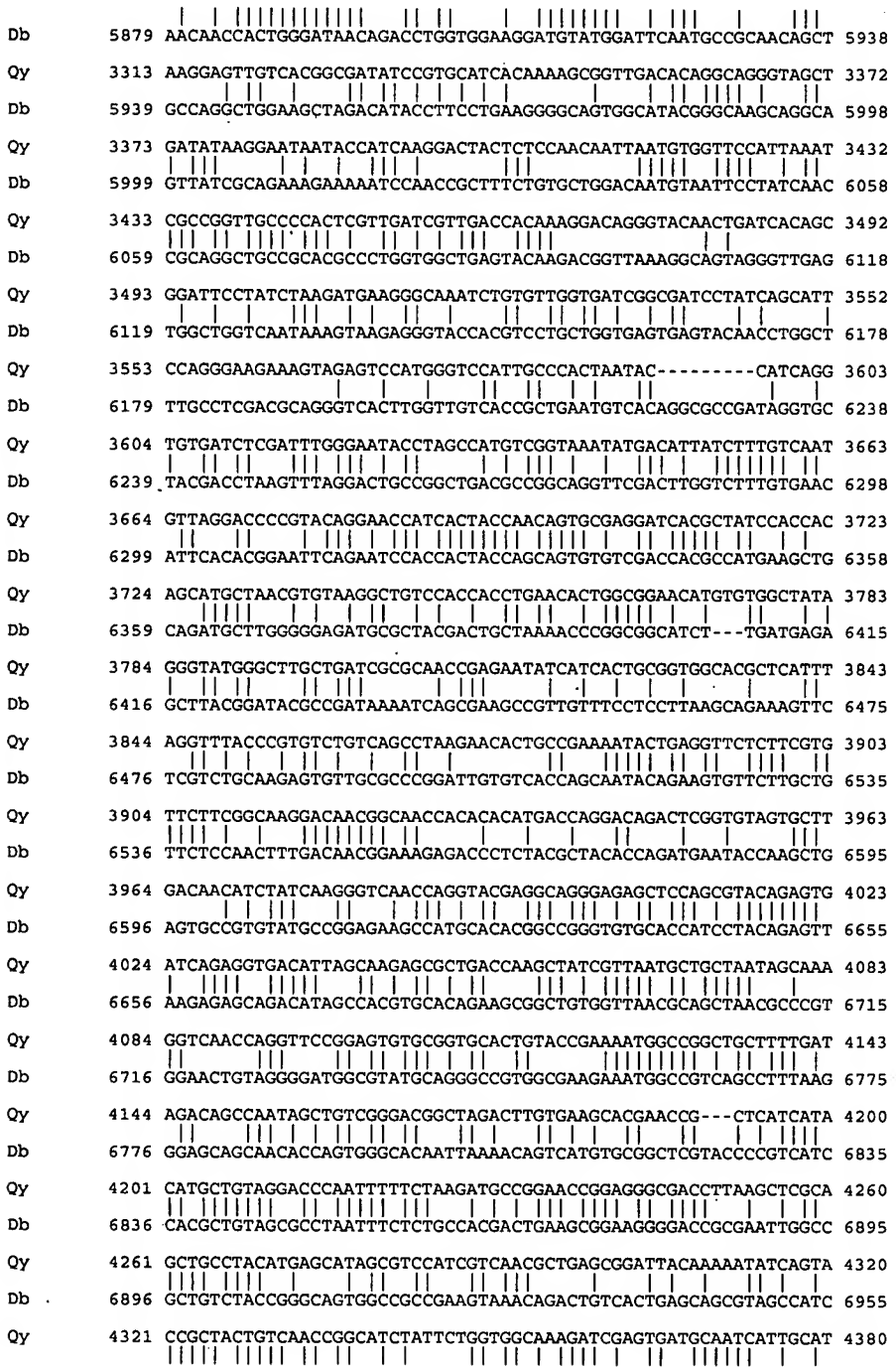


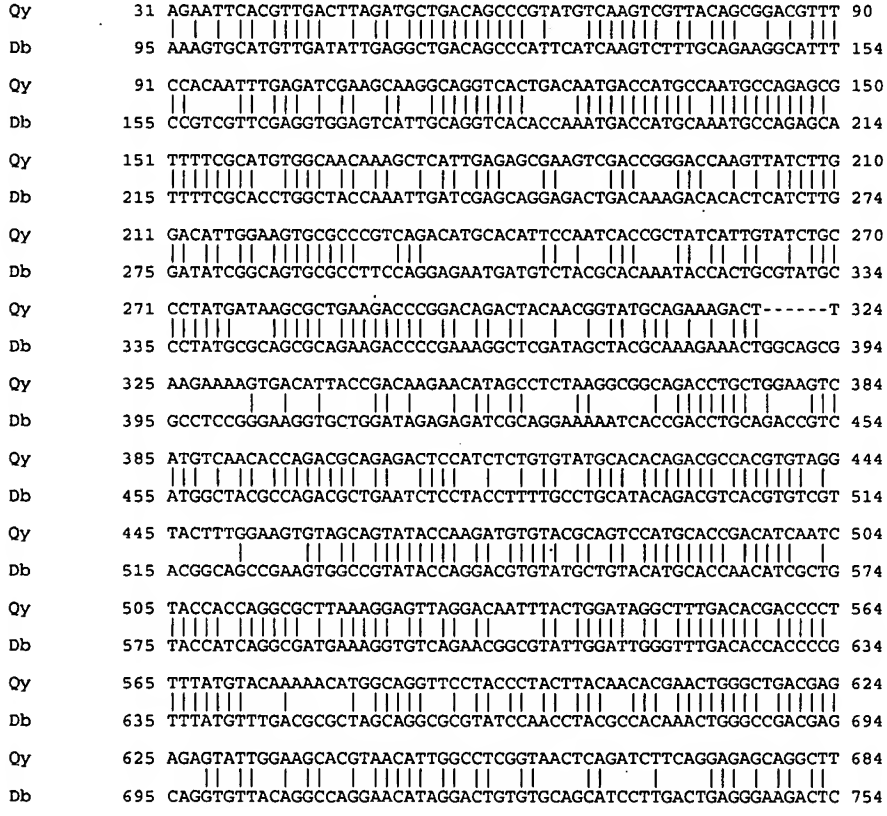


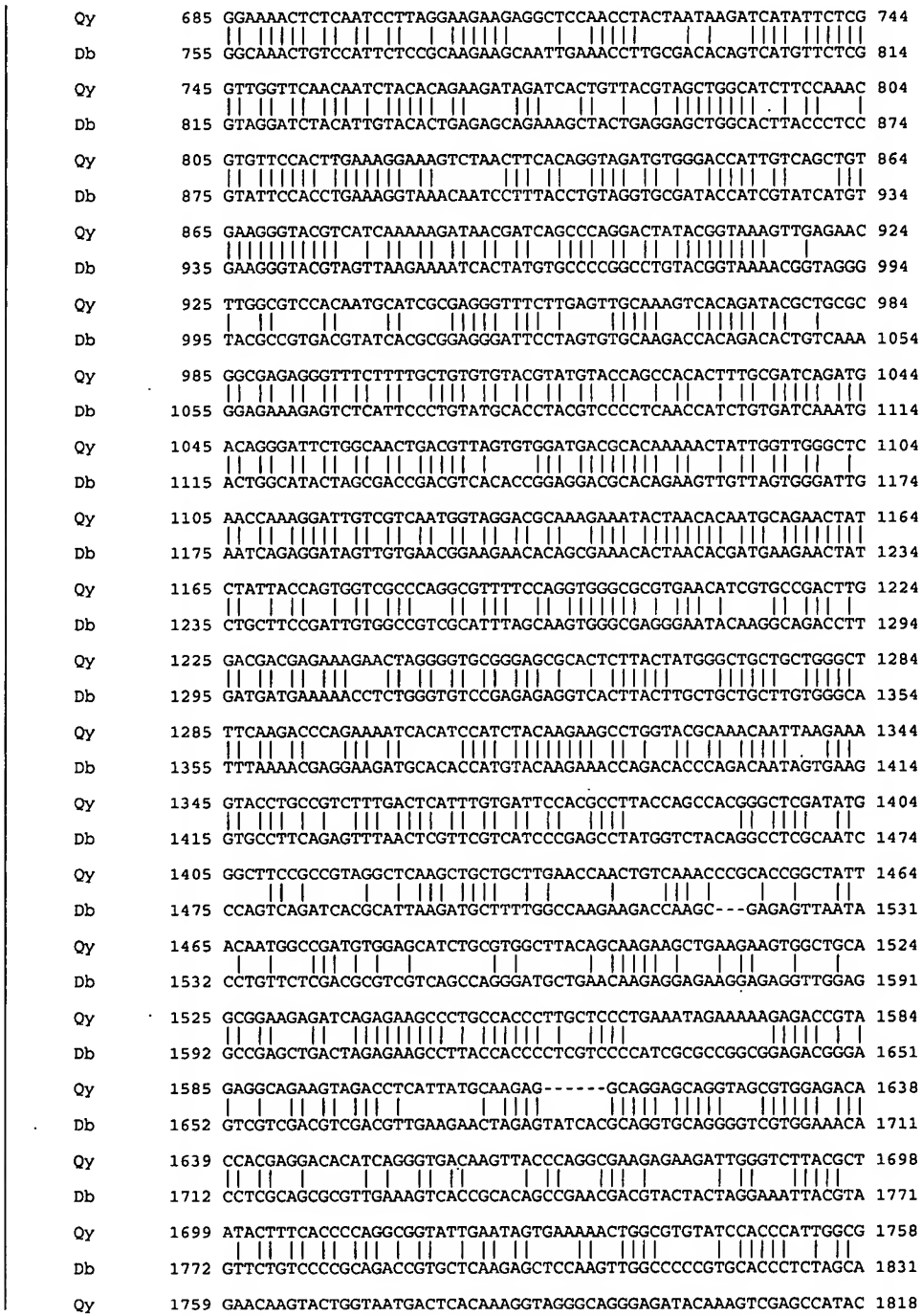


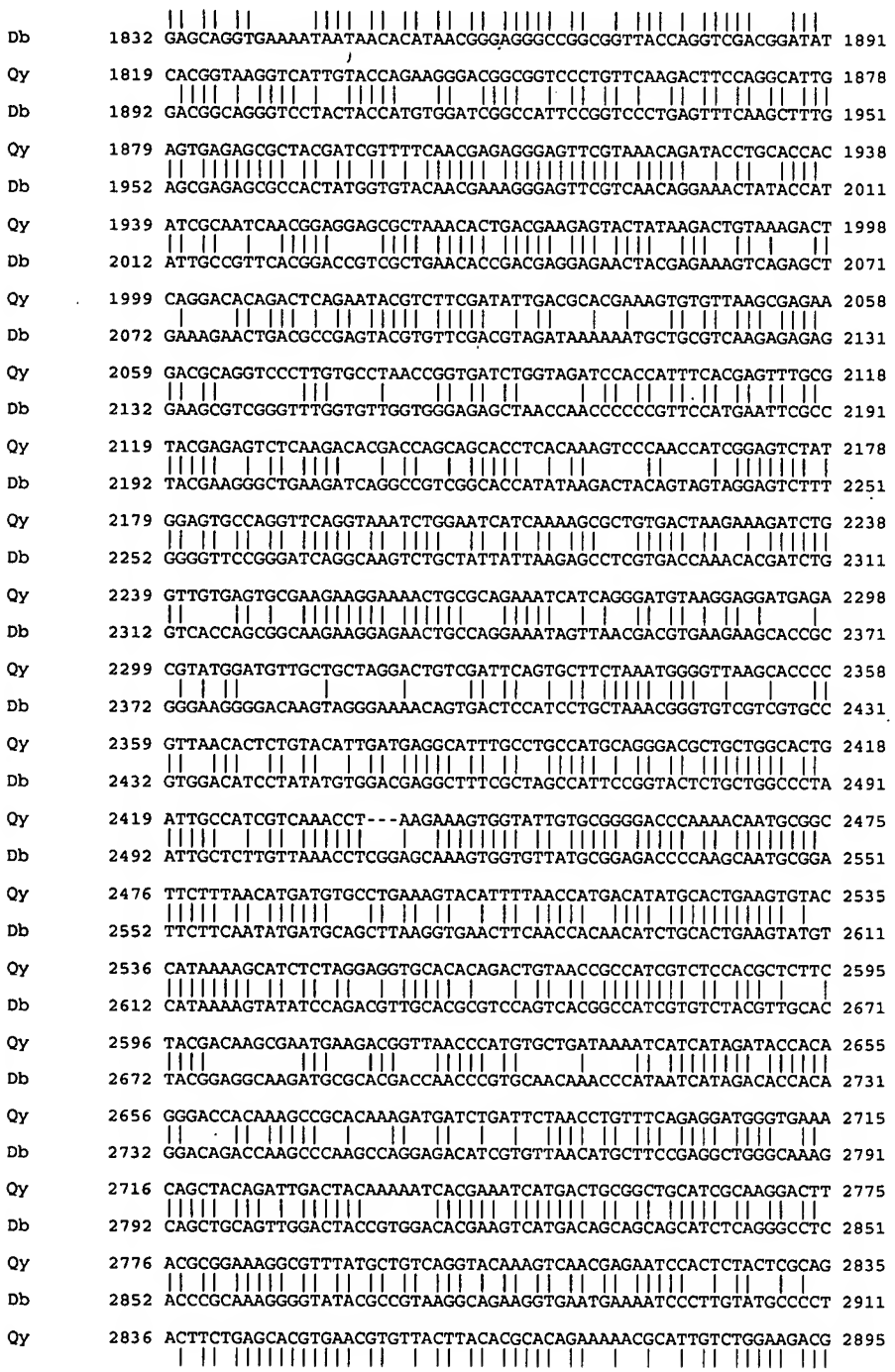
RESULT 12
ABN86687
ID ABN86687 standard; DNA; 11489 BP.
XX
AC ABN86687;
XX
DT 05-NOV-2002 (first entry)
XX
DE Nucleotide sequence of a pSCA1 suicide DNA vector.
XX
KW Major histocompatibility complex; MHC; antigen presenting cell; APC;
KW antigen; cytostatic; virucide; gene therapy; CD8; vaccine; therapeutic;
KW cancer; viral infection; ds.
XX
OS Synthetic.
XX
PN WO200261113-A2.
XX
PD 08-AUG-2002.
XX
PF 01-FEB-2002; 2002WO-US02598.
XX
PR 01-FEB-2001; 2001US-265334P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Wu T, Hung C;
XX
DR WPI; 2002-619261/66.
XX

PT Nucleic acid molecule encoding a fusion polypeptide that promotes
PT processing via the Major Histocompatibility Complex class I pathway
PT and/or promotes activity of an antigen presenting cell, useful as
PT vaccine for cancer and viral infections -
XX
PS Claim 32; Page 25-27; 127pp; English.
XX
CC The invention relates to a new nucleic acid molecule (I) encoding a
CC fusion polypeptide useful as a vaccine composition. (I) comprises a first
CC nucleic acid sequence encoding a first polypeptide or peptide that
CC promotes processing via the Major Histocompatibility Complex (MHC) class
CC I pathway (MHC-I-PP) and/or promotes development or activity of an
CC antigen presenting cell (APC). The second nucleic acid sequence is linked
CC in frame to the first nucleic acid sequence or to a linker nucleic acid
CC sequence and encodes an antigenic polypeptide or peptide. The methods and
CC compositions of the present invention are useful as therapeutic vaccine
CC for cancer and for major viral infections, such as hepatoma and cervical
CC cancer, that cause morbidity and mortality. They can also be used in
CC treating animal diseases, such as equine herpesvirus, bovine viruses,
CC Marek's disease, retroviral and lentiviral diseases and rabies, in the
CC veterinary medicine context. The present sequence represents the
CC nucleotide sequence of a pSCA1 suicide DNA vector.
XX
SQ Sequence 11489 BP; 3105 A; 2908 C; 2988 G; 2488 T; 0 other;

Query Match 31.2%; Score 1562.4; DB 24; Length 11489;
Best Local Similarity 58.3%; Pred. No. 0;
Matches 2903; Conservative 0; Mismatches 2041; Indels 36; Gaps 8;



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RESULT 13
ABN86690
ID ABN86690 standard; DNA; 13599 BP.
XX
AC ABN86690;
XX
DT 05-NOV-2002 (first entry)
XX
DE Nucleotide sequence of vector pSCA1-E7-Hsp70.
XX
KW Major histocompatibility complex; MHC; antigen presenting cell; APC;
KW antigen; cytostatic; virucide; gene therapy; CD8; vaccine; therapeutic;
KW cancer; viral infection; HPV; E7; heat shock protein 70; Hsp70; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 7405..9509
FT /*tag= a
FT /note= "E7-Hsp70 fusion sequence"
XX
PN WO200261113-A2.
XX
PD 08-AUG-2002.
XX
PF 01-FEB-2002; 2002WO-US02598.
XX
PR 01-FEB-2001; 2001US-265334P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Wu T, Hung C;
XX
DR WPI; 2002-619261/66.
XX
PT Nucleic acid molecule encoding a fusion polypeptide that promotes
PT processing via the Major Histocompatibility Complex class I pathway
PT and/or promotes activity of an antigen presenting cell, useful as
PT vaccine for cancer and viral infections -
XX
PS Claim 37; Page 34-37; 127pp; English.
XX
CC The invention relates to a new nucleic acid molecule (I) encoding a
CC fusion polypeptide useful as a vaccine composition. (I) comprises a first
CC nucleic acid sequence encoding a first polypeptide or peptide that
CC promotes processing via the Major Histocompatibility Complex (MHC) class
CC I pathway (MHC-I-PP) and/or promotes development or activity of an
CC antigen presenting cell (APC). The second nucleic acid sequence is linked
CC in frame to the first nucleic acid sequence or to a linker nucleic acid
CC sequence and encodes an antigenic polypeptide or peptide. The methods and
CC compositions of the present invention are useful as therapeutic vaccine
CC for cancer and for major viral infections, such as hepatoma and cervical
CC cancer, that cause morbidity and mortality. They can also be used in
CC treating animal diseases, such as equine herpesvirus, bovine viruses,
CC Marek's disease, retroviral and lentiviral diseases and rabies, in the
CC veterinary medicine context. The present sequence represents the
CC nucleotide sequence of vector pSCA1-E7-Hsp70 comprising the human
CC papillomavirus (HPV) E7 antigenic protein and M. tuberculosis heat
CC shock protein 70 (Hsp70) fusion sequence.
XX
SQ Sequence 13599 BP; 3582 A; 3516 C; 3647 G; 2854 T; 0 other;

Query Match 31.2%; Score 1562.4; DB 24; Length 13599;
Best Local Similarity 58.3%; Pred. No. 0;
Matches 2903; Conservative 0; Mismatches 2041; Indels 36; Gaps 8;

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Qy         91 CCACAATTTGAGATCGAAGCAAGGCAGGTCACTGACAATGACCATGCCAATGCCAGAGCG 150
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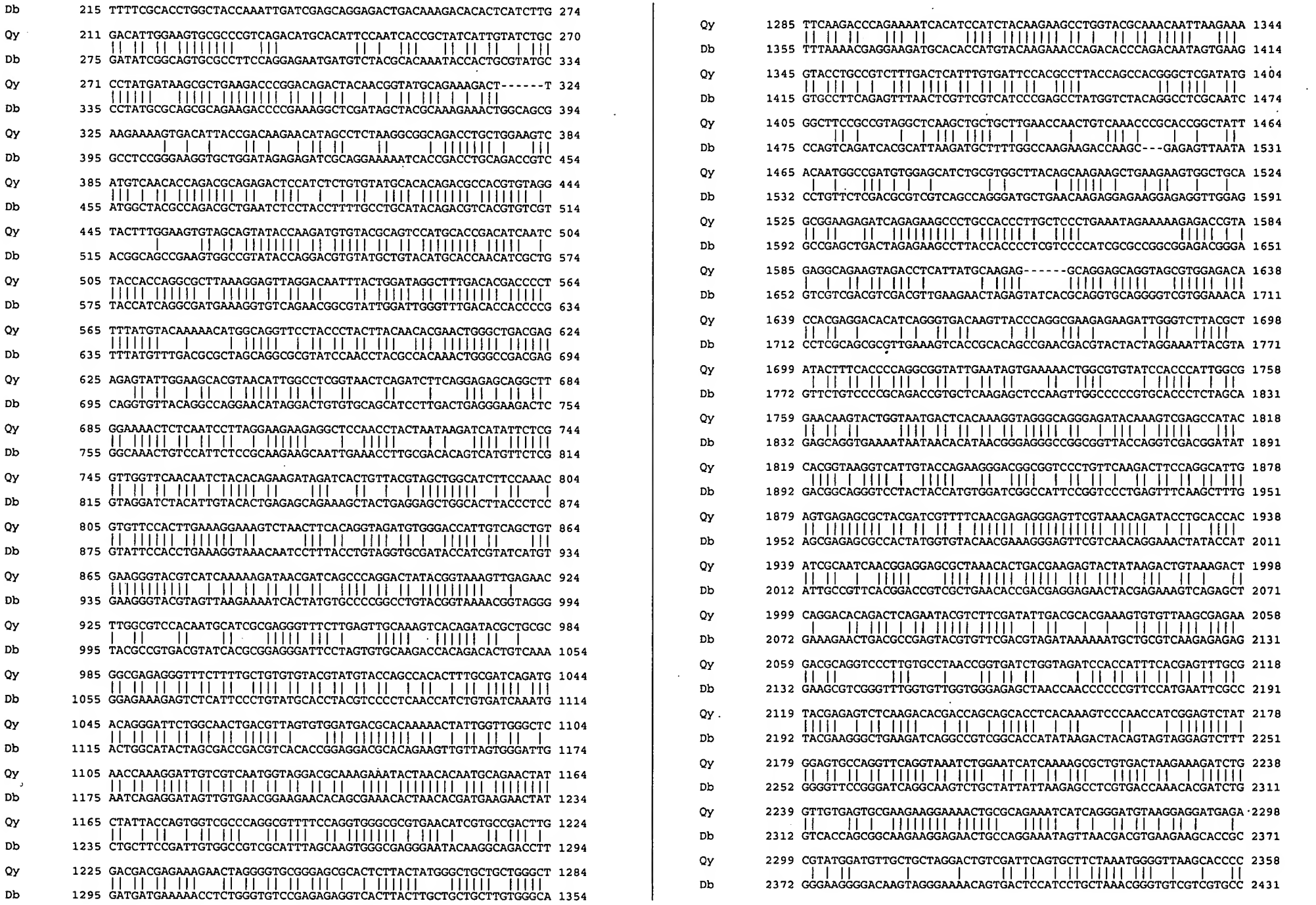

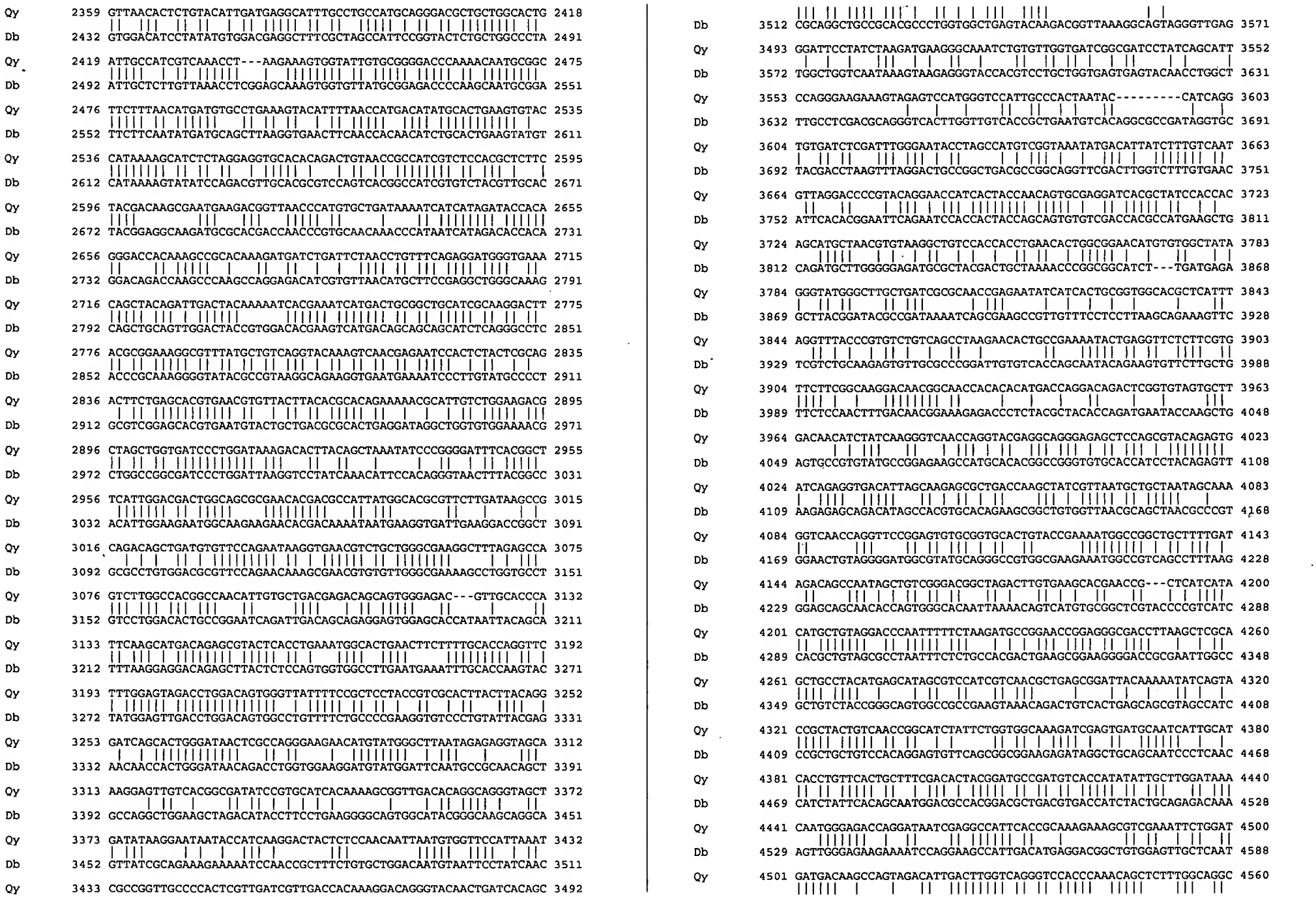

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Db       4649 CGTAAGGGCTACAGTACCACTGACGGGTCGCTGTACTCGTACTTTGAAGGTACGAAATTC 4708

Qy       4621 CATCAGACCGCCAAGGACATTGCCGAAATCCATGCAATGTGGCCCAACAAATCTGAGGCT 4680

Db       4709 AACCAGGCTGCTATTGATATGGCAGAGATACTGACGTTGTGGCCCAGACTGCAAGAGGCA 4768

Qy       4681 AATGAGCAGATTTGCTTGTACATCCTGGGGGAGAGTATGTCCAGCATCCGCTCCAAATGC 4740

Db       4769 AACGAACAGATATGCCTATACGCGCTGGGCGAAACAATGGACAACATCAGATCCAAATGT 4828

Qy       4741 CCAGTAGAGGAGTCAGAGGCGTCTGCTCCACCTCACACACTTCCATGCCTGTGTAATTAC 4800

Db       4829 CCGGTGAACGATTCCGATTCATCAACACCTCCCAGGACAGTGCCCTGCCTGTGCCGCTAC 4888

Qy       4801 GCTATGACGGCTGAGCGCGTATACAGGTTGCGCTCTGCGAAGAAAGAACAGTTCGCCGTA 4860

Db       4889 GCAATGACAGCAGAACGGATCGCCCGCCTTAGGTCACACCAAGTTAAAAGCATGGTGGTT 4948

Qy       4861 TGCTCATCATTCCTGTTGCCGAAGTACAGGATCACAGGCGTGCAGAAGCTACAGTGCAGC 4920

Db       4949 TGCTCATCTTTTCCCCTCCCGAAATACCATGTAGATGGGGTGCAGAAGGTAAAGTGCGAG 5008

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RESULT 14
AAQ26021
ID AAQ26021 standard; DNA; 11517 BP.
XX
AC AAQ26021;
XX
DT 25-MAR-2003 (updated)
DT 05-JAN-1993 (first entry)
XX
DE pSP6-SFV4 RNA transcript as DNA.
XX
KW Semliki forest virus; SFV; SP6 expression vector; RNA polymerase; ss.
XX
OS Synthetic.
XX

FH	Key	Location/Qualifiers
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FT		/label= Non-structural_polyprotein
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PD 25-JUN-1992.
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XX
PA (BIOP-) BIOPTION AB.
XX
PI Garoff H, Liljestroem P;
XX
DR WPI; 1992-234633/28.
DR P-PSDB; AAR25138, AAR28337.
XX
PT RNA mol. derived from alphavirus RNA genome - chimeric alphavirus
PT antigen and vaccine for immunisation against viral infections
XX
PS Disclosure; Fig 5; 94pp; English.

XX
CC The sequence given contains a full length Semliki forest virus (SFV)
CC cDNA clone within an SP6 expression vector. The SP6 RNA polymerase
CC promoter allows in vitro transcription of full length and infectious
CC transcripts.
CC (Updated on 25-MAR-2003 to correct PN field.)
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 11517 BP; 3130 A; 2985 C; 3091 G; 2311 T; 0 other;

Query Match 31.1%; Score 1554.4; DB 13; Length 11517;
Best Local Similarity 58.2%; Pred. No. 0;
Matches 2898; Conservative 0; Mismatches 2046; Indels 36; Gaps 8;

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Qy         91 CCACAATTTGAGATCGAAGCAAGGCAGGTCACTGACAATGACCATGCCAATGCCAGAGCG 150

Db        156 CCGTCGTTCGAGGTGGAGTCATTGCAGGTCACACCAAATGACCATGCAAATGCCAGAGCA 215

Qy        151 TTTTCGCATGTGGCAACAAAGCTCATTGAGAGCGAAGTCGACCGGGACCAAGTTATCTTG 210

Db        216 TTTTCGCACCTGGCTACCAAATTGATCGAGCAGGAGACTGACAAAGACACACTCATCTTG 275

Qy        211 GACATTGGAAGTGCGCCCGTCAGACATGCACATTCCAATCACCGCTATCATTGTATCTGC 270

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Qy        385 ATGTCAACACCAGACGCAGAGACTCCATCTCTGTGTATGCACACAGACGCCACGTGTAGG 444

Db        456 ATGGCTACGCCAGACGCTGAATCTCCTACCTTTTGCCTGCATACAGACGTCACGTGTCGT 515

Qy        445 TACTTTGGAAGTGTAGCAGTATACCAAGATGTGTACGCAGTCCATGCACCGACATCAATC 504

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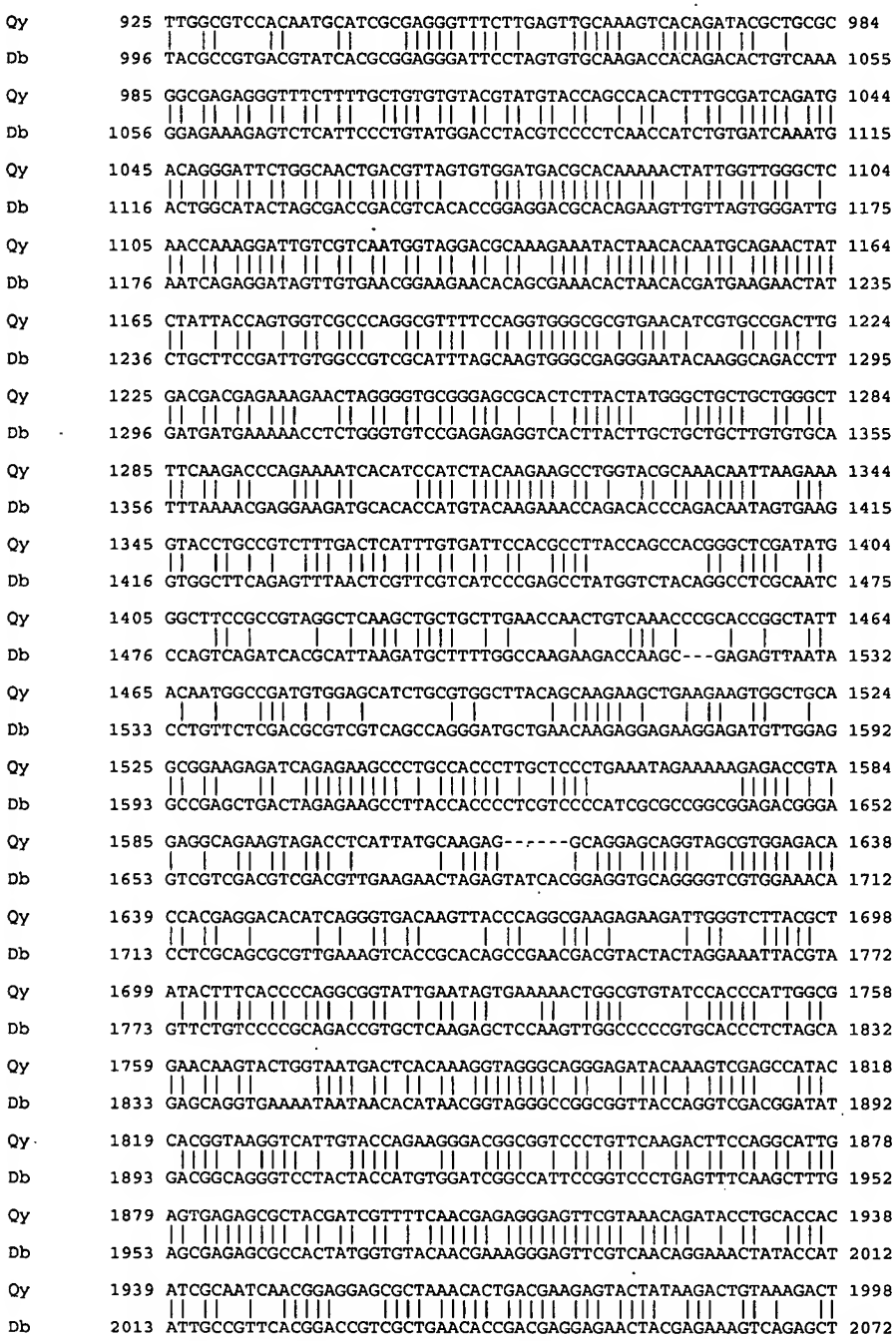
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Qy 1585 GAGGCAGAAGTAGACCTCATTATGCAAGAG-----GCAGGAGCAGGTAGCGTGGAGACA 1638
Db 1653 GTCGTCGACGTCGACGTTGAAGAACTAGAGTATCACGGAGGTGCAGGGGTCGTGGAAACA 1712
Qy 1639 CCACGAGGACACATCAGGGTGACAAGTTACCCAGGCGAAGAGAAGATTGGGTCTTACGCT 1698
Db 1713 CCTCGCAGCGCGTTGAAAGTCACCGCACAGCCGAACGACGTACTACTAGGAAATTACGTA 1772
Qy 1699 ATACTTTCACCCCAGGCGGTATTGAATAGTGAAAAACTGGCGTGTATCCACCCATTGGCG 1758
Db 1773 GTTCTGTCCCCGCAGACCGTGCTCAAGAGCTCCAAGTTGGCCCCCGTGCACCCTCTAGCA 1832
Qy 1759 GAACAAGTACTGGTAATGACTCACAAAGGTAGGGCAGGGAGATACAAAGTCGAGCCATAC 1818
Db 1833 GAGCAGGTGAAAATAATAACACATAACGGTAGGGCCGGCGGTTACCAGGTCGACGGATAT 1892
Qy 1819 CACGGTAAGGTCATTGTACCAGAAGGGACGGCGGTCCCTGTTCAAGACTTCCAGGCATTG 1878
Db 1893 GACGGCAGGGTCCTACTACCATGTGGATCGGCCATTCCGGTCCCTGAGTTTCAAGCTTTG 1952
Qy 1879 AGTGAGAGCGCTACGATCGTTTTCAACGAGAGGGAGTTCGTAAACAGATACCTGCACCAC 1938
Db 1953 AGCGAGAGCGCCACTATGGTGTACAACGAAAGGGAGTTCGTCAACAGGAAACTATACCAT 2012
Qy 1939 ATCGCAATCAACGGAGGAGCGCTAAACACTGACGAAGAGTACTATAAGACTGTAAAGACT 1998
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Db 2073 GAAAGAACTGACGCCGAGTACGTGTTCGACGTAGATAAAAAATGCTGCGTCAAGAGAGAG 2132
Qy 2059 GACGCAGGTCCCTTGTGCCTAACCGGTGATCTGGTAGATCCACCATTTCACGAGTTTGCG 2118
Db 2133 GAAGCGTCGGGTTTGGTGTTGGTGGGAGAGCTAACCAACCCCCCGTTCCATGAATTCGCC 2192
Qy 2119 TACGAGAGTCTCAAGACACGACCAGCAGCACCTCACAAAGTCCCAACCATCGGAGTCTAT 2178
Db 2193 TACGAAGGGCTGAAGATCAGGCCGTCGGCACCATATAAGACTACAGTAGTAGGAGTCTTT 2252
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Qy 2956 TCATTGGACGACTGGCAGCGCGAACACGACGCCATTATGGCACGCGTTCTTGATAAGCCG 3015
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Qy 3076 GTCTTGGCCACGGCCAACATTGTGCTGACGAGACAGCAGTGGGAGAC---GTTGCACCCA 3132

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Qy       3253 GATCAGCACTGGGATAACTCGCCAGGGAAGAACATGTATGGGCTTAATAGAGAGGTAGCA 3312
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Qy       3313 AAGGAGTTGTCACGGCGATATCCGTGCATCACAAAAGCGGTTGACACAGGCAGGGTAGCT 3372
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Qy       3373 GATATAAGGAATAATACCATCAAGGACTACTCTCCAACAATTAATGTGGTTCCATTAAAT 3432
Db       3453 GTTATCGCAGAAAGAAAAATCCAACCGCTTTCTGTGCTGGACAATGTAAATCCTATCAAC 3512
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Db       3513 CGCAGGCTGCCGCACGCCCTGGTGGCTGAGTACAAGACGGTTAAAGGCAGTAGGGTTGAG 3572
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Db       3573 TGGCTGGTCAATAAAGTAAGAGGCTACCACGTCCTGCTGGTGAGTGAGTACAACCTGGCT 3632
Qy       3553 CCAGGGAAGAAAGTAGAGTCCATGGGTCCATTGCCCACTAATAC---------CATCAGG 3603
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Qy       3604 TGTGATCTCGATTTGGGAATACCTAGCCATGTCGGTAAATATGACATTATCTTTGTCAAT 3663
Db       3693 TACGACCTAAGTTTAGGACTGCCGGCTGACGCCGGCAGGTTCGACTTGGTCTTTGTGAAC 3752
Qy       3664 GTTAGGACCCCGTACAGGAACCATCACTACCAACAGTGCGAGGATCACGCTATCCACCAC 3723
Db       3753 ATTCACACGGAATTCAGAATCCACCACTACCAGCAGTGTGTCGACCACGCCATGAAGCTG 3812
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Db       3813 CAGATGCTTGGGGGAGATGCGCTACGACTGCTAAAACCCGGCGGCATCT---TGATGAGA 3869
Qy       3784 GGGTATGGGCTTGCTGATCGCGCAACCGAGAATATCATCACTGCGGTGGCACGCTCATTT 3843
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Qy       4144 AGACAGCCAATAGCTGTCGGGACGGCTAGACTTGTGAAGCACGAACCG---CTCATCATA 4200
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Qy       4201 CATGCTGTAGGACCCAATTTTTCTAAGATGCCGGAACCGGAGGGCGACCTTAAGCTCGCA 4260
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Db       4410 CCGCTGCTGTCCACAGGAGTGTTCAGCGGCGGAAGAGATAGGCTGCAGCAATCCCTCAAC 4469
Qy       4381 CACCTGTTCACTGCTTTCGACACTACGGATGCCGATGTCACCATATATTGCTTGGATAAA 4440
Db       4470 CATCTATTCACAGCAATGGACGCCACGGACGCTGACGTGACCATCTACTGCAGAGACAAA 4529
Qy       4441 CAATGGGAGACCAGGATAATCGAGGCCATTCACCGCAAAGAAAGCGTCGAAATTCTGGAT 4500
Db       4530 AGTTGGGAGAAGAAAATCCAGGAAGCCATTGACATGAGGACGGCTGTGGAGTTGCTCAAT 4589
Qy       4501 GATGACAAGCCAGTAGACATTGACTTGGTCAGGGTCCACCCAAACAGCTCTTTGGCAGGC 4560
Db       4590 GATGACGTGGAGCTGACCACAGACTTGGTGAGAGTGCACCCGGACAGCAGCCTGGTGGGT 4649
Qy       4561 AGACCAGGTTACTCCGTCAATGAGGGCAAGTTGTATTCATACCTGGAAGGTACACGATTC 4620
Db       4650 CGTAAGGGCTACAGTACCACTGACGGGTCGCTGTACTCGTACTTTGAAGGTACGAAATTC 4709
Qy       4621 CATCAGACCGCCAAGGACATTGCCGAAATCCATGCAATGTGGCCCAACAAATCTGAGGCT 4680
Db       4710 AACCAGGCTGCTATTGATATGGCAGAGATACTGACGTTGTGGCCCAGACTGCAAGAGGCA 4769
Qy       4681 AATGAGCAGATTTGCTTGTACATCCTGGGGGAGAGTATGTCCAGCATCCGCTCCAAATGC 4740
Db       4770 AACGAACAGATATGCCTATACGCGCTGGGCGAAACAATGGACAACATCAGATCCAAATGT 4829
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Db       4890 GCAATGACAGCAGAACGGATCGGCCGGCTTAGGTCACACCAAGTTAAAAGCATGGTGGTT 4949
Qy       4861 TGCTCATCATTCCTGTTGCCGAAGTACAGGATCACAGGCGTGCAGAAGCTACAGTGCAGC 4920
Db       4950 TGCTCATCTTTTCCCCTCCCGAAATACCATGTAGATGGGGTGCAGAAGGTAAAGTGCGAG 5009
Qy       4921 AAACCAGTCCTGTTTTCAGGCGTCGTACCACCGGCTGTACACCCCAGGAAGTACGCGGAA 4980
Db       5010 AAGGTTCTCCTGTTCGACCCGACGGTACCTTCAGTGGTTAGTCGGCGGAAGTATGCCGCA 5069
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RESULT 15
AAX78129
ID AAX78129 standard; DNA; 8010 BP.
XX
AC AAX78129;
XX
DT 20-AUG-1999 (first entry)
XX
DE Semliki Forest virus replicon fragment.
XX
KW Alphavirus; replicon; expression vector; heterologous splice site;
KW RNA splicing; viral RNA replication; antigen; vaccination; therapy; ss.
XX
OS Semliki forest virus.
XX
PN WO9925859-A1.
XX
PD 27-MAY-1999.

XX
PF 13-NOV-1998; 98WO-CA01065.
XX
PR 14-NOV-1997; 97US-0065793.
XX
PA (CONN-) CONNAUGHT LAB LTD.
XX
PI Parrington M;
XX
DR WPI; 1999-385140/32.
XX
PT New vector (EV) used to express an antigen for vaccination, e.g.
PT against human immune deficiency virus
XX
PS Disclosure; Fig 3A-F; 60pp; English.
XX
CC This invention describes the construction of a novel expression vector
CC (EV) containing an alphavirus replicon having a heterologous splice site.
CC The expression vector contains (i) a DNA molecule (I) complementary to
CC at least part of an alphavirus RNA genome, and (ii) inserted into a
CC region of (I) that is not essential for its replication, a heterologous
CC DNA (II), under control of a promoter. (I) includes at least one
CC heterologous splice site (HSS) to prevent aberrant RNA splicing of the
CC alphavirus and is the complement of the complete alphavirus genomic
CC region essential for replication of viral RNA. The expression vector is
CC used to express (II) in humans or animals, e.g. to express an antigen
CC for vaccination (against human immune deficiency virus) or to produce a
CC therapeutically active protein or peptide. Introducing an HSS: (1) makes
CC it more likely that any splicing will occur at this site, rather than at
CC a cryptic splice site; (2) restores function of the alphavirus when
CC eliminated, and (3) may improve transport of RNA from the nucleus.
XX
SQ Sequence 8010 BP; 2213 A; 2036 C; 2158 G; 1603 T; 0 other;

Query Match 29.5%; Score 1473.8; DB 20; Length 8010;
Best Local Similarity 57.9%; Pred. No. 0;
Matches 2779; Conservative 0; Mismatches 1982; Indels 36; Gaps 8;

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Qy        214 ATTGGAAGTGCGCCCGTCAGACATGCACATTCCAATCACCGCTATCATTGTATCTGCCCT 273
              || || ||||||||   |||         || |  |||   || || ||  | ||||||
Db          1 ATCGGCAGTGCGCCTTCCAGGAGAATGATGTCTACGCACAAATACCACTGCGTATGCCCT 60

Qy        274 ATGATAAGCGCTGAAGACCCGGACAGACTACAACGGTATGCAGAAAGACTTAAGAAAA-- 331
              |||   ||||| |||||||| || ||  ||   |  | || ||| | | |||
Db         61 ATGCGCAGCGCAGAAGACCCCGAAAGGCTCGATAGCTACGCAAAGAAACTGGCAGCGGCC 120

Qy        332 ----GTGACATTACCGACAAGAACATAGCCTCTAAGGCGGCAGACCTGCTGGAAGTCATG 387
                  |  |  |    || |   | || ||     ||      | |||||||  |   ||||||
Db        121 TCCGGGAAGGTGCTGGATAGAGAGATCGCAGGAAAAATCACCGACCTGCAGACCGTCATG 180

Qy        388 TCAACACCAGACGCAGAGACTCCATCTCTGTGTATGCACACAGACGCCACGTGTAGGTAC 447
              | || |||||||| ||  ||||  |  | ||  |||| ||||||| ||||||| |
Db        181 GCTACGCCAGACGCTGAATCTCCTACCTTTTGCCTGCATACAGACGTCACGTGTCGTACG 240

Qy        448 TTTGGAAGTGTAGCAGTATACCAAGATGTGTACGCAGTCCATGCACCGACATCAATCTAC 507
                |    || || |||||||| || ||||| || || |||||||| |||||   | |||
Db        241 GCAGCCGAAGTGGCCGTATACCAGGACGTGTATGCTGTACATGCACCAACATCGCTGTAC 300

Qy        508 CACCAGGCGCTTAAAGGAGTTAGGACAATTTACTGGATAGGCTTTGACACGACCCCTTTT 567
              || |||||| | ||||| || || ||    || ||||| || |||||||| ||||| |||
Db        301 CATCAGGCGATGAAAGGTGTCAGAACGGCGTATTGGATTGGGTTTGACACCACCCCGTTT 360

Qy        568 ATGTACAAAAACATGGCAGGTTCCTACCCTACTTACAACACGAACTGGGCTGACGAGAGA 627
              ||||   |     | |||||  | || || || |||  ||| |||||||| ||||||
Db        361 ATGTTTGACGCGCTAGCAGGCGCGTATCCAACCTACGCCACAAACTGGGCCGACGAGCAG 420

Qy        628 GTATTGGAAGCACGTAACATTGGCCTCGGTAACTCAGATCTTCAGGAGAGCAGGCTTGGA 687
              || ||  | ||  | ||||| || ||  ||     ||     |    ||| | || || ||
Db        421 GTGTTACAGGCCAGGAACATAGGACTGTGTGCAGCATCCTTGACTGAGGGAAGACTCGGC 480

Qy        688 AAACTCTCAATCCTTAGGAAGAAGAGGCTCCAACCTACTAATAAGATCATATTCTCGGTT 747
              |||| || || ||  | ||||||    |  |||||    | |   |||| ||||||||
Db        481 AAACTGTCCATTCTCCGCAAGAAGCAATTGAAACCTTGCGACACAGTCATGTTCTCGGTA 540

Qy        748 GGTTCAACAATCTACACAGAAGATAGATCACTGTTACGTAGCTGGCATCTTCCAAACGTG 807
              || || ||| | ||||| ||    |||   ||  |  | ||||||||  | ||   |||
Db        541 GGATCTACATTGTACACTGAGAGCAGAAAGCTACTGAGGAGCTGGCACTTACCCTCCGTA 600

Qy        808 TTCCACTTGAAAGGAAAGTCTAACTTCACAGGTAGATGTGGGACCATTGTCAGCTGTGAA 867
              |||||| ||||||| ||      ||| ||  |||| || |  ||||| ||     ||||||
Db        601 TTCCACCTGAAAGGTAAACAATCCTTTACCTGTAGGTGCGATACCATCGTATCATGTGAA 660

Qy        868 GGGTACGTCATCAAAAAGATAACGATCAGCCCAGGACTATACGGTAAAGTTGAGAACTTG 927
              |||||||  | || || || || ||  |||| || || |||||||||   |     |
Db        661 GGGTACGTAGTTAAGAAAATCACTATGTGCCCCGGCCTGTACGGTAAAACGGTAGGGTAC 720

Qy        928 GCGTCCACAATGCATCGCGAGGGTTTCTTGAGTTGCAAAGTCACAGATACGCTGCGCGGC 987
              ||    ||    ||    ||||| ||| |    |||||   |||||| ||  |    ||
Db        721 GCCGTGACGTATCACGCGGAGGGATTCCTAGTGTGCAAGACCACAGACACTGTCAAAGGA 780

Qy        988 GAGAGGGTTTCTTTTGCTGTGTGTACGTATGTACCAGCCACACTTTGCGATCAGATGACA 1047
              || || || || ||  |||| || || || || ||  | ||  | || ||||| |||||
Db        781 GAAAGAGTCTCATTCCCTGTATGCACCTACGTCCCCTCAACCATCTGTGATCAAATGACT 840

Qy       1048 GGGATTCTGGCAACTGACGTTAGTGTGGATGACGCACAAAAACTATTGGTTGGGCTCAAC 1107
              || || || || || ||||| |     ||| |||||||| ||  | || || ||  | ||
Db        841 GGCATACTAGCGACCGACGTCACACCGGAGGACGCACAGAAGTTGTTAGTGGGATTGAAT 900

Qy       1108 CAAAGGATTGTCGTCAATGGTAGGACGCAAAGAAATACTAACACAATGCAGAACTATCTA 1167
              || ||||| || || || || || || || ||  |||| |||||||| ||| ||||||||||
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Qy       1168 TTACCAGTGGTCGCCCAGGCGTTTTCCAGGTGGGCGCGTGAACATCGTGCCGACTTGGAC 1227
              | ||  | || |||   || |||  || |||||| | |||  |    || ||| | ||
Db        961 CTTCCGATTGTGGCCGTCGCATTTAGCAAGTGGGCGAGGGAATACAAGGCAGACCTTGAT 1020

Qy       1228 GACGAGAAAGAACTAGGGGTGCGGGAGCGCACTCTTACTATGGGCTGCTGCTGGGCTTTC 1287
              || || |||   || || || || || ||| |  | ||||||    ||||||  ||||| ||
Db        1021 GATGAAAAACCTCTGGGTGTCCGAGAGAGGTCACTTACTTGCTGCTGCTTGTGGGCATTT 1080

Qy       1288 AAGACCCAGAAAATCACATCCATCTACAAGAAGCCTGGTACGCAAACAATTAAGAAAGTA 1347
              || ||   ||| ||      |||| |||||||| || |  || || |||||   ||| ||
Db        1081 AAAACGAGGAAGATGCACACCATGTACAAGAAACCAGACACCCAGACAATAGTGAAGGTG 1140

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              || |     |  | ||| ||||  | |      |   ||| |  |   |  ||  |
Db        1201 GTCAGATCACGCATTAAGATGCTTTTGGCCAAGAAGACCAAGCGAGA---GTTAATACCT 1257

Qy       1468 ATGGCCGATGTGGAGCATCTGCGTGGCTTACAGCAAGAAGCTGAAGAAGTGGCTGCAGCG 1527
              |   ||| | |  |        | |      | |||||  |  | |||  |  |  ||
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Qy       1528 GAAGAGATCAGAGAAGCCCTGCCACCCTTGCTCCCTGAAATAGAAAAAGAGACCGTAGAG 1587
              ||  ||  |||||||||  | ||||||  |  ||||                |||||  | ||
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Qy       1588 GCAGAAGTAGACCTCATTATGCAAGAG------GCAGGAGCAGGTAGCGTGGAGACACCA 1641
              |  || || |||  |       | ||||      |||||  |||||   ||||||  |||||
Db        1378 GTCGACGTCGACGTTGAAGAACTAGAGTATCACGCAGGTGCAGGGGTCGTGGAAACACCT 1437

Qy       1642 CGAGGACACATCAGGGTGACAAGTTACCCAGGCGAAGAGAAGATTGGGTCTTACGCTATA 1701
              ||  |     | |  || ||      | ||   ||| |      | ||   ||||   |
Db        1438 CGCAGCGCGTTGAAAGTCACCGCACAGCCGAACGACGTACTACTAGGAAATTACGTAGTT 1497

Qy       1702 CTTTCACCCCAGGCGGTATTGAATAGTGAAAAACTGGCGTGTATCCACCCATTGGCGGAA 1761
              || || || ||| | ||  | || ||     ||  ||||      | |||||  | || ||
Db        1498 CTGTCCCCGCAGACCGTGCTCAAGAGCTCCAAGTTGGCCCCCGTGCACCCTCTAGCAGAG 1557

Qy       1762 CAAGTACTGGTAATGACTCACAAAGGTAGGGCAGGGAGATACAAAGTCGAGCCATACCAC 1821
              || ||      |||| || || || || ||||| ||  | ||| | |||||   ||| ||
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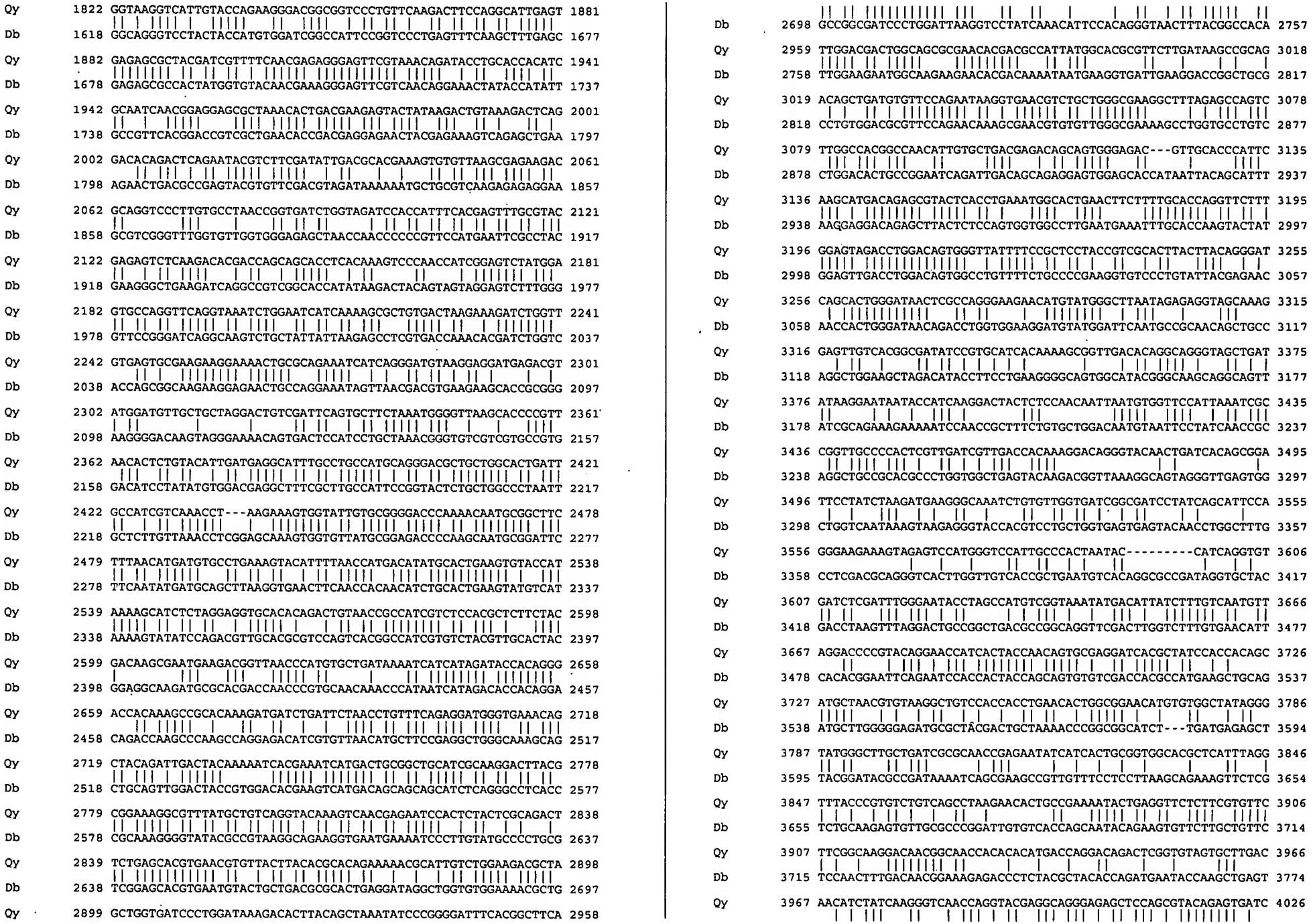

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Qy       4027 AGAGGTGACATTAGCAAGAGCGCTGACCAAGCTATCGTTAATGCTGCTAATAGCAAAGGT 4086

Db       3835 AGAGCAGACATAGCCACGTGCACAGAAGCGGCTGTGGTTAACGCAGCTAACGCCCGTGGA 3894

Qy       4087 CAACCAGGTTCCGGAGTGTGCGGTGCACTGTACCGAAAATGGCCGGCTGCTTTTGATAGA 4146

Db       3895 ACTGTAGGGGATGGCGTATGCAGGGCCGTGGCGAAGAAATGGCCGTCAGCCTTTAAGGGA 3954

Qy       4147 CAGCCAATAGCTGTCGGGACGGCTAGACTTGTGAAGCACGAACCG---CTCATCATACAT 4203

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Qy       4204 GCTGTAGGACCCAATTTTTCTAAGATGCCGGAACCGGAGGGCGACCTTAAGCTCGCAGCT 4263

Db       4015 GCTGTAGCGCCTAATTTCTCTGCCACGACTGAAGCGGAAGGGGACCGCGAATTGGCCGCT 4074

Qy       4264 GCCTACATGAGCATAGCGTCCATCGTCAACGCTGAGCGGATTACAAAAATATCAGTACCG 4323

Db       4075 GTCTACCGGGCAGTGGCCGCCGAAGTAAACAGACTGTCACTGAGCAGCGTAGCCATCCCG 4134

Qy       4324 CTACTGTCAACCGGCATCTATTCTGGTGGCAAAGATCGAGTGATGCAATCATTGCATCAC 4383

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Qy       4384 CTGTTCACTGCTTTCGACACTACGGATGCCGATGTCACCATATATTGCTTGGATAAACAA 4443

Db       4195 CTATTCACAGCAATGGACGCCACGGACGCTGACGTGACCATCTACTGCAGAGACAAAAGT 4254

Qy       4444 TGGGAGACCAGGATAATCGAGGCCATTCACCGCAAAGAAAGCGTCGAAATTCTGGATGAT 4503

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Db       4315 GACGTGGAGCTGACCACAGACTTGGTGAGAGTGCACCCGGACAGCAGCCTGGTGGGTCGT 4374

Qy       4564 CCAGGTTACTCCGTCAATGAGGGCAAGTTGTATTCATACCTGGAAGGTACACGATTCCAT 4623

Db       4375 AAGGGCTACAGTACCACTGACGGGTCGCTGTACTCGTACTTTGAAGGTACGAAATTCAAC 4434

Qy       4624 CAGACCGCCAAGGACATTGCCGAAATCCATGCAATGTGGCCCAACAAATCTGAGGCTAAT 4683

Db       4435 CAGGCTGCTATTGATATGGCAGAGATACTGACGTTGTGGCCCAGACTGCAAGAGGCAAAC 4494

Qy       4684 GAGCAGATTTGCTTGTACATCCTGGGGGAGAGTATGTCCAGCATCCGCTCCAAATGCCCA 4743

Db       4495 GAACAGATATGCCTATACGCGCTGGGCGAAACAATGGACAACATCAGATCCAAATGTCCG 4554

Qy       4744 GTAGAGGAGTCAGAGGCGTCTGCTCCACCTCACACACTTCCATGCCTGTGTAATTACGCT 4803

Db       4555 GTGAACGATTCCGATTCATCAACACCTCCCAGGACAGTGCCCTGCCTGTGCCGCTACGCA 4614

Qy       4804 ATGACGGCTGAGCGCGTATACAGGTTGCGCTCTGCGAAGAAAGAACAGTTCGCCGTATGC 4863

Db       4615 ATGACAGCAGAACGGATCGCCCGCCTTAGGTCACACCAAGTTAAAAGCATGGTGGTTTGC 4674

Qy       4864 TCATCATTCCTGTTGCCGAAGTACAGGATCACAGGCGTGCAGAAGCTACAGTGCAGCAAA 4923

Db       4675 TCATCTTTTCCCCTCCCGAAATACCATGTAGATGGGGTGCAGAAGGTAAAGTGCGAGAAG 4734

Qy       4924 CCAGTCCTGTTTTCAGGCGTCGTACCACCGGCTGTACACCCCAGGAAGTACGCGGAA 4980

Db       4735 GTTCTCCTGTTCGACCCGACGGTACCTTCAGTGGTTAGTCCGCGGAAGTATGCCGCA 4791


Search completed: November 15, 2003, 12:34:31
Job time : 1215 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2003, 20:27:52 ; Search time 1505 Seconds
(without alignments)
11631.798 Million cell updates/sec

Title: US-10-023-649-1_COPY_5000_11484
Perfect score: 6485
Sequence: 1 caccgccagcaacgacaacc.....tattttgtttttaaaatttc 6485

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5877.6	90.6	11492	20	AAV74107	Western equine enc
2	2397.6	37.0	11663	19	AAV33475	South African Arbo
3	2396	36.9	11663	19	AAV33473	South African Arbo
4	2388.4	36.8	11703	19	AAV33476	Sindbis virus clon
5	2386.4	36.8	11717	19	AAV33474	Girdwood S.A.virus
6	2383.6	36.8	11703	21	AAC64506	Alphavirus SinDCCh
7	2382	36.7	11703	21	AAC64507	Alphavirus SinChir
8	2381.6	36.7	11663	18	AAT47668	South African Arbo
9	2380.4	36.7	11740	25	ABX81526	Sindbis virus cDNA
10	2370.8	36.6	16656	17	AAT30787	Alphavirus-based e
11	2370.6	36.6	11717	21	AAA70577	Sindbis-like virus
12	2369.2	36.5	16656	19	AAV60125	Representative euk
13	2369.2	36.5	16656	19	AAV42364	Representative euk
14	2369.2	36.5	16656	20	AAV70684	Representative euk
15	2369.2	36.5	16656	21	AAZ92765	Representative euk
16	2369.2	36.5	16656	21	AAZ92892	Representative euk
17	2369.2	36.5	16656	24	AAL38772	DNA of eukaryotic
18	2367.6	36.5	16656	24	ABK46238	Eukaryotic Layered
19	2364.4	36.5	16656	16	AAQ86154	Eukaryotic layered
20	2331	35.9	11626	21	AAA70607	Sindbis-like virus
21	2322.4	35.8	16958	25	AAL55269	DNA of expression
22	2225.2	34.3	11687	24	AAD25136	SinChironLP virus
23	2198.4	33.9	11684	24	AAD25135	SinDCchiron virus
24	2122.6	32.7	13905	20	AAX77358	Polynucleotide seq
25	2122.6	32.7	13905	21	AAA90390	Plasmid pTE5'2J DN
26	1738.8	26.8	11464	20	AAV74108	Venezuelan equine
27	1728.6	26.7	11459	21	AAA49442	Venezuelan equine
28	1650.8	25.5	7970	20	AAX77357	Polynucleotide seq
29	1650.8	25.5	7970	21	AAA90389	Plasmid pDH-EB DNA
30	1646.6	25.4	9542	20	AAX77359	Polynucleotide seq
31	1646.6	25.4	9542	21	AAA90391	987BBneo DNA seque
32	1415.4	21.8	11517	13	AAQ26021	pSP6-SFV4 RNA tran
33	926.2	14.3	12523	24	AAD29131	Venezuelan equine
34	924.6	14.3	12379	24	AAD29139	Human immunodefici
35	924.6	14.3	13584	24	AAD29141	Venezuelan equine
36	916.2	14.1	7479	24	AAD29132	Venezuelan equine
37	863.2	13.3	4003	20	AAV74109	Venezuelan equine
38	827.6	12.8	8000	25	ABX81525	Sindbis virus cDNA
39	824.4	12.7	8000	18	AAX59321	Sindbis virus vari
40	824.4	12.7	8000	20	AAX58571	Sindbis virus vari
41	824.4	12.7	8000	25	ABX81524	Sindbis virus cDNA
42	819.2	12.6	9951	20	AAX77354	Polynucleotide seq
43	819.2	12.6	9951	21	AAA90386	Sindbis expression
44	819.2	12.6	9951	22	AAD04742	Alphaviral vector
45	819.2	12.6	9951	24	ABV73174	Nucleotide sequenc

ALIGNMENTS

RESULT 1
AAV74107
ID AAV74107 standard; cDNA; 11492 BP.
XX
AC AAV74107;
XX
DT 12-APR-1999 (first entry)
XX
DE Western equine encephalitis virus cDNA.
XX
KW WEE virus; vaccine; ds.
XX
OS Western equine encephalitis virus.
XX
PN WO9853077-A1.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WO-US10645.
XX
PR 16-DEC-1997; 97US-0991840.
PR 20-MAY-1997; 97US-0047162.
PR 24-JUL-1997; 97US-0053652.
XX
PA (REED-) REED ARMY INST RES WALTER.
XX
PI Crise BJ, Oberste MS, Parker MD, Schmura SM, Smith JF;
XX
DR WPI; 1999-045316/04.
XX
PT New DNA encoding infectious Western or Venezuelan equine

PT encephalitis virus genome - useful for the production of live or
PT attenuated vaccines for human or veterinary medicine
XX
PS Example 1; Page 54-67; 112pp; English.
XX
CC This cDNA sequence codes for an infectious western equine
CC encephalitis (WEE) virus RNA transcript. DNA representing the
CC entire genome was prepared by PCR using primers (see AAV74110-21)
CC based on partial genome sequences. 5' Sequences were obtained by
CC RACE. The full-length infectious clone is useful in the production
CC of virulent WEE virus, and for introducing and testing attenuating
CC mutations. Also new are: infectious or attenuated WEE RNA
CC transcripts and WEE viral particles; cDNA (see AAV74108) encoding an
CC infectious Venezuelan equine encephalitis (VEE) variant IE viral
CC genome; infectious or attenuated VEE RNA transcripts and viral
CC particles; an attenuated chimeric virus containing non-structural
CC sequences from a first alpha-virus (aV) and structural sequences
CC from a second aV, resulting in attenuation of the second aV; a method
CC for expressing a protein (especially an antigen to protect against
CC a pathogen) by cloning its gene into an attenuated WEE or VEE IE
CC replicon so that transcription of the replicon produces RNA able to
CC infect the cells in which protein is to be produced; methods for
CC diagnosing WEE and VEE infections; and polypeptides encoded by VEE
CC variant IIIA. Attenuated WEE and VEE are used in live or inactivated
CC vaccines, for use in human or veterinary medicine. Chimeric viruses
CC are also useful as vaccines, directed against the second aV which is
CC particularly Eastern equine encephalitis (EEE) virus or some variant
CC of VEE. WEE and VEE nucleic acids are used as primers and probes to
CC diagnose virus infections and to define natural variants, also for
CC production of protein antigens which can be used as diagnostic
CC reagents, to generate antibodies, and in vaccines. The attenuated
CC viruses are highly immunogenic and provide long-lasting protection.
XX
SQ Sequence 11492 BP; 3257 A; 2854 C; 2794 G; 2570 T; 17 other;

Query Match 90.6%; Score 5877.6; DB 20; Length 11492;
Best Local Similarity 96.1%; Pred. No. 0;
Matches 6238; Conservative 0; Mismatches 221; Indels 29; Gaps 20;

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Qy          1 CACCGCCAGCAACGACAACCGTAATATGTGAACCAACTGTGCCAGAACGTATACCCAGTC 60
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Db       5012 CATCGCCAACAACGACAACCGTAATATGTGAACCAACTGTGCCAGAACGTATACCCAGTC 5071

Qy         61 CGGTGATTTCTAGAGCACCAAGTGCGGAATCACTGCTATCGCTTGGCGGCGTCTCGTTCT 120
              |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
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Qy        121 CTAGCTCTGCCACACGCTCGTCAACCGCCTGGAGCGACTATGACAGGCGGTTTGTGGTTA 180
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       5132 CTAGCTCTGCCACACGCTCGTCAACTGCCTGGAGCGACTATGACAGGCGGTTTGTGGTTA 5191

Qy        181 CAGCTGATGTGCATCAAGCGAACACGTCTACGTGGAGCATCCCTAGTGCTCCTGGCTTGG 240
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Qy        241 ACGTCCAGCTGCCTTCTGACGTCACTGATTCCCACTGGAGTATTCCAAGTGCATCAGGCT 300
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Qy        301 TTGAAGTGAGAACACCATCTGTACAGGACCTAACTGCGGAGTGTGCGAAGCCTCGTGGAC 360
              |||||||||||||||| |||||||||||||||||||| |||||||||| ||||||||||||
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Qy        361 TGGCCGAAATAATGCAAGACTTCAATACTGCTCCTTTCCAGTTTCTTTCGGACTACAGAC 420
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Qy        421 CAGTACCGGCACCACGGAGACGCCCCATCCCATCACCTAGATCGACGGCTTCCGCACCTC 480
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Qy        481 CAGTTCCAAAGCCACGCAGGACTAAGTACCAACAACCACCAGGAGTCGCTAGAGCGATCT 540
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Qy .      541 CAGAAGCGGAGTTGGACGAGTACATCCGTCAACACTCCAACTGACGGTATGAAGCGGGAG 600
              |||||||||||  |||||||||||||||||||||||  |||||  |||||||||||||| ||||
Db       5552 CAGAAGCGGAGCTGGACGAGTACATCCGTCAACATTCCAATTGACGGTATGAAGC-GGAG 5610

Qy        601 CGTATATTTTCTCATCGGAAACAGGCCAAGGTCACCTTCAACAGAAATCAGTACGTCAAT 660
              ||||||||   ||       ||   | | ||||||||||||||||||||||||||||||||||
Db       5611 CGTATATT---TCTCATCGAAACAGGCCAGGTCACCTTCAACAGAAATCAGTACGTCAAT 5667

Qy        661 GTAAACTACAAGAACCTATATTGGATCGGGCCGTCCATGAGAAGTATTACGCCCCGCGCC 720
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Qy        721 TCGATCTCGAAAGAGAGAAAATGTTACAGAAGAAACTGCAATTATGCGCCTC-TGAAGGA 779
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Db       5727 TCGATCTCGAAAGAGAGAAGATGTTACAGAAGAAACTGCAATTATGCGCCTCNTGAAGGA 5786

Qy        780 AATAGAAGCAGGTATCAATCACGAAAAGTA-GAAAATATGAAAGCAATTACAGCGGAGCG 838
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Db       5787 AATAGAAGCAGGTATCAATCACGAAAAGTANGAAAATATGAAAGCAATTACAGCGGAGCG 5846

Qy        839 ACTCATTTCTGGATTGGGCACATATCTATCATCAGAAGTGAATCCTGTCGAGTGTTACAG 898
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Db       5847 ACTCATTTCTGGATTGGGCACATATCTATCATCAGAAGTGAATCCTGTCGAGTGTTACAG 5906

Qy        899 AGTCAATTATCCTGTACCAATCTACTCGTCAACGGTAATTAACAGGTTTACATCTGCAGA 958
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Qy        959 GGTCGCGGTTAAAACGTGCAACTTAGTTATCCAAGAGAATTACCCTACAGTAGCCAGTTA 1018
              || || || |||   |||||||||||| |||||||||||||||||||||||||||| |||
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Qy       1019 TTGTATAACAGATGAATACGATGCGTATCTTGACATGGTGGACGGCGCATCGTGCTGTCT 1078
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Qy       1079 AGATACAGCCACTTTTTGTCCGGCTAAACTGAGAAGCTACCCAAAGAAGCATAGCTATTT 1138
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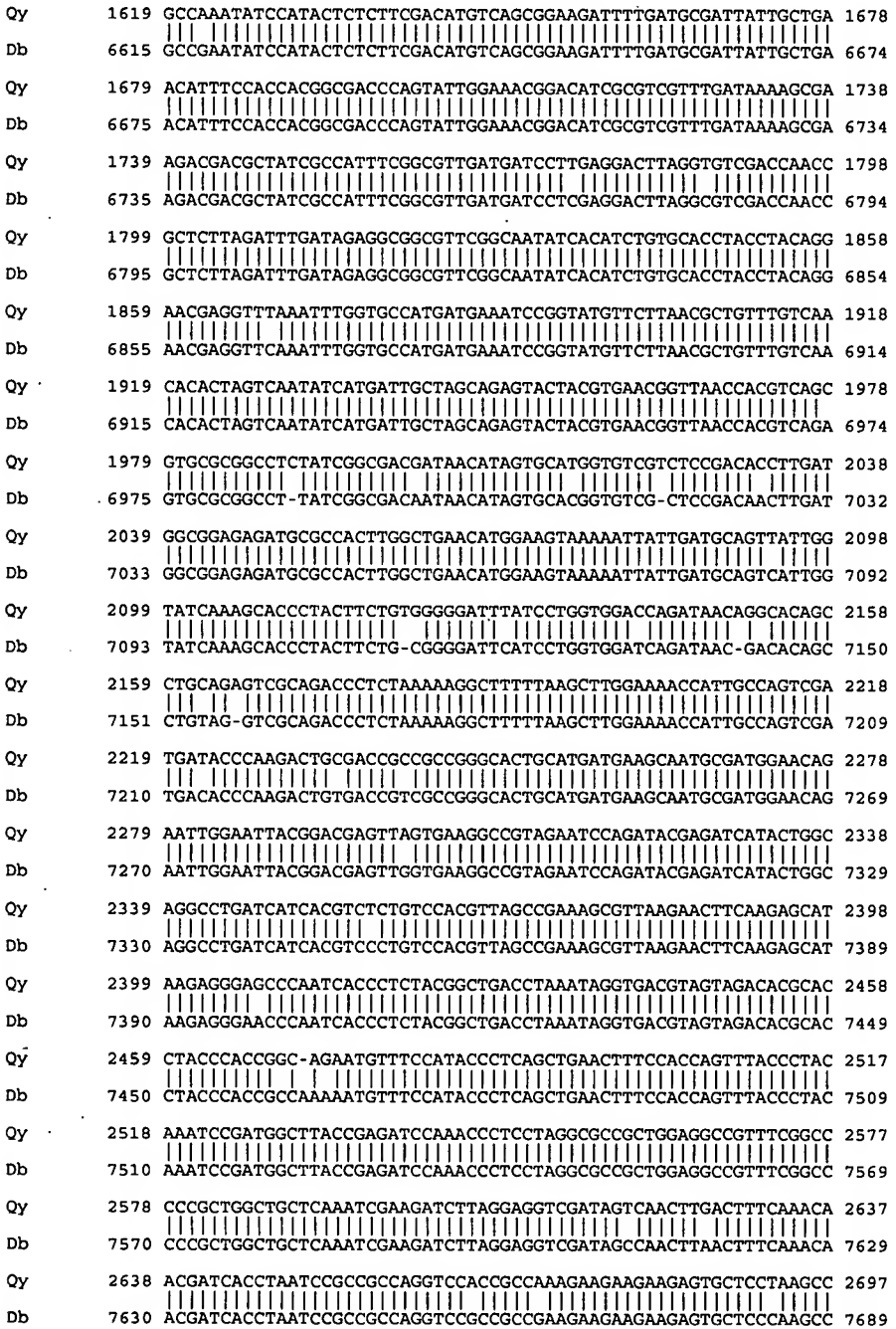
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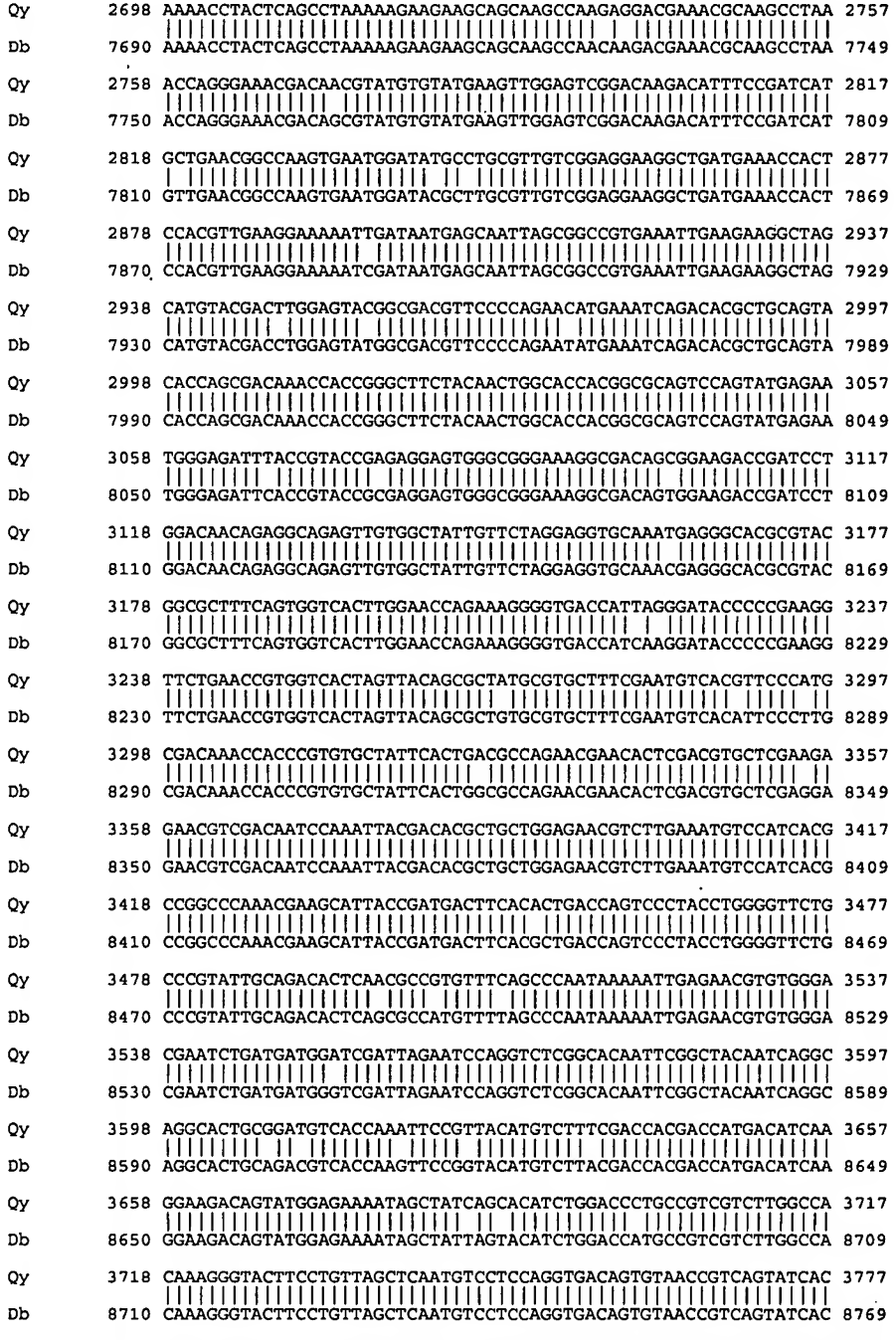
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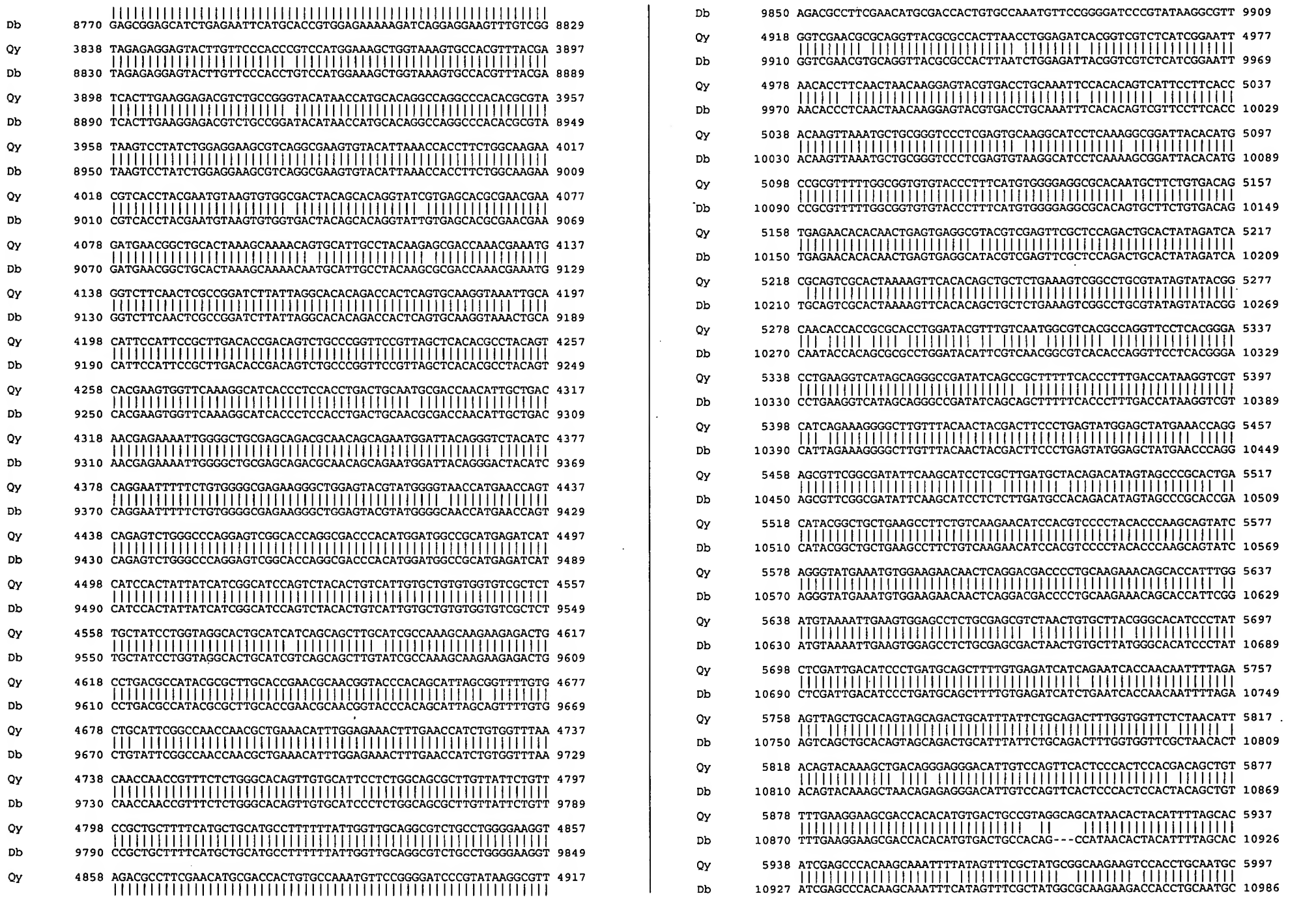
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RESULT 2
AAV33475
ID AAV33475 standard; cDNA; 11663 BP.
XX
AC AAV33475;
XX
DT 10-DEC-1998 (first entry)
XX
DE South African Arbovirus strain No. 86 cDNA clone pS55 sequence.
XX
KW Bone marrow cell; alphavirus; South African Arbovirus strain No. 86;
KW S.A.AR86; reverse transcriptase-PCR; nsP1; nsP2; nsP3; nsP4; capsid;
KW E3; E2; 6K; E1; growth hormone; growth factor; interleukin; cytokine;
KW chemokine; enzyme; ribozyme; antisense oligonucleotide; ss.
XX
OS South african arbovirus.
XX
FH Key   Location/Qualifiers
FT variation   215
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FT   to the S.A.AR86 cDNA sequence given in AAV33473"
FT variation   3863
FT   /*tag= b
FT   /note= "This nucleotide varies from C to G with respect
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FT variation   5984
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FT   /note= "This nucleotide varies from A to G with respect
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FT variation   9113
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FT   /note= "This nucleotide varies from T to C with respect
FT   to the S.A.AR86 cDNA sequence given in AAV33473"
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PN WO9836779-A2.
XX
PD 27-AUG-1998.
XX
PF 18-FEB-1998; 98WO-US02945.
XX
PR 19-FEB-1997; 97US-0801263.
XX
PA (UYNC-) UNIV NORTH CAROLINA.
XX
PI Davis NL, Johnston RE, Simpson DA;
XX
DR WPI; 1998-495361/42.
DR P-PSDB; AAW70471, AAW70472.
XX
PT Expression of heterologous RNA in bone marrow cells - using a
PT recombinant alphavirus comprising a promoter operable in bone marrow
PT cells operably associated with heterologous RNA.
XX
PS Example 5; Fig 5A-5B; 68pp; English.
XX
CC The present sequence represents the South African Arbovirus strain
CC No. 86 (S.A.AR86) cDNA clone pS55 sequence used in the method of
CC the invention. The invention provides a method for introducing and
CC expressing heterologous RNA in bone marrow cells using alphavirus
CC vectors. S.A.AR86 is an alphavirus whose cDNA sequence (AAV33474) was
CC determined from uncloned reverse transcriptase-PCR reaction fragments
CC amplified from the virion RNA. The S.A.AR86 cDNA clone pS55 sequence
CC has four nucleotide variations when compared with the S.A.AR86 cDNA
CC sequence derived from genomic RNA. The variations, however, do not
CC alter the the sequence of the protein encoded with respect to the
CC S.A.SR86 genomic RNA. The S.A.AR86 cDNA encodes nonstructural
CC and structural polyproteins. The nonstructural polyprotein is,
CC presumably, post-translationally modified into four different protein
CC products, namely nsP1 (AAW70460), nsP2 (AAW70461), nsP3 (AAW70466), nsP4
CC (AAW70467) proteins. The structural polyprotein is, presumably,
CC post-translationally modified into five different protein products,
CC namely capsid (AAW70468), E3 (AAW70469), E2 (AAW70470), 6K (AAW70471),
CC E1 (AAW70472) proteins. The S.A.AR86 cDNA was used in the method of the
CC invention. The inventors claim the transformed bone marrow cells are
CC useful for expressing a protein or peptide suitable for protecting the
CC subject against a disease such as a microbial, bacterial, protozoal,
CC parasitic or viral disease. The transformed bone marrow cells are also
CC claimed to be useful for expressing proteins and peptides such as
CC hormones, growth hormones, growth factors, interleukins, cytokines,
CC chemokines, enzymes, ribozymes or antisense oligonucleotides.
XX
SQ Sequence 11663 BP; 3289 A; 3105 C; 2910 G; 2359 T; 0 other;

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  Matches 3752;  Conservative    0;  Mismatches 1984;  Indels   74;  Gaps    9;

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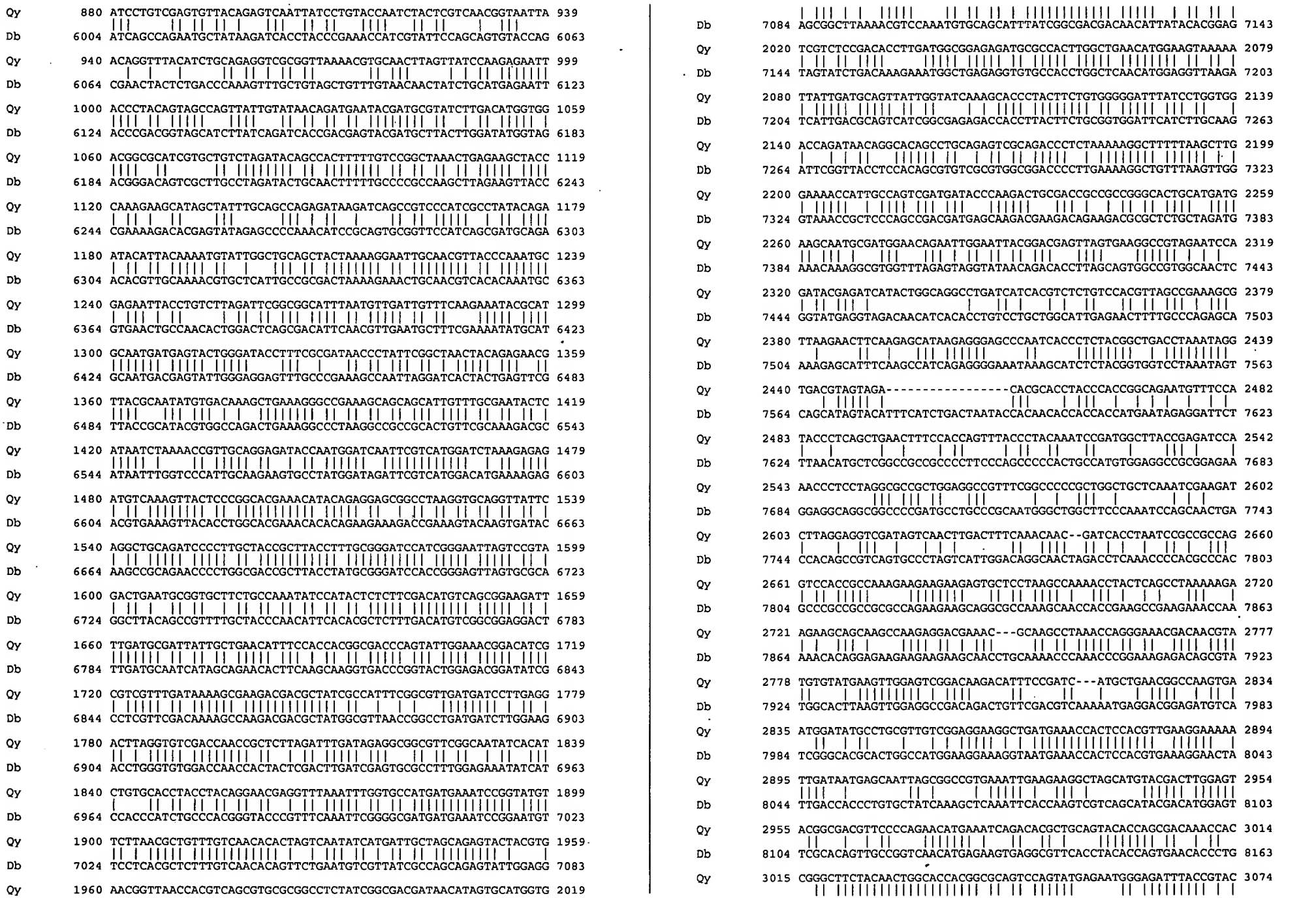

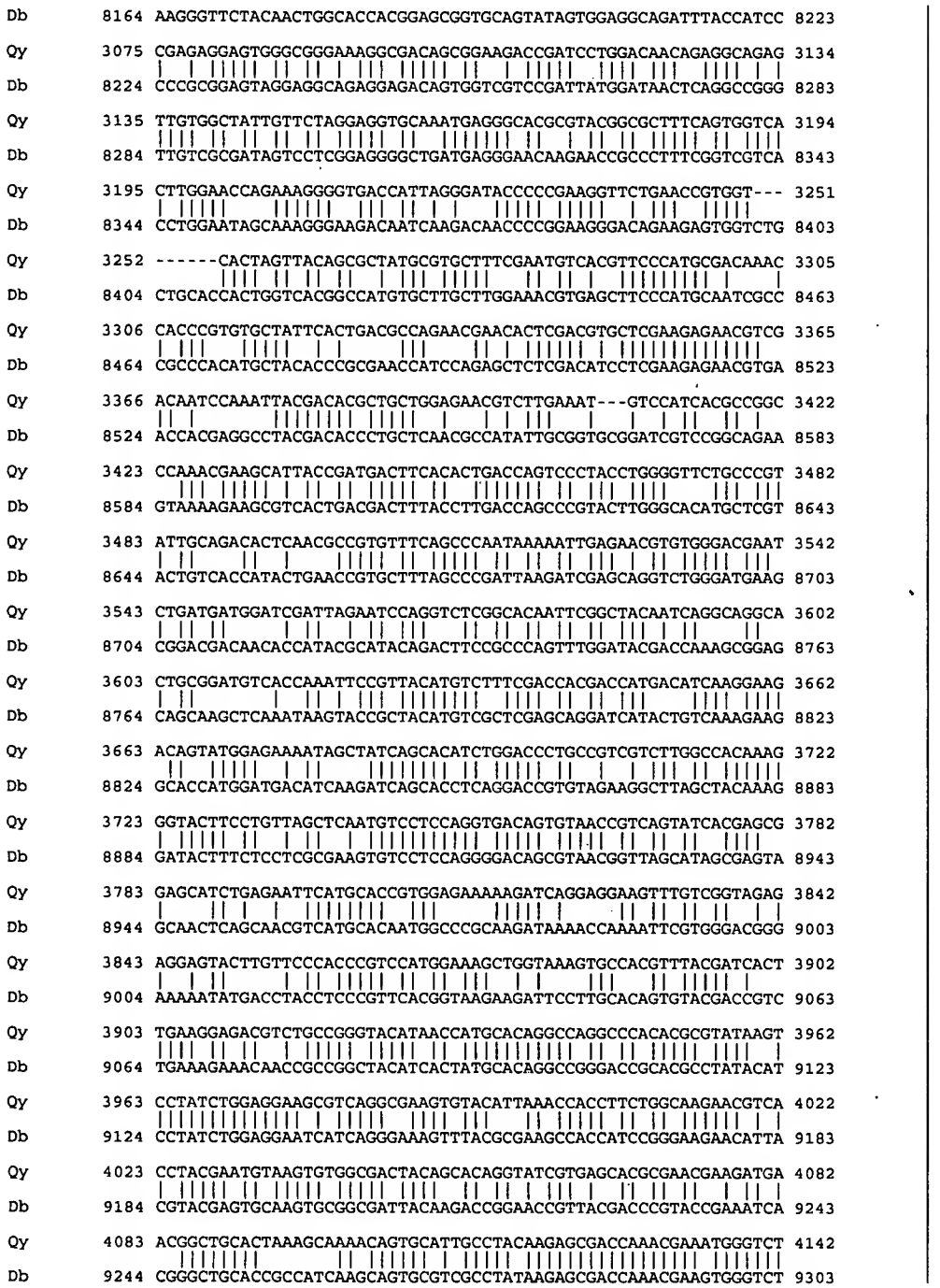
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Qy 4023 CCTACGAATGTAAGTGTGGCGACTACAGCACAGGTATCGTGAGCACGCGAACGAAGATGA 4082
Db 9184 CGTACGAGTGCAAGTGCGGCGATTACAAGACCGGAACCGTTACGACCCGTACCGAAATCA 9243
Qy 4083 ACGGCTGCACTAAAGCAAAACAGTGCATTGCCTACAAGAGCGACCAAACGAAATGGGTCT 4142
Db 9244 CGGGCTGCACCGCCATCAAGCAGTGCGTCGCCTATAAGAGCGACCAAACGAAGTGGGTCT 9303
Qy 4143 TCAACTCGCCGGATCTTATTAGGCACACAGACCACTCAGTGCAAGGTAAATTGCACATTC 4202
Db 9304 TCAACTCGCCGGACTCGATCAGACACGCCGACCACACGGCCCAAGGGAAATTGCATTTGC 9363
Qy 4203 CATTCCGCTTGACACCGACAGTCTGCCCGGTTCCGTTAGCTCACACGCCTACAGTCACGA 4262
Db 9364 CTTTCAAGCTGATCCCGAGTACCTGCATGGTCCCTGTTGCCCACGCGCCGAACGTAGTAC 9423
Qy 4263 AGTGGTTCAAAGGCATCACCCTCCACCTGACTGCAATGCGACCAACATTGCTGACAACGA 4322
Db 9424 ACGGCTTTAAACACATCAGCCTCCAATTAGACACAGACCATCTGACATTGCTCACCACCA 9483
Qy 4323 GAAAATTGGGGCTGCGAGCAGACGCAACAGCAGAATGGATTACAGGGTCTACATCCAGGA 4382
Db 9484 GGAGACTAGGGGCAAACCCGGAACCAACCACTGAATGGATCATCGGAAACACGGTTAGAA 9543
Qy 4383 ATTTTTCTGTGGGGCGAGAAGGGCTGGAGTACGTATGGGGTAACCATGAACCAGTCAGAG 4442
Db 9544 ACTTCACCGTCGACCGAGATGGCCTGGAATACATATGGGGCAATCACGAACCAGTAAGGG 9603
Qy 4443 TCTGGGCCCAGGAGTCGGCACCAGGCGACCCACATGGATGGCCGCATGAGATCATCATCC 4502
Db 9604 TCTATGCCCAAGAGTCTGCACCAGGAGACCCTCACGGATGGCCACACGAAATAGTACAGC 9663
Qy 4503 ACTATTATCATCGGCATCCAGTCTACACTGTCATTGTGCTGTGTGGTGTCGCTCTTGCTA 4562
Db 9664 ATTACTATCATCGCCATCCTGTGTACACCATCTTAGCCGTCGCATCAGCTGCTGTGGCGA 9723
Qy 4563 TCCTGGTAGGCACTGCATCATCAGCAGCTTGCATCGCCAAAGCAAGAAGAGACTGCCTGA 4622
Db 9724 TGATGATTGGCGTAACTGTTGCAGCATTATGTGCCTGTAAAGCGCGCCGTGAGTGCCTGA 9783
Qy 4623 CGCCATACGCGCTTGCACCGAACGCAACGGTACCCACAGCATTAGCGGTTTTGTGCTGCA 4682
Db 9784 CGCCATATGCCCTGGCCCCAAATGCCGTGATTCCAACTTCGCTGGCACTTTTGTGCTGTG 9843
Qy 4683 TTCGGCCAACCAACGCTGAAACATTTGGAGAAACTTTGAACCATCTGTGGTTTAACAACC 4742
Db 9844 TTAGGTCGGCTAATGCTGAAACATTCACCGAGACCATGAGTTACTTATGGTCGAACAGCC 9903
Qy 4743 AACCGTTTCTCTGGGCACAGTTGTGCATTCCTCTGGCAGCGCTTGTTATTCTGTTCCGCT 4802
Db 9904 AGCCGTTCTTCTGGGTCCAGCTGTGTATACCTCTGGCCGCTGTCGTCGTTCTAATGCGCT 9963
Qy 4803 GCTTTTCATGCTGCATGCCTTTTTTATTGGTTGCAGGCGTCTGCCTGGGGAAGGTAGACG 4862
Db 9964 GTTGCTCATGCTGCCTGCCTTTTTTAGTGGTTGCCGGCGCCTACCTGGCGAAGGTAGACG 10023
Qy 4863 CCTTCGAACATGCGACCACTGTGCCAAATGTTCCGGGGATCCCGTATAAGGCGTTGGTCG 4922
Db 10024 CCTACGAACATGCGACCACTGTTCCAAATGTGCCACAGATACCGTATAAGGCACTTGTTG 10083
Qy 4923 AACGCGCAGGTTACGCGCCACTTAACCTGGAGATCACGGTCGTCTCATCGGAATTAACAC 4982
Db 10084 AAAGGGCAGGGTACGCCCCGCTCAATTTGGAGATTACTGTCATGTCCTCGGAGGTTTTGC 10143
Qy 4983 CTTCAACTAACAAGGAGTACGTGACCTGCAAATTCCACACAGTCATTCCTTCACCACAAG 5042
Db 10144 CTTCCACCAACCAAGAGTACATTACCTGCAAATTCACCACTGTGGTCCCCTCCCCTAAAG 10203
Qy 5043 TTAAATGCTGCGGGTCCCTCGAGTGCAAGGCATCCTCAAAGGCGGATTACACATGCCGCG 5102
Db 10204 TCAGATGCTGCGGCTCCTTGGAATGTCAGCCCGCCGCTCACGCAGACTATACCTGCAAGG 10263
Qy 5103 TTTTTGGCGGTGTGTACCCTTTCATGTGGGGAGGCGCACAATGCTTCTGTGACAGTGAGA 5162
Db 10264 TCTTTGGAGGGGTGTACCCCTTCATGTGGGGAGGAGCACAATGTTTTTGCGACAGTGAGA 10323
Qy 5163 ACACACAACTGAGTGAGGCGTACGTCGAGTTCGCTCCAGACTGCACTATAGATCACGCAG 5222
Db 10324 ACAGCCAGATGAGTGAGGCGTACGTCGAATTGTCAGTAGATTGCGCGACTGACCACGCGC 10383

```
Qy       5223 TCGCACTAAAAGTTCACACAGCTGCTCTGAAAGTCGGCCTGCGTATAGTATACGGCAACA 5282
Db      10384 AGGCGATTAAGGTGCATACTGCCGCGATGAAAGTAGGACTGCGTATAGTGTACGGGAACA 10443

Qy       5283 CCACCGCGCACCTGGATACGTTTGTCAATGGCGTCACGCCAGGTTCCTCACGGGACCTGA 5342
Db      10444 CTACCAGTTTCCTAGATGTGTACGTGAACGGAGTCACACCAGGAACGTCTAAAGACCTGA 10503

Qy       5343 AGGTCATAGCAGGGCCGATATCAGCCGCTTTTTCACCCTTTGACCATAAGGTCGTCATCA 5402
Db      10504 AAGTCATAGCTGGACCAATTTCAGCATTGTTTACACCATTCGATCACAAGGTCGTTATCA 10563

Qy       5403 GAAAGGGGCTTGTTTACAACTACGACTTCCCTGAGTATGGAGCTATGAAACCAGGAGCGT 5462
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Qy       5463 TCGGCGATATTCAAGCATCCTCGCTTGATGCTACAGACATAGTAGCCCGCACTGACATAC 5522
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Qy       5583 ATGAAATGTGGAAGAACAACTCAGGACGACCCCTGCAAGAAACAGCACCATTTGGATGTA 5642
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Qy       5643 AAATTGAAGTGGAGCCTCTGCGAGCGTCTAACTGTGCTTACGGGCACATCCCTATCTCGA 5702
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Qy       5703 TTGACATCCCTGATGCAGCTTTTGTGAGATCATCAGAATCACCAACAATTTTAGAAGTTA 5762
Db      10864 TTGACATCCCGAACGCTGCCTTTATCAGGACATCAGATGCACCACTGGTCTCAACAGTCA 10923

Qy       5763 GCTGCACAGTAGCAGACTGCATTTATTCTGCAGACTTTGGTGGTTCTCTAACATTACAGT 5822
Db      10924 AATGTGATGTCAGTGAGTGCACTTATTCAGCGGACTTCGGAGGGATGGCTACCCTGCAGT 10983

Qy       5823 ACAAAGCTGACAGGGAGGGACATTGTCCAGTTCACTCCCACTCCACGACAGCTGTTTTGA 5882
Db      10984 ATGTATCCGACCGCGAAGGACAATGCCCTGTACATTCGCATTCGAGCACAGCAACCCTCC 11043

Qy       5883 AGGAAGCGACCACACATGTGACTGCCGTAGGCAGCATAACACTACATTTTAGCACATCGA 5942
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Qy       5943 GCCCACAAGCAAATTTTATAGTTTCGCTATGCGGCAAGAAGTCCACCTGCAATGCTGAAT 6002
Db      11104 GCCCACAGGCGAACTTCATTGTATCGCTGTGTGGTAAGAAGACAACATGCAATGCAGAAT 11163

Qy       6003 GTAAACCACCGGCCGACCACATAATTGGAGAACCACATAAAGTCGACCAAGAATTCCAGG 6062
Db      11164 GCAAACCACCAGCTGATCATATCGTGAGCACCCCGCACAAAAATGACCAAGAATTCCAAG 11223

Qy       6063 CGGCAGTTTCCAAAACATCTTGGAACTGGCTGCTTGCACTGTTTGGGGGAGCATCATCCC 6122
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Qy       6123 TCATTGTTGTAGGACTTATAGTGTTGGTCTGCAGCTCTATGCTTATAAACACACGTAGAT 6182
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Qy       6183 GACTGAGCGCGGACACTGA-CATAGCGGTAAAACTCGATGTACTTCCGAGGAAGCGTGGT 6241
Db      11344 GACCGCTACGCCCCAATGACCCGACCAGCAAAACTCGATGTACTTCCGAGGAACTGATGT 11403

Qy       6242 GCATAATGCCACGCGCCGCT--------------------------------TGACACT 6268
Db      11404 GCATAATGCATCAGGCTGGTATATTAGATCCCCGCTTACCGCGGGCAATATAGCAACACC 11463

Qy       6269 AAAACTCGATGTATTTCCGAGGAAGCACAGTGCATAATGCTGTGCAGTGT 6318
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Db      11464 AAAACTCGACGTATTTCCGAGGAAGCGCAGTGCATAATGCTGCGCAGTGT 11513
```

RESULT 3
AAV33473
ID AAV33473 standard; cDNA; 11663 BP.
XX
AC AAV33473;
XX
DT 10-DEC-1998 (first entry)
XX
DE South African Arbovirus strain No. 86 cDNA sequence.
XX
KW Bone marrow cell; alphavirus; South African Arbovirus strain No. 86;
KW S.A.AR86; reverse transcriptase-PCR; nsP1; nsP2; nsP3; nsP4; capsid;
KW E3; E2; 6K; E1; growth hormone; growth factor; interleukin; cytokine;
KW chemokine; enzyme; ribozyme; antisense oligonucleotide; ss.
XX
OS South african arbovirus
XX
FH Key Location/Qualifiers
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FT /*tag= a
FT CDS 60..7662
FT /*tag= b
FT /product= "Non-structural polyprotein"
FT CDS 7608..11345
FT /*tag= c
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FT 3'UTR 11346..11663
FT /*tag= d
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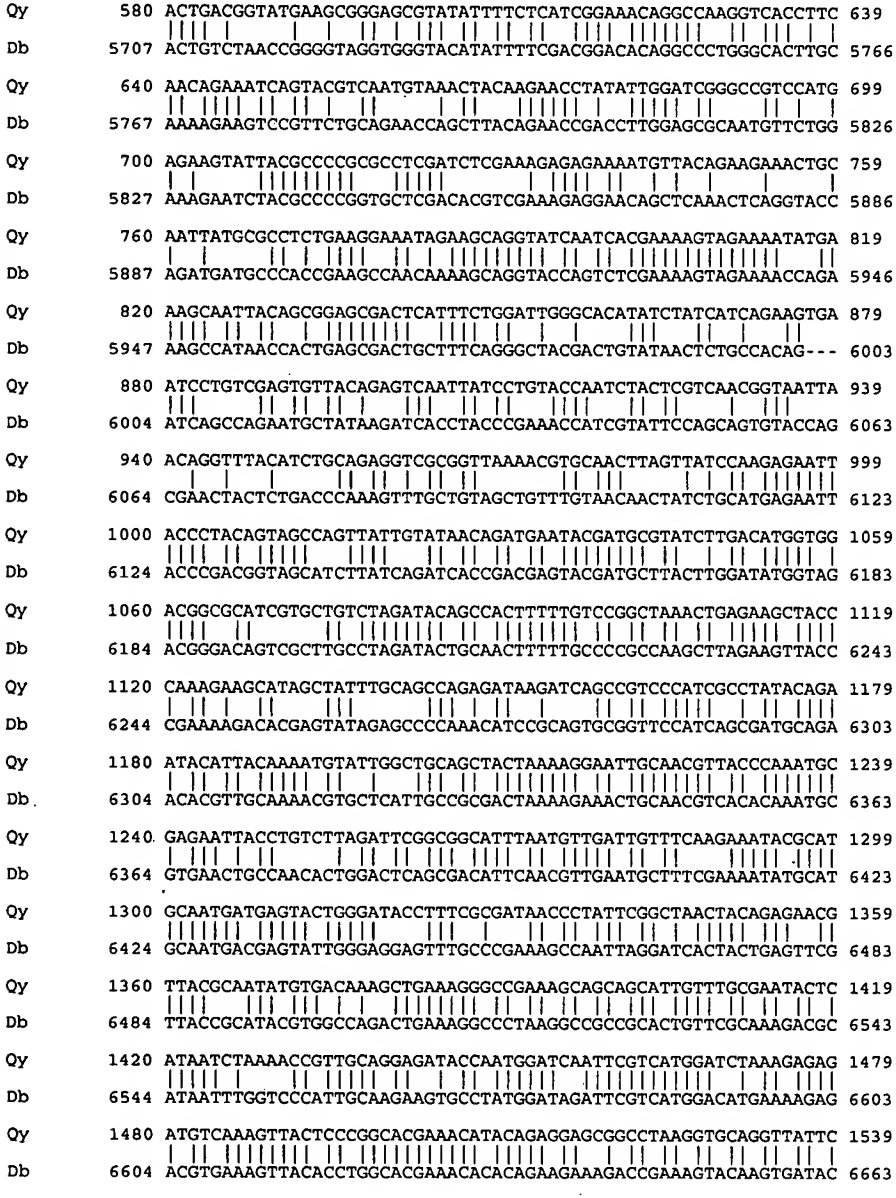
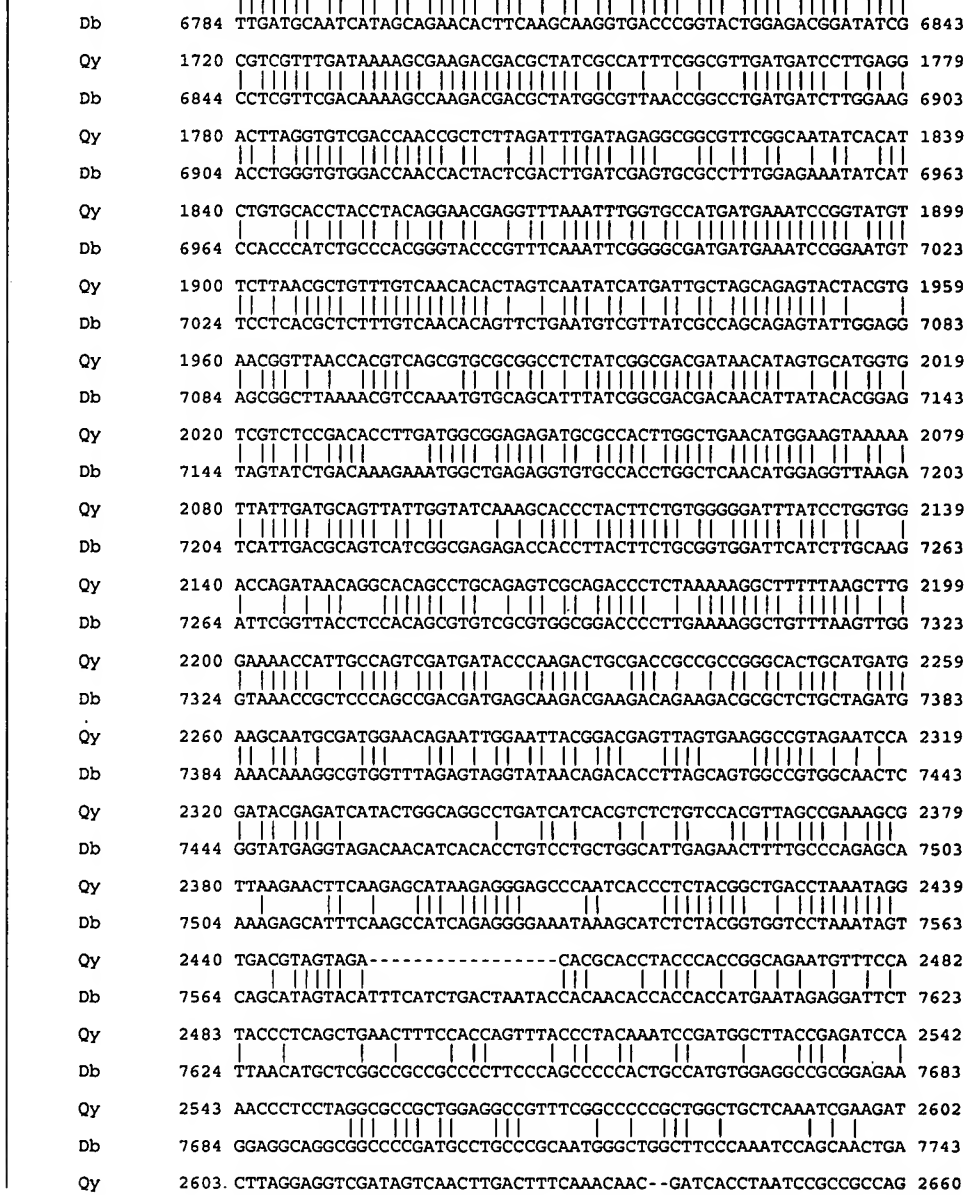
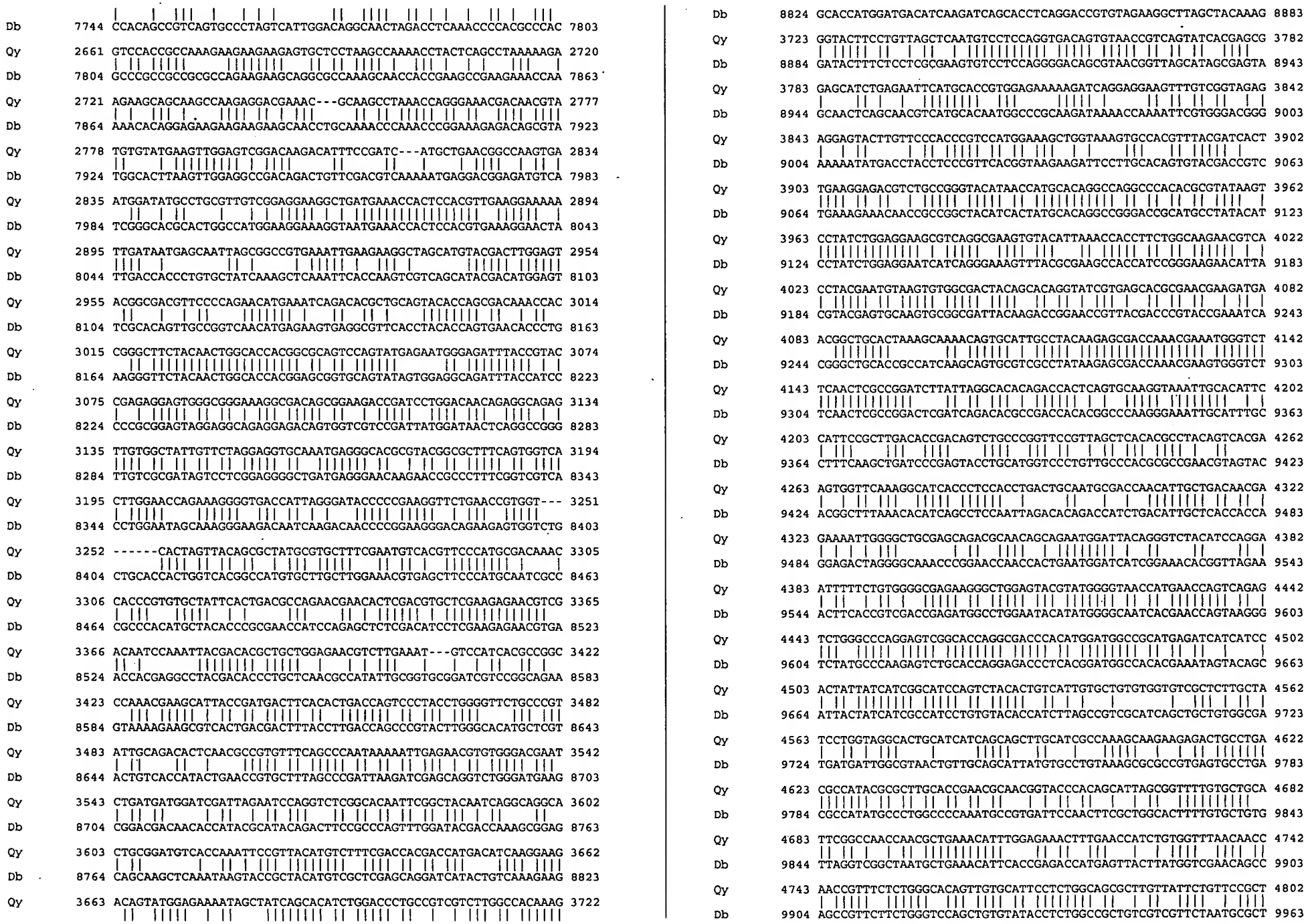
PN WO9836779-A2.
XX
PD 27-AUG-1998.
XX
PF 18-FEB-1998; 98WO-US02945.
XX
PR 19-FEB-1997; 97US-0801263.
XX
PA (UYNC-) UNIV NORTH CAROLINA.
XX
PI Davis NL, Johnston RE, Simpson DA;
XX
DR WPI; 1998-495361/42.
DR P-PSDB; AAW70460, AAW70461, AAW70466, AAW70467, AAW70468, AAW70469,
DR AAW70470, AAW70471, AAW70472.
XX
PT Expression of heterologous RNA in bone marrow cells - using a
PT recombinant alphavirus comprising a promoter operable in bone marrow
PT cells operably associated with heterologous RNA.
XX
PS Example 2; Fig 1A-1C; 68pp; English.
XX
CC The invention provides a method for introducing and expressing
CC heterologous RNA in bone marrow cells using alphavirus vectors.
CC The South African Arbovirus strain No. 86 (S.A.AR86) is an
CC alphavirus whose cDNA sequence was determined from uncloned reverse
CC transcriptase-PCR reaction fragments amplified from the virion RNA.
CC The S.A.AR86 cDNA encodes nonstructural and structural polyproteins.
CC The nonstructural polyprotein is, presumably, post-translationally
CC modified into four different protein products, namely nsP1 (AAW70460),
CC nsP2 (AAW70461), nsP3 (AAW70466), nsP4 (AAW70467) proteins. The
CC structural polyprotein is, presumably, post-translationally modified into
CC five different protein products, namely capsid (AAW70468), E3
CC (AAW70469), E2 (AAW70470), 6K (AAW70471), E1 (AAW70472) proteins. The
CC S.A.AR86 cDNA was used in the method of the invention. The inventors
CC claim the transformed bone marrow cells are useful for expressing a
CC protein or peptide suitable for protecting the subject against a disease
CC such as a microbial, bacterial, protozoal, parasitic or viral disease.
CC The transformed bone marrow cells are also claimed to be useful for
CC expressing proteins and peptides such as hormones, growth hormones,

CC growth factors, interleukins, cytokines, chemokines, enzymes, ribozymes
CC or antisense oligonucleotides.
XX
SQ Sequence 11663 BP; 3291 A; 3105 C; 2907 G; 2360 T; 0 other;

Query Match 36.9%; Score 2396; DB 19; Length 11663;
Best Local Similarity 64.6%; Pred. No. 0;
Matches 3751; Conservative 0; Mismatches 1985; Indels 74; Gaps 9;







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Db       9964 GTTGCTCATGCTGCCTGCCTTTTTTAGTGGTTGCCGGCGCCTACCTGGCGAAGGTAGACG 10023

Qy       4863 CCTTCGAACATGCGACCACTGTGCCAAATGTTCCGGGGATCCCGTATAAGGCGTTGGTCG 4922
             ||| |||||||||||||||| |||||||| ||   ||| ||||||||||  | || |
Db      10024 CCTACGAACATGCGACCACTGTTCCAAATGTGCCACAGATACCGTATAAGGCACTTGTTG 10083

Qy       4923 AACGCGCAGGTTACGCGCCACTTAACCTGGAGATCACGGTCGTCTCATCGGAATTAACAC 4982
             || | ||||| ||||| || || ||  ||||||| || ||| | || |||||    |
Db      10084 AAAGGGCAGGGTACGCCCCGCTCAATTTGGAGATTACTGTCATGTCCTCGGAGGTTTTGC 10143

Qy       4983 CTTCAACTAACAAGGAGTACGTGACCTGCAAATTCCACACAGTCATTCCTTCACCACAAG 5042
             |||| || ||| | |||||| | |||||||||||  ||| ||  | || || ||  |||
Db      10144 CTTCCACCAACCAAGAGTACATTACCTGCAAATTCACCACTGTGGTCCCCTCCCCTAAAG 10203

Qy       5043 TTAAATGCTGCGGGTCCCTCGAGTGCAAGGCATCCTCAAAGGCGGATTACACATGCCGCG 5102
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Db      10204 TCAGATGCTGCGGCTCCTTGGAATGTCAGCCCGCCGCTCACGCAGACTATACCTGCAAGG 10263

Qy       5103 TTTTTGGCGGTGTGTACCCTTTCATGTGGGGAGGCGCACAATGCTTCTGTGACAGTGAGA 5162
             | ||||| || |||||||| |||||||||||||| |||||||| || || ||||||||||
Db      10264 TCTTTGGAGGGGTGTACCCCTTCATGTGGGGAGGAGCACAATGTTTTTGCGACAGTGAGA 10323

Qy       5163 ACACACAACTGAGTGAGGCGTACGTCGAGTTCGCTCCAGACTGCACTATAGATCACGCAG 5222
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Db      10324 ACAGCCAGATGAGTGAGGCGTACGTCGAATTGTCAGTAGATTGCGCGACTGACCACGCGC 10383

Qy       5223 TCGCACTAAAAGTTCACACAGCTGCTCTGAAAGTCGGCCTGCGTATAGTATACGGCAACA 5282
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Db      10384 AGGCGATTAAGGTGCATACTGCCGCGATGAAAGTAGGACTGCGTATAGTGTACGGGAACA 10443

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Qy       5343 AGGTCATAGCAGGGCCGATATCAGCCGCTTTTTCACCCTTTGACCATAAGGTCGTCATCA 5402
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Qy       5403 GAAAGGGGCTTGTTTACAACTACGACTTCCCTGAGTATGGAGCTATGAAACCAGGAGCGT 5462
                || || || |||||||| ||||| || || || ||||| ||||||||||||||||
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Qy       5463 TCGGCGATATTCAAGCATCCTCGCTTGATGCTACAGACATAGTAGCCCGCACTGACATAC 5522
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Qy       5523 GGCTGCTGAAGCCTTCTGTCAAGAACATCCACGTCCCCTACACCCAAGCAGTATCAGGGT 5582
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Db      10684 GGCTACTCAAGCCTTCCGCCAAGAACGTGCATGTCCCGTACACGCAGGCCGCATCTGGAT 10743

Qy       5583 ATGAAATGTGGAAGAACAACTCAGGACGACCCCTGCAAGAAACAGCACCATTTGGATGTA 5642
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Db      10804 AGATTGCAGTCAATCCGCTTCGAGCGGTGGACTGCTCATACGGGAACATTCCCATTTCTA 10863

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Qy       5763 GCTGCACAGTAGCAGACTGCATTTATTCTGCAGACTTTGGTGGTTCTCTAACATTACAGT 5822
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Qy       5823 ACAAAGCTGACAGGGAGGGACATTGTCCAGTTCACTCCCACTCCACGACAGCTGTTTTGA 5882
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Db      10984 ATGTATCCGACCGCGAAGGACAATGCCCTGTACATTCGCATTCGAGCACAGCAACCCTCC 11043

Qy       5883 AGGAAGCGACCACACATGTGACTGCCGTAGGCAGCATAACACTACATTTTAGCACATCGA 5942
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Db      11044 AAGAGTCGACAGTTCATGTCCTGGAGAAAGGAGCGGTGACAGTACACTTCAGCACCGCGA 11103

Qy       5943 GCCCACAAGCAAATTTTATAGTTTCGCTATGCGGCAAGAAGTCCACCTGCAATGCTGAAT 6002
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Db      11104 GCCCACAGGCGAACTTCATTGTATCGCTGTGTGGTAAGAAGACAACATGCAATGCAGAAT 11163

Qy       6003 GTAAACCACCGGCCGACCACATAATTGGAGAACCACATAAAGTCGACCAAGAATTCCAGG 6062
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Db      11164 GCAAACCACCAGCTGATCATATCGTGAGCACCCCGCACAAAAATGACCAAGAATTCCAAG 11223

Qy       6063 CGGCAGTTTCCAAAACATCTTGGAACTGGCTGCTTGCACTGTTTGGGGGAGCATCATCCC 6122
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Db      11224 CCGCCATCTCAAAAACTTCATGGAGTTGGCTGTTTGCCCTTTTCGGCGGCGCCTCGTCGC 11283

Qy       6123 TCATTGTTGTAGGACTTATAGTGTTGGTCTGCAGCTCTATGCTTATAAACACACGTAGAT 6182
             | | || ||||||||||  | || |  ||||||   ||||| |  | ||||| ||||
Db      11284 TATTAATTATAGGACTTATGATTTTTGCTTGCAGCATGATGCTGACTAGCACACGAAGAT 11343

Qy       6183 GACTGAGCGCGGACACTGA-CATAGCGGTAAAACTCGATGTACTTCCGAGGAAGCGTGGT 6241
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Db      11344 GACCGCTACGCCCCAATGACCCGACCAGCAAAACTCGATGTACTTCCGAGGAACTGATGT 11403

Qy       6242 GCATAATGCCACGCGCCGCT--------------------------------TGACACT 6268
             |||||||||  |  || | |                                ||||
Db      11404 GCATAATGCATCAGGCTGGTATATTAGATCCCCGCTTACCGCGGGCAATATAGCAACACC 11463

Qy       6269 AAAACTCGATGTATTTCCGAGGAAGCACAGTGCATAATGCTGTGCAGTGT 6318
             ||||||||| |||||||||||||| |||||||||||||| |||||||
Db      11464 AAAACTCGACGTATTTCCGAGGAAGCGCAGTGCATAATGCTGCGCAGTGT 11513
```

RESULT 4
AAV33476
ID AAV33476 standard; cDNA; 11703 BP.
XX
AC AAV33476;
XX
DT 10-DEC-1998 (first entry)
XX
DE Sindbis virus clone TR339 cDNA sequence.
XX
KW Bone marrow cell; alphavirus; Sindbis virus; cytokine; capsid;
KW reverse transcriptase-PCR; nsP1; nsP2; nsP3; nsP4; E3; E2; 6K; E1;
KW growth hormone; growth factor; interleukin; chemokine; enzyme;
KW ribozyme; antisense oligonucleotide; ss.
XX
OS Sindbis virus.
XX

FH	Key	Location/Qualifiers
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FT	CDS	60..7601
FT		/*tag= b
FT		/product= "Non-structural polyprotein"
FT		/note= "Internal stop codon present at nucleotides 5748-5750"
FT	CDS	7647..11384
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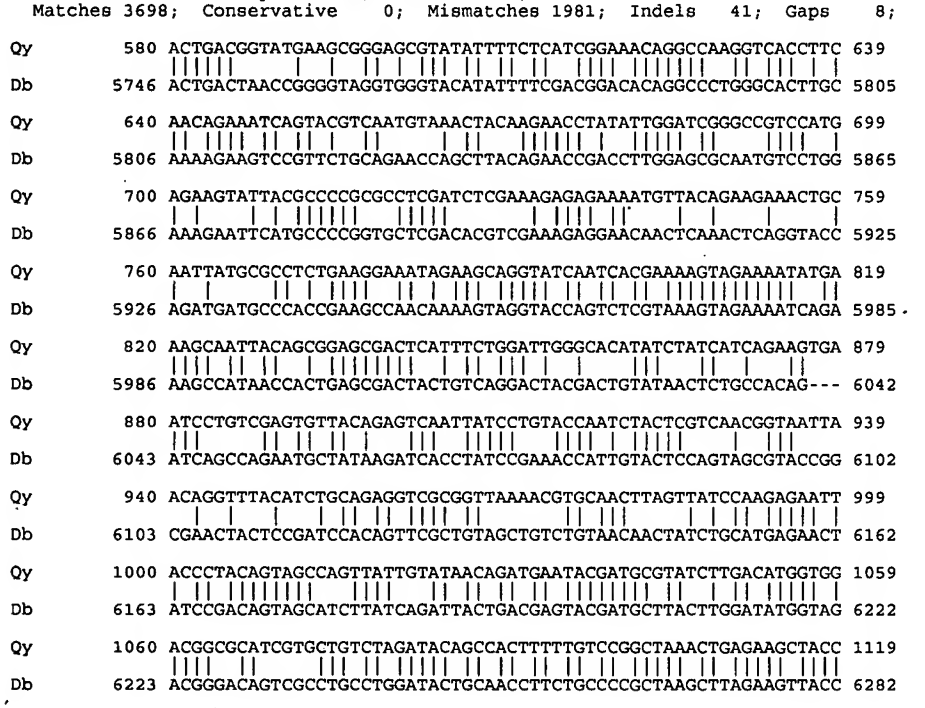
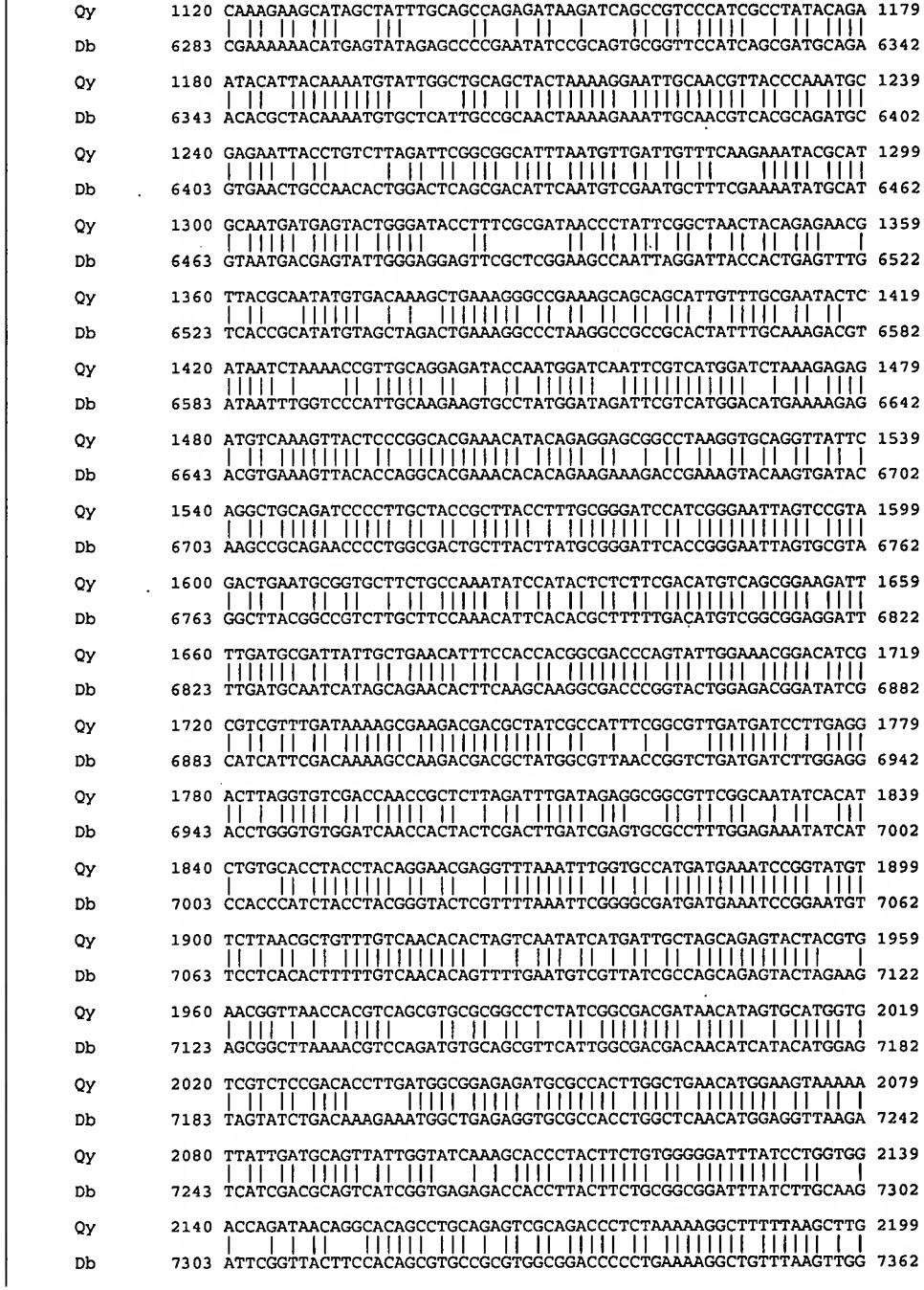
FT		/product= "Structural polyprotein"
FT	3'UTR	11382..11703
FT		/*tag= d

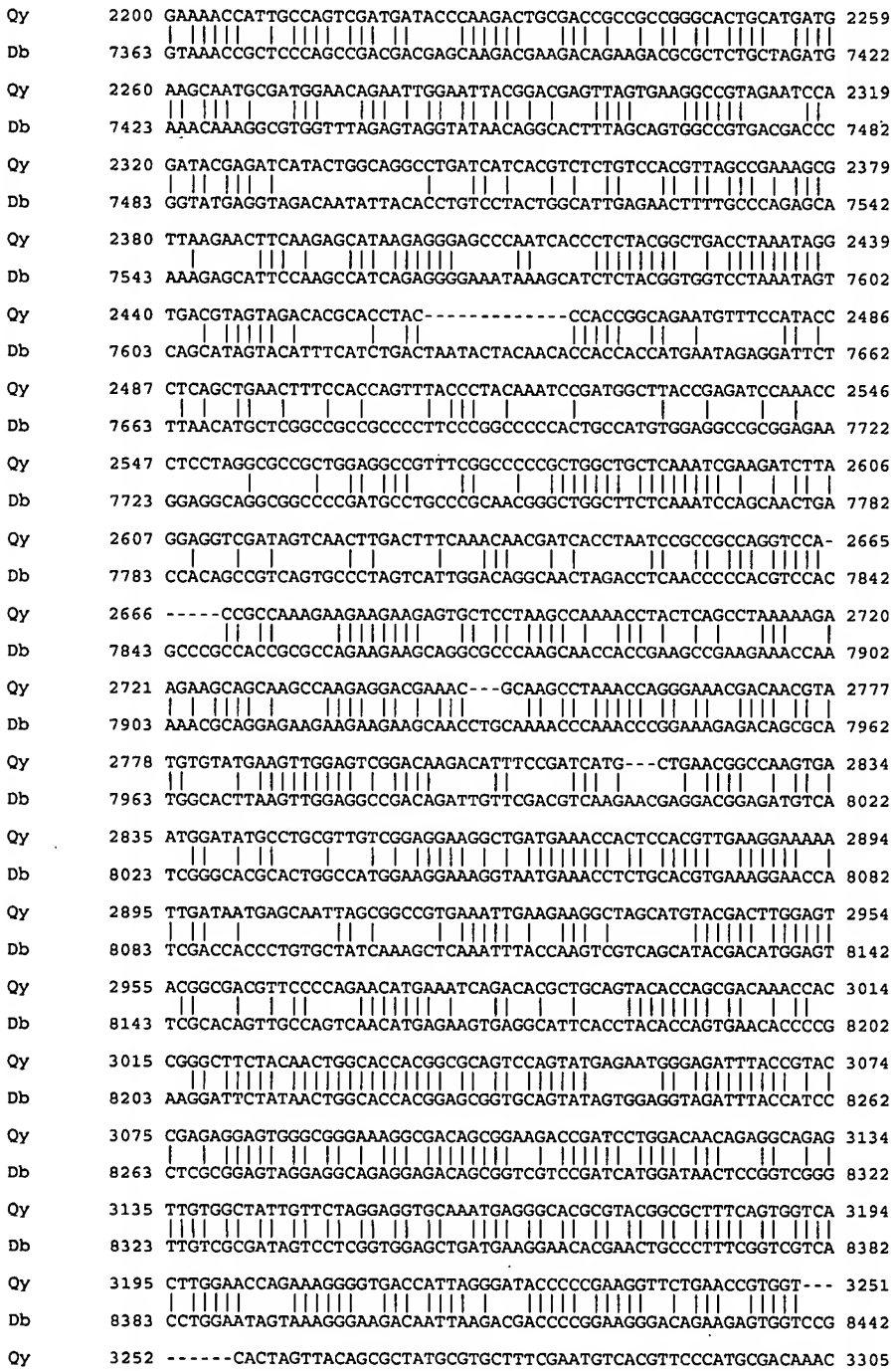
XX
PN WO9836779-A2.
XX
PD 27-AUG-1998.
XX
PF 18-FEB-1998; 98WO-US02945.
XX
PR 19-FEB-1997; 97US-0801263.
XX
PA (UYNC-) UNIV NORTH CAROLINA.

XX
PI Davis NL, Johnston RE, Simpson DA;
XX
DR WPI; 1998-495361/42.
DR P-PSDB; AAW70464, AAW70465, AAW70480, AAW70481, AAW70482, AAW70483,
DR AAW70484, AAW70485, AAW70486.
XX
PT Expression of heterologous RNA in bone marrow cells - using a
PT recombinant alphavirus comprising a promoter operable in bone marrow
PT cells operably associated with heterologous RNA.
XX
PS Example 6; Fig 6A-6B; 68pp; English.
XX
CC The invention provides a method for introducing and expressing
CC heterologous RNA in bone marrow cells using alphavirus vectors.
CC The present sequence represents the Sindbis virus clone TR339 cDNA
CC sequence. The Sindbis virus cDNA encodes nonstructural and structural
CC polyproteins. The nonstructural polyprotein is, presumably,
CC post-translationally modified into four different protein products,
CC namely nsP1 (AAW70464), nsP2 (AAW70465), nsP3 (AAW70480), nsP4
CC (AAW70481) proteins. The structural polyprotein is, presumably, post-
CC translationally modified into five different protein products, namely
CC capsid (AAW70482), E3 (AAW70483), E2 (AAW70484), 6K (AAW70485), E1
CC (AAW70486) proteins. The Sindbis virus cDNA was used in the method of
CC the invention. The inventors claim the transformed bone marrow cells
CC are useful for expressing a protein or peptide suitable for protecting
CC the subject against a disease such as a microbial, bacterial, protozoal,
CC parasitic or viral disease. The transformed bone marrow cells are also
CC claimed to be useful for expressing proteins and peptides such as
CC hormones, growth hormones, growth factors, interleukins, cytokines,
CC chemokines, enzymes, ribozymes or antisense oligonucleotides.
XX
SQ Sequence 11703 BP; 3306 A; 3051 C; 2913 G; 2433 T; 0 other;

Query Match 36.8%; Score 2388.4; DB 19; Length 11703;
Best Local Similarity 64.7%; Pred. No. 0;
Matches 3698; Conservative 0; Mismatches 1981; Indels 41; Gaps 8;



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Qy 2260 AAGCAATGCGATGGAACAGAATTGGAATTACGGACGAGTTAGTGAAGGCCGTAGAATCCA 2319
Db 7423 AAACAAAGGCGTGGTTTAGAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCC 7482
Qy 2320 GATACGAGATCATACTGGCAGGCCTGATCATCACGTCTCTGTCCACGTTAGCCGAAAGCG 2379
Db 7483 GGTATGAGGTAGACAATATTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCA 7542
Qy 2380 TTAAGAACTTCAAGAGCATAAGAGGGAGCCCAATCACCCTCTACGGCTGACCTAAATAGG 2439
Db 7543 AAAGAGCATTCCAAGCCATCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGT 7602
Qy 2440 TGACGTAGTAGACACGCACCTAC----------CCACCGGCAGAATGTTTCCATACC 2486
Db 7603 CAGCATAGTACATTTCATCTGACTAATACTACAACACCACCACCATGAATAGAGGATTCT 7662
Qy 2487 CTCAGCTGAACTTTCCACCAGTTTACCCTACAAATCCGATGGCTTACCGAGATCCAAACC 2546
Db 7663 TTAACATGCTCGGCCGCCGCCCCTTCCCGGCCCCCACTGCCATGTGGAGGCCGCGGAGAA 7722
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Qy 2666 -----CCGCCAAAGAAGAAGAAGAGTGCTCCTAAGCCAAAACCTACTCAGCCTAAAAAGA 2720
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Qy 3135 TTGTGGCTATTGTTCTAGGAGGTGCAAATGAGGGCACGCGTACGGCGCTTTCAGTGGTCA 3194
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Qy 3783 GAGCATCTGAGAATTCATGCACCGTGGAGAAAAAGATCAGGAGGAAGTTTGTCGGTAGAG 3842
Db 8983 GCAACTCAGCAACGTCATGTACACTGGCCCGCAAGATAAAACCAAAATTCGTGGGACGGG 9042
Qy 3843 AGGAGTACTTGTTCCCACCCGTCCATGGAAAGCTGGTAAAGTGCCACGTTTACGATCACT 3902
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Qy 4023 CCTACGAATGTAAGTGTGGCGACTACAGCACAGGTATCGTGAGCACGCGAACGAAGATGA 4082
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Qy 4083 ACGGCTGCACTAAAGCAAAACAGTGCATTGCCTACAAGAGCGACCAAACGAAATGGGTCT 4142
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Qy 4263 AGTGGTTCAAAGGCATCACCCTCCACCTGACTGCAATGCGACCAACATTGCTGACAACGA 4322
Db 9463 ATGGCTTTAAACACATCAGCCTCCAATTAGATACAGACCACTTGACATTGCTCACCACCA 9522
Qy 4323 GAAAATTGGGGCTGCGAGCAGACGCAACAGCAGAATGGATTACAGGGTCTACATCCAGGA 4382

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Db       9523 GGAGACTAGGGGCAAACCCGGAACCAACCACTGAATGGATCGTCGGAAAGACGGTCAGAA 9582
Qy       4383 ATTTTTCTGTGGGGCGAGAAGGGCTGGAGTACGTATGGGGTAACCATGAACCAGTCAGAG 4442
Db       9583 ACTTCACCGTCGACCGAGATGGCCTGGAATACATATGGGGAAATCATGAGCCAGTGAGGG 9642
Qy       4443 TCTGGGCCCAGGAGTCGGCACCAGGCGACCCACATGGATGGCCGCATGAGATCATCATCC 4502
Db       9643 TCTATGCCCAAGAGTCAGCACCAGGAGACCCTCACGGATGGCCACACGAAATAGTACAGC 9702
Qy       4503 ACTATTATCATCGGCATCCAGTCTACACTGTCATTGTGCTGTGTGGTGTCGCTCTTGCTA 4562
Db       9703 ATTACTACCATCGCCATCCTGTGTACACCATCTTAGCCGTCGCATCAGCTACCGTGGCGA 9762
Qy       4563 TCCTGGTAGGCACTGCATCATCAGCAGCTTGCATCGCCAAAGCAAGAAGAGACTGCCTGA 4622
Db       9763 TGATGATTGGCGTAACCGTTGCAGTGTTATGTGCCTGTAAAGCGCGCCGTGAGTGCCTGA 9822
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Db       9823 CGCCATACGCCCTGGCCCCAAACGCCGTAATCCCAACTTCGCTGGCACTCTTGTGCTGCG 9882
Qy       4683 TTCGGCCAACCAACGCTGAAACATTTGGAGAAACTTTGAACCATCTGTGGTTTAACAACC 4742
Db       9883 TTAGGTCGGCCAATGCTGAAACGTTCACCGAGACCATGAGTTACTTGTGGTCGAACAGTC 9942
Qy       4743 AACCGTTTCTCTGGGCACAGTTGTGCATTCCTCTGGCAGCGCTTGTTATTCTGTTCCGCT 4802
Db       9943 AGCCGTTCTTCTGGGTCCAGTTGTGCATACCTTTGGCCGCTTTCATCGTTCTAATGCGCT 10002
Qy       4803 GCTTTTCATGCTGCATGCCTTTTTTATTGGTTGCAGGCGTCTGCCTGGGGAAGGTAGACG 4862
Db      10003 GCTGCTCCTGCTGCCTGCCTTTTTTAGTGGTTGCCGGCGCCTACCTGGCGAAGGTAGACG 10062
Qy       4863 CCTTCGAACATGCGACCACTGTGCCAAATGTTCCGGGGATCCCGTATAAGGCGTTGGTCG 4922
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Qy       4923 AACGCGCAGGTTACGCGCCACTTAACCTGGAGATCACGGTCGTCTCATCGGAATTAACAC 4982
Db      10123 AAAGGGCAGGGTATGCCCCGCTCAATTTGGAGATCACTGTCATGTCCTCGGAGGTTTTGC 10182
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Qy       5043 TTAAATGCTGCGGGTCCCTCGAGTGCAAGGCATCCTCAAAGGCGGATTACACATGCCGCG 5102
Db      10243 TCAAATGCTGCGGCTCCTTGGAATGTCAGCCGGCCGCTCATGCAGACTATACCTGCAAGG 10302
Qy       5103 TTTTTGGCGGTGTGTACCCTTTCATGTGGGGAGGCGCACAATGCTTCTGTGACAGTGAGA 5162
Db      10303 TCTTCGGAGGGGTCTACCCCTTTATGTGGGGAGGAGCGCAATGTTTTTGCGACAGTGAGA 10362
Qy       5163 ACACACAACTGAGTGAGGCGTACGTCGAGTTCGCTCCAGACTGCACTATAGATCACGCAG 5222
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Qy       5223 TCGCACTAAAAGTTCACACAGCTGCTCTGAAAGTCGGCCTGCGTATAGTATACGGCAACA 5282
Db      10423 AGGCGATTAAGGTGCACACTGCCGCGATGAAAGTAGGACTGCGTATAGTGTACGGGAACA 10482
Qy       5283 CCACCGCGCACCTGGATACGTTTGTCAATGGCGTCACGCCAGGTTCCTCACGGGACCTGA 5342
Db      10483 CTACCAGTTTCCTAGATGTGTACGTGAACGGAGTCACACCAGGAACGTCTAAAGACTTGA 10542
Qy       5343 AGGTCATAGCAGGGCCGATATCAGCCGCTTTTTCACCCTTTGACCATAAGGTCGTCATCA 5402
Db      10543 AAGTCATAGCTGGACCAATTTCAGCATCGTTTACGCCATTCGATCATAAGGTCGTTATCC 10602
Qy       5403 GAAAGGGGCTTGTTTACAACTACGACTTCCCTGAGTATGGAGCTATGAAACCAGGAGCGT 5462
Db      10603 ATCGCGGCCTGGTGTACAACTATGACTTCCCGGAATATGGAGCGATGAAACCAGGAGCGT 10662
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Qy       5463 TCGGCGATATTCAAGCATCCTCGCTTGATGCTACAGACATAGTAGCCCGCACTGACATAC 5522
Db      10663 TTGGAGACATTCAAGCTACCTCCTTGACTAGCAAGGATCTCATCGCCAGCACAGACATTA 10722
Qy       5523 GGCTGCTGAAGCCTTCTGTCAAGAACATCCACGTCCCCTACACCCAAGCAGTATCAGGGT 5582
Db      10723 GGCTACTCAAGCCTTCCGCCAAGAACGTGCATGTCCCGTACACGCAGGCCGCATCAGGAT 10782
Qy       5583 ATGAAATGTGGAAGAACAACTCAGGACGACCCCTGCAAGAAACAGCACCATTTGGATGTA 5642
Db      10783 TTGAGATGTGGAAAAACAACTCAGGCCGCCCACTGCAGGAAACCGCACCTTTCGGGTGTA 10842
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Qy       5763 GCTGCACAGTAGCAGACTGCATTTATTCTGCAGACTTTGGTGGTTCTCTAACATTACAGT 5822
Db      10963 AATGTGAAGTCAGTGAGTGCACTTATTCAGCAGACTTCGGCGGGATGGCCACCCTGCAGT 11022
Qy       5823 ACAAAGCTGACAGGGAGGGACATTGTCCAGTTCACTCCCACTCCACGACAGCTGTTTTGA 5882
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Qy       5883 AGGAAGCGACCACACATGTGACTGCCGTAGGCAGCATAACACTACATTTTAGCACATCGA 5942
Db      11083 AAGAGTCGACAGTACATGTCCTGGAGAAAGGAGCGGTGACAGTACACTTTAGCACCGCGA 11142
Qy       5943 GCCCACAAGCAAATTTTATAGTTTCGCTATGCGGCAAGAAGTCCACCTGCAATGCTGAAT 6002
Db      11143 GTCCACAGGCGAACTTTATCGTATCGCTGTGTGGGAAGAAGACAACATGCAATGCAGAAT 11202
Qy       6003 GTAAACCACCGGCCGACCACATAATTGGAGAACCACATAAAGTCGACCAAGAATTCCAGG 6062
Db      11203 GTAAACCACCAGCTGACCATATCGTGAGCACCCCGCACAAAAATGACCAAGAATTTCAAG 11262
Qy       6063 CGGCAGTTTCCAAAACATCTTGGAACTGGCTGCTTGCACTGTTTGGGGGAGCATCATCCC 6122
Db      11263 CCGCCATCTCAAAAACATCATGGAGTTGGCTGTTTGCCCTTTTCGGCGGCGCCTCGTCGC 11322
Qy       6123 TCATTGTTGTAGGACTTATAGTGTTGGTCTGCAGCTCTATGCTTATAAACACACGTAGAT 6182
Db      11323 TATTAATTATAGGACTTATGATTTTTGCTTGCAGCATGATGCTGACTAGCACACGAAGAT 11382
Qy       6183 GACTGAGCGCGGACACTGA-CATAGCGGTAAAACTCGATGTACTTCCGAGGAAGCGTGGT 6241
Db      11383 GACCGCTACGCCCCAATGATCCGACCAGCAAAACTCGATGTACTTCCGAGGAACTGATGT 11442
Qy       6242 GCATAATGCCACGCGCCGCT 6261
Db      11443 GCATAATGCATCAGGCTGGT 11462
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RESULT 5
AAV33474
ID   AAV33474 standard; cDNA; 11717 BP.
XX
AC   AAV33474;
XX
DT   10-DEC-1998  (first entry)
XX
DE   Girdwood S.A.virus cDNA sequence.
XX
KW   Bone marrow cell; alphavirus; Girdwood S.A.virus; cytokine; capsid;
KW   reverse transcriptase-PCR; nsP1; nsP2; nsP3; nsP4; E3; E2; 6K; E1;
KW   growth hormone; growth factor; interleukin; chemokine; enzyme;
KW   ribozyme; antisense oligonucleotide; ss.
XX
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OS   Girdwood S.A. virus.
XX
FH   Key             Location/Qualifiers
FT   5'UTR           1..59
FT                   /*tag=  a
FT   CDS             60..7616
FT                   /*tag=  b
FT                   /product= "Non-structural polyprotein"
FT                   /note= "Internal stop codon present at nucleotides
FT                        5763-5765"
FT   CDS             7662..11399
FT                   /*tag=  c
FT                   /product= "Structural polyprotein"
FT   3'UTR           11400..11717
FT                   /*tag=  d
XX
PN   WO9836779-A2.
XX
PD   27-AUG-1998.
XX
PF   18-FEB-1998;   98WO-US02945.
XX
PR   19-FEB-1997;   97US-0801263.
XX
PA   (UYNC-) UNIV NORTH CAROLINA.
XX
PI   Davis NL,  Johnston RE,  Simpson DA;
XX
DR   WPI; 1998-495361/42.
DR   P-PSDB; AAW70462, AAW70463, AAW70473, AAW70474, AAW70475, AAW70476,
DR   AAW70477, AAW70478, AAW70479.
XX
PT   Expression of heterologous RNA in bone marrow cells - using a
PT   recombinant alphavirus comprising a promoter operable in bone marrow
PT   cells operably associated with heterologous RNA.
XX
PS   Example 2; Fig 3A-3C; 68pp; English.
XX
CC   The invention provides a method for introducing and expressing
CC   heterologous RNA in bone marrow cells using alphavirus vectors.  The
CC   Girdwood S.A.virus is an alphavirus whose cDNA sequence was determined
CC   from uncloned reverse transcriptase-PCR reaction fragments amplified
CC   from the virion RNA.  The Girdwood S.A.virus cDNA encodes nonstructural
CC   and structural polyproteins.  The nonstructural polyprotein is,
CC   presumably, post-translationally modified into four different protein
CC   products, namely nsP1 (AAW70462), nsP2 (AAW70463), nsP3 (AAW70473), nsP4
CC   (AAW70474) proteins.  The structural polyprotein is, presumably, post-
CC   translationally modified into five different protein products, namely
CC   capsid (AAW70475), E3 (AAW70476), E2 (AAW70477), 6K (AAW70478), E1
CC   (AAW70479) proteins.  The Girdwood S.A.virus cDNA was used in the method
CC   of the invention.  The inventors claim the transformed bone marrow cells
CC   are useful for expressing a protein or peptide suitable for protecting
CC   the subject against a disease such as a microbial, bacterial, protozoal,
CC   parasitic or viral disease.  The transformed bone marrow cells are also
CC   claimed to be useful for expressing proteins and peptides such as
CC   hormones, growth hormones, growth factors, interleukins, cytokines,
CC   chemokines, enzymes, ribozymes or antisense oligonucleotides.
XX
SQ   Sequence 11717 BP; 3297 A; 3130 C; 2927 G; 2360 T; 3 other;

  Query Match           36.8%;  Score 2386.4;  DB 19;  Length 11717;
  Best Local Similarity  64.5%;  Pred. No. 0;
  Matches 3745;  Conservative    0;  Mismatches 1991;  Indels   74;  Gaps    9;

Qy        580 ACTGACGGTATGAAGCGGGAGCGTATATTTTCTCATCGGAAACAGGCCAAGGTCACCTTC 639
              ||||||     |  |  || | ||| || || ||  |||| |||||||  || ||| | |
Db       5761 ACTGACTAACCGGGGTAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGC 5820

Qy        640 AACAGAAATCAGTACGTCAATGTAAACTACAAGAACCTATATTGGATCGGGCCGTCCATG 699
              ||  | | || || |  ||   | | ||   |||||| |  ||||| ||    || |  |
Db       5821 AAATGGAGTCCGTTCTGCAGAATCAGCTTACAGAACCGACCTTGGAGCGCAATGTTCTGG 5880

Qy        700 AGAAGTATTACGCCCCGCGCCTCGATCTCGAAAGAGAGAAAATGTTACAGAAGAAACTGC 759
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              | |    |||||||||   |||||       | |||| || | |  |    |    |
Db       5881 AAAGAATCTACGCCCCGGTGCTCGACACGTCGAAAGAGGAACAGCTCAAACTCAGGTACC 5940

Qy        760 AATTATGCGCCTCTGAAGGAAATAGAAGCAGGTATCAATCACGAAAAGTAGAAAATATGA 819
              |  |      || | |||| || | |||||||||| || ||  |||||||||||||  ||
Db       5941 AGATGATGCCCACCGAAGCCAACAAAAGCAGGTACCAGTCTAGAAAAGTAGAAAATCAGA 6000

Qy        820 AAGCAATTACAGCGGAGCGACTCATTTCTGGATTGGGCACATATCTATCATCAGAAGTGA 879
              |||| || ||  | |||||||  |||| ||  |  |    |||   ||  |   ||
Db       6001 AAGCCATAACCACTGAGCGACTGCTTTCAGGGCTACGACTGTATAACTCTGCCACAG--- 6057

Qy        880 ATCCTGTCGAGTGTTACAGAGTCAATTATCCTGTACCAATCTACTCGTCAACGGTAATTA 939
              |||     || || || |   |||  || ||   ||||   || ||     |  |||
Db       6058 ATCAGCCAGAATGCTATAAGATCACCTACCCGAAACCATCGTATTCCAGCAGTGTACCGG 6117

Qy        940 ACAGGTTTACATCTGCAGAGGTCGCGGTTAAAACGTGCAACTTAGTTATCCAAGAGAATT 999
              |  |   |     || || | || ||      ||||||    | | || |||||||
Db       6118 CGAACTACTCTGACCCAAAGTTTGCTGTAGCTGTTTGCAACAACTATCTGCATGAGAATT 6177

Qy       1000 ACCCTACAGTAGCCAGTTATTGTATAACAGATGAATACGATGCGTATCTTGACATGGTGG 1059
              |||| || |||||   ||||  || || || || |||||||| ||  | || ||||| |
Db       6178 ACCCGACGGTAGCATCTTATCAGATCACCGACGAGTACGATGCTTACTTGGATATGGTAG 6237

Qy       1060 ACGGCGCATCGTGCTGTCTAGATACAGCCACTTTTTGTCCGGCTAAACTGAGAAGCTACC 1119
              ||||  ||      || |||||||| || |||||||| || || || || ||||| ||||
Db       6238 ACGGGACAGTCGCTTGCCTAGATACTGCAACTTTTTGCCCCGCCAAGCTTAGAAGTTACC 6297

Qy       1120 CAAAGAAGCATAGCTATTTGCAGCCAGAGATAAGATCAGCCGTCCCATCGCCTATACAGA 1179
              | || |  ||   |||  . ||| | |   |  || || |||||  | || ||||
Db       6298 CGAAAAGACACGAGTATAGAGCCCCAAACACTCGCAGTGCGGTTCCATCAGCGATGCAGA 6357

Qy       1180 ATACATTACAAAATGTATTGGCTGCAGCTACTAAAAGGAATTGCAACGTTACCCAAATGC 1239
              | || || ||||| ||  |   ||| || |||||||| || |||||||| || |||||||
Db       6358 ACACGTTGCAAAACGTGCTCATTGCCGCGACTAAAAGAAACTGCAACGTCACACAAATGC 6417

Qy       1240 GAGAATTACCTGTCTTAGATTCGGCGGCATTTAATGTTGATTGTTTCAAGAAATACGCAT 1299
              | ||||| ||     | || || ||| |||| || ||||| || ||    ||||| ||||
Db       6418 GTGAATTGCCAACACTGGACTCAGCGACATTCAACGTTGAATGCTTTCGAAAATATGCAT 6477

Qy       1300 GCAATGATGAGTACTGGGATACCTTTCGCGATAACCCTATTCGGCTAACTACAGAGAACG 1359
              | ||||| ||||| |||||   |||  |   || || ||| || | |||| |||  ||
Db       6478 GTAATGACGAGTATTGGGAGGAGTTTGCCCGAAAGCCAATTAGGATCACTACTGAGTTCG 6537

Qy       1360 TTACGCAATATGTGACAAAGCTGAAAGGGCCGAAAGCAGCAGCATTGTTTGCGAATACTC 1419
              ||||   ||| ||| | |  |||||||| || || || || ||| |||| || || || |
Db       6538 TTACCGCATACGTGGCCAGACTGAAAGGCCCTAAGGCCGCCGCACTGTTCGCAAAGACGC 6597

Qy       1420 ATAATCTAAAACCGTTGCAGGAGATACCAATGGATCAATTCGTCATGGATCTAAAGAGAG 1479
              |||||  |    || ||||| ||  | || ||||||   |||||||||||  | || ||||
Db       6598 ATAATTTGGTCCCATTGCAAGAAGTGCCTATGGATAGGTTCGTCATGGACATGAAAAGAG 6657

Qy       1480 ATGTCAAAGTTACTCCCGGCACGAAACATACAGAGGAGCGGCCTAAGGTGCAGGTTATTC 1539
              | || |||||||| || |||||||||| ||||| ||  | || || || || || | |
Db       6658 ACGTGAAAGTTACACCTGGCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGCTAC 6717

Qy       1540 AGGCTGCAGATCCCCTTGCTACCGCTTACCTTTGCGGGATCCATCGGGAATTAGTCCGTA 1599
              | || ||||| ||||| || |||||||||| |||||||||| ||||| ||||| || |
Db       6718 AAGCCGCAGAACCCCTGGCGACCGCTTACCTGTGCGGGATCCACCGGGAGTTAGTGCGCA 6777

Qy       1600 GACTGAATGCGGTGCTTCTGCCAAATATCCATACTCTCTTCGACATGTCAGCGGAAGATT 1659
              | || |  || ||  | || || || || || || || || || |||||||| ||||| || |
Db       6778 GGCTTACAGCCGTCTTGCTACCCAACATTCACACGCTTTTTGACATGTCGGCGGAGGACT 6837

Qy       1660 TTGATGCGATTATTGCTGAACATTTCCACCACGGCGACCCAGTATTGGAAACGGACATCG 1719
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              | ||||| || |||||| |||||||||||||| ||  |  | |  |||||||| | || |
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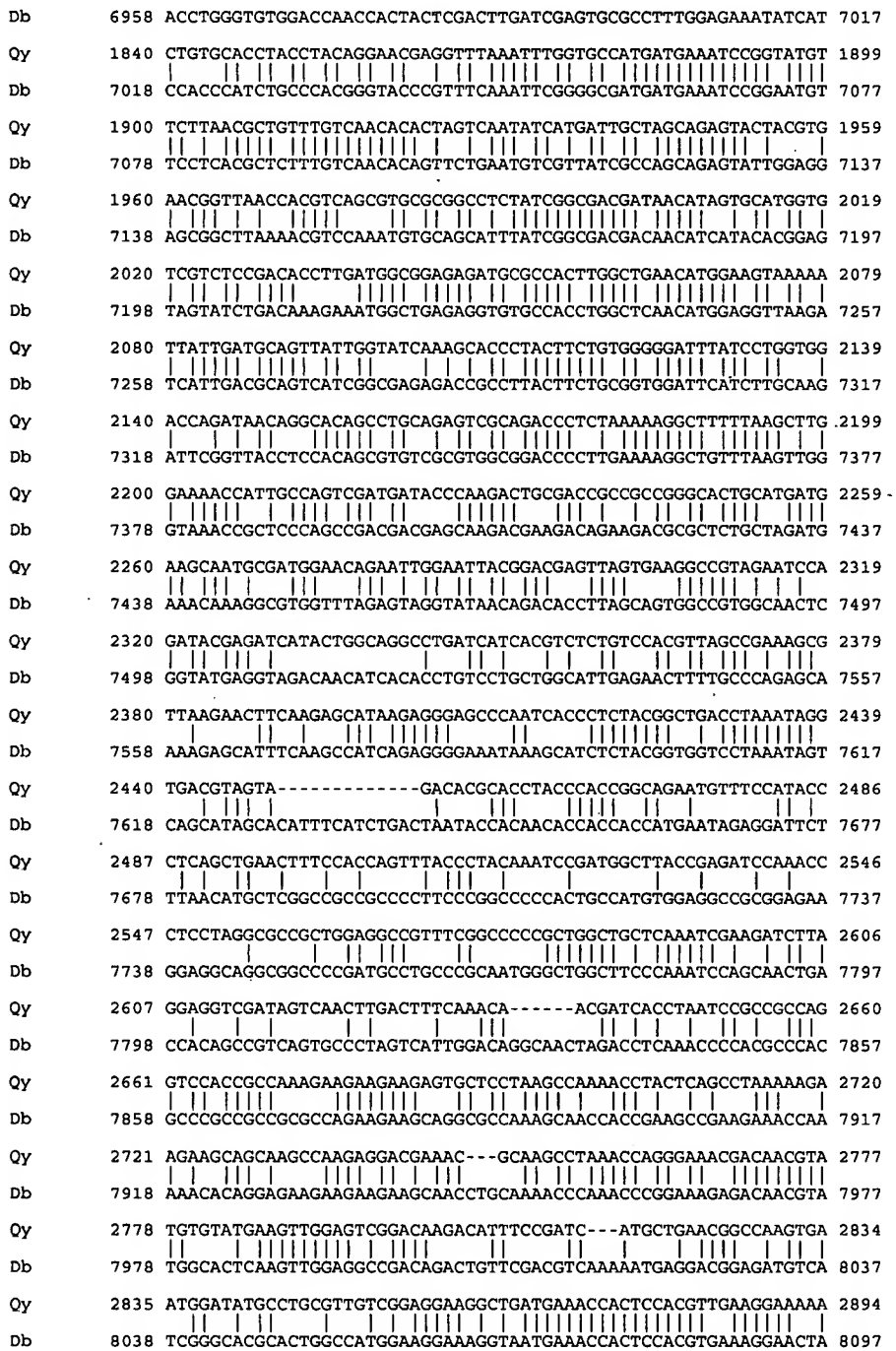
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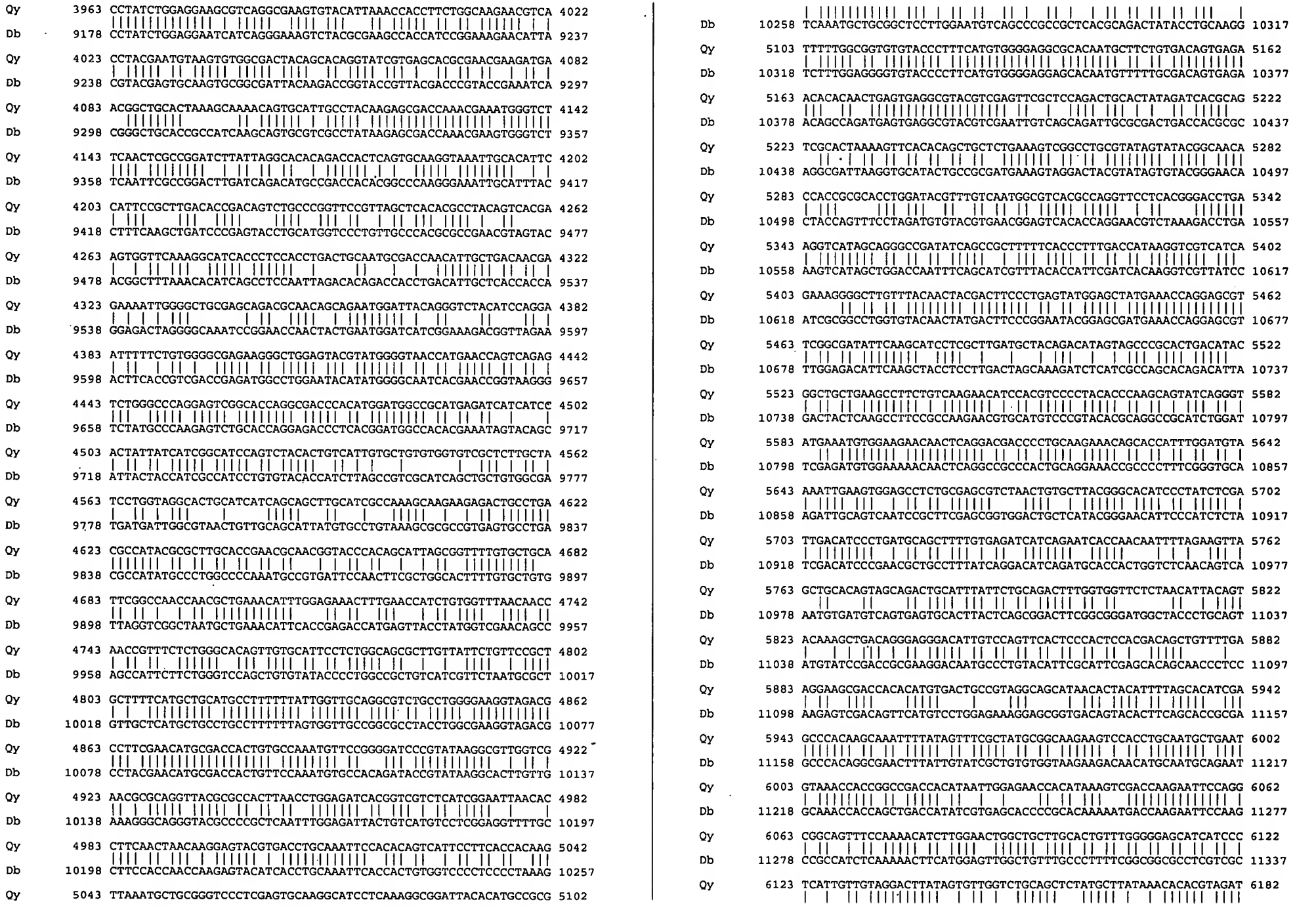

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Qy       6242 GCATAATGCCACGCGCCGCT--------------------------------TGACACT 6268
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Db      11518 AAAACTCGACGTATTTCCGAGGAAGCGCAGTGCATAATGCTGCGCAGTGT 11567


RESULT 6
AAC64506
ID   AAC64506 standard; DNA; 11703 BP.
XX
AC   AAC64506;
XX
DT   14-FEB-2001  (first entry)
XX
DE   Alphavirus SinDCChiron virus nucleotide sequence.
XX
KW   Alphavirus; SinDCChiron virus; SinChironLP virus; immune response;
KW   infection; human dendritic cell; immunostimulatory; cytostatic;
KW   virucide; fungicide; antibacterial; antiparasitic; vaccine; cancer;
KW   pathogen; antigen presenting cell; ds.
XX
OS   Alphavirus.
XX
PN   WO200061772-A2.
XX
PD   19-OCT-2000.
XX
PF   14-APR-2000; 2000WO-US10722.
XX
PR   14-APR-1999;   99US-0129498.
PR   09-AUG-1999;   99US-0148086.
PR   22-MAR-2000; 2000US-0191363.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Polo JM,  Dubensky TW,  Frolov I,  Gardner JP,  Otten G,  Barnett S;
PI   Driver DA;
XX
DR   WPI; 2000-619231/59.
XX
PT   New alphavirus that infects human dendritic cells for use in generating
PT   an immune response to pathogenic agents such as bacteria, viruses,
PT   fungi, parasites and cancer and for biological assays -
XX
PS   Claim 9; Fig 2B; 83pp; English.
XX
CC   The present invention describes an isolated alphavirus (AV) which
CC   infects human dendritic cells and is not of American Type Culture
CC   Collection (ATCC) number VR-2526. AAC64506 and AAC64507 represent the
CC   nucleotide sequence of the specifically claimed SinDCChiron virus and
CC   SinChironLP virus. The new AVs have immunostimulatory, cytostatic,
CC   virucide, fungicide, antibacterial and antiparasitic activities and
CC   can be used in vaccines. The AVs are used to infect dendritic cells,
CC   preferably human cells. A heterologous sequence can be introduced and
CC   expressed in human macrophages or antigen presenting cells in vivo and
CC   in vitro, for use in biological assays. The AV-based vector systems
CC   are used to generate an immune response to cancer or a pathogenic
CC   agent, such as, bacteria, fungi, parasites or viruses. The AV can be
CC   used to infect human dendritic cells, macrophages or antigen
CC   presenting cells that previously could not be infected using an AV or
CC   AV variant. The AV vectors are targeted directly to antigen presenting
CC   cells.
XX
SQ   Sequence 11703 BP; 3310 A; 3049 C; 2910 G; 2434 T; 0 other;
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  Query Match             36.8%;  Score 2383.6;  DB 21;  Length 11703;
  Best Local Similarity   64.6%;  Pred. No. 0;
  Matches 3695;  Conservative    0;  Mismatches 1984;  Indels   41;  Gaps    8;

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Qy        640 AACAGAAATCAGTACGTCAATGTAAACTACAAGAACCTATATTGGATCGGGCCGTCCATG 699
              || |||| || ||  |  ||      | ||   ||||||  |  |||||  ||    ||||  |
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Qy        700 AGAAGTATTACGCCCCGCGCCTCGATCTCGAAAGAGAGAAAATGTTACAGAAGAAACTGC 759
              | |    | | ||||||   |||||        | ||||  ||    |  |    |     |
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Qy        760 AATTATGCGCCTCTGAAGGAAATAGAAGCAGGTATCAATCACGAAAAGTAGAAAATATGA 819
              |  |      || | ||||  || | ||| |||||  || || || ||||||||||||  ||
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Qy        820 AAGCAATTACAGCGGAGCGACTCATTTCTGGATTGGGCACATATCTATCATCAGAAGTGA 879
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Qy        880 ATCCTGTCGAGTGTTACAGAGTCAATTATCCTGTACCAATCTACTCGTCAACGGTAATTA 939
              |||     || || || |   |||  |||||   |||| | |||||     |  |||
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Qy        940 ACAGGTTTACATCTGCAGAGGTCGCGGTTAAAACGTGCAACTTAGTTATCCAAGAGAATT 999
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Qy       1000 ACCCTACAGTAGCCAGTTATTGTATAACAGATGAATACGATGCGTATCTTGACATGGTGG 1059
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Qy       1060 ACGGCGCATCGTGCTGTCTAGATACAGCCACTTTTTGTCCGGCTAAACTGAGAAGCTACC 1119
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Qy       1120 CAAAGAAGCATAGCTATTTGCAGCCAGAGATAAGATCAGCCGTCCCATCGCCTATACAGA 1179
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Qy       1420 ATAATCTAAAACCGTTGCAGGAGATACCAATGGATCAATTCGTCATGGATCTAAAGAGAG 1479
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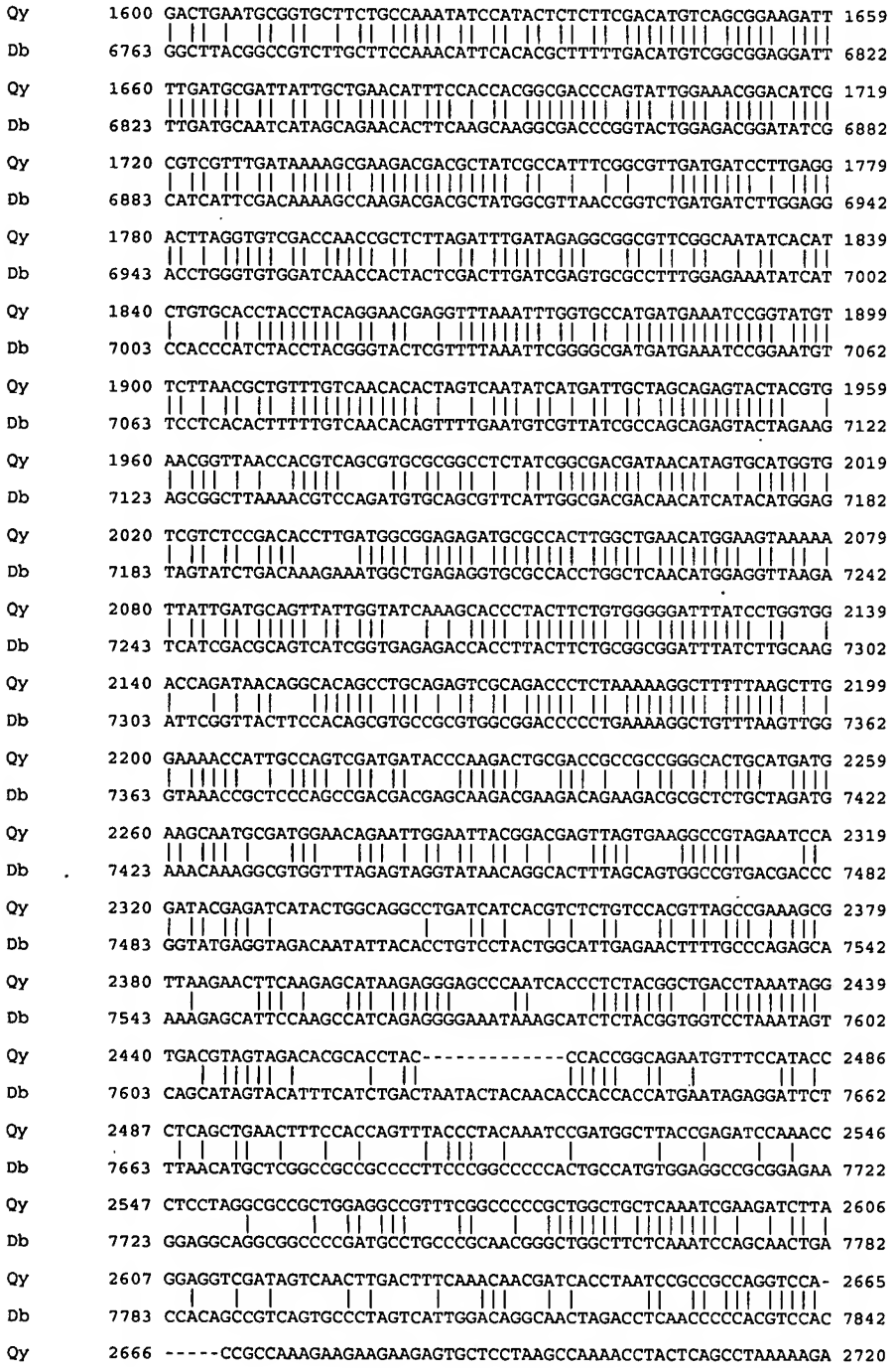

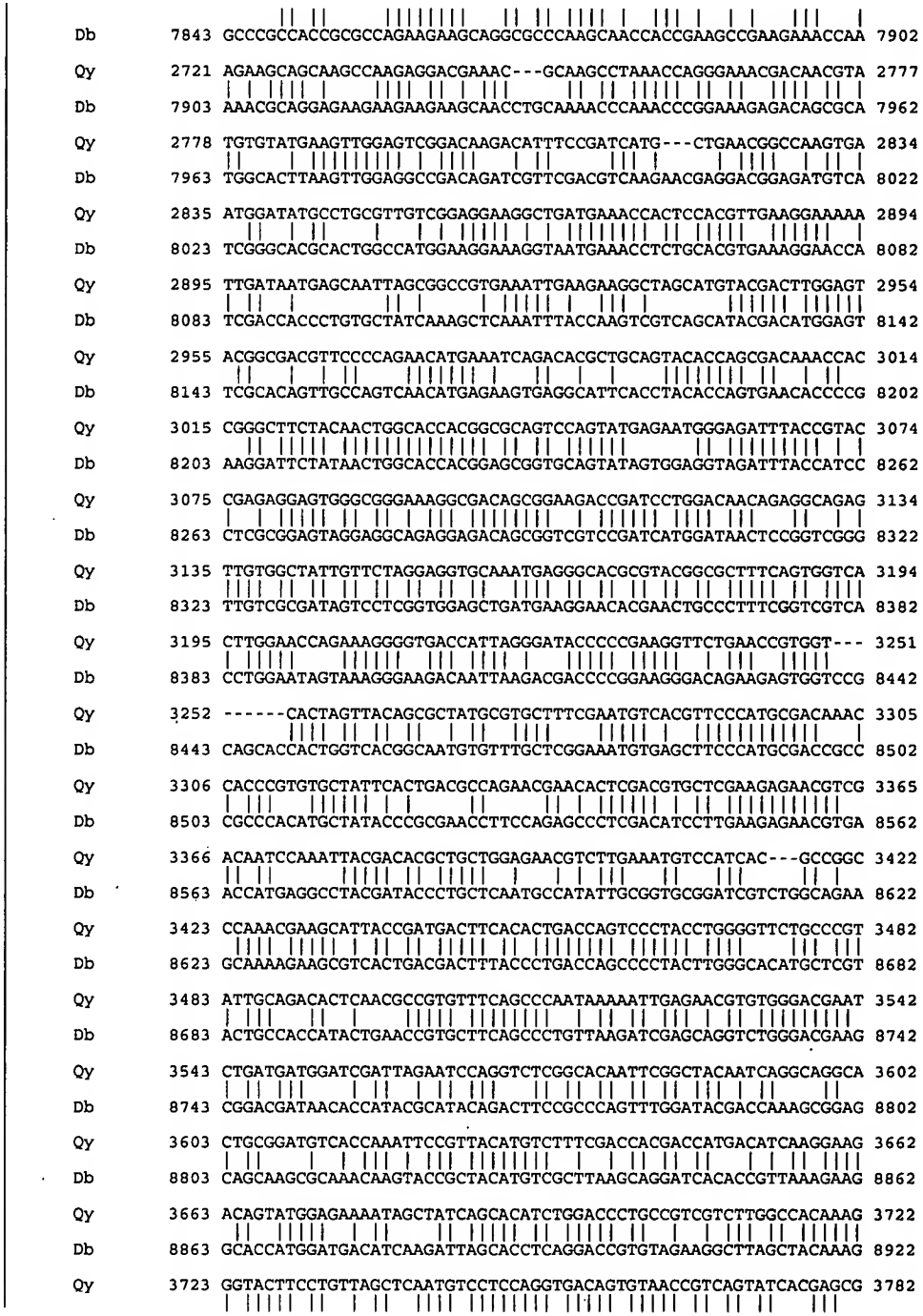

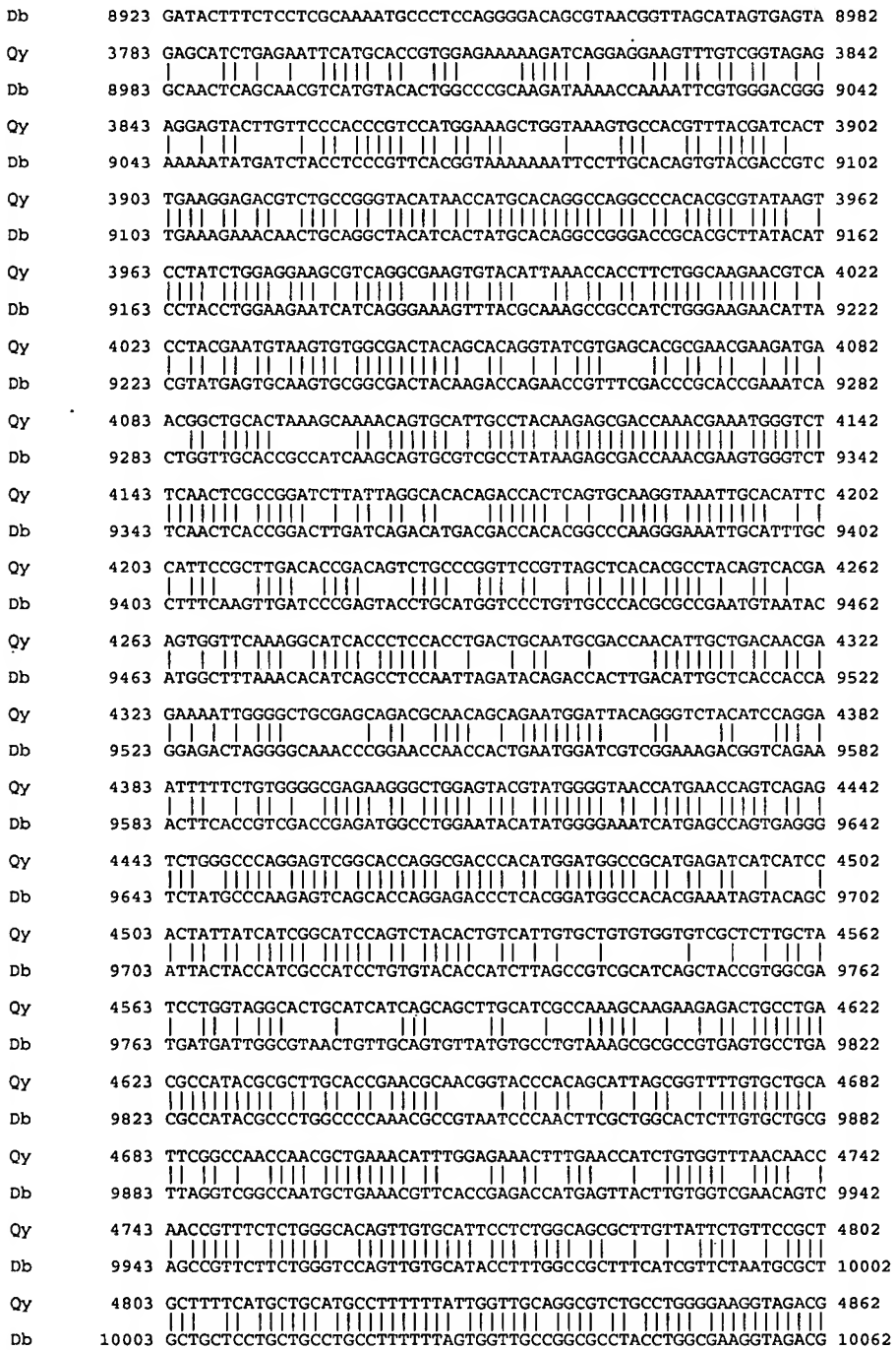
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Db 10363 ACAGCCAGATGAGTGAGGCGTACGTCGAACTGTCAGCAGATTGCGCGTCTGACCACGCGC 10422
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Db 10783 TTGAGATGTGGAAAAACAACTCAGGCCGCCCACTGCAGGAAACCGCACCTTTCGGGTGTA 10842
Qy 5643 AAATTGAAGTGGAGCCTCTGCGAGCGTCTAACTGTGCTTACGGGCACATCCCTATCTCGA 5702
Db 10843 AGATTGCAGTAAATCCGCTCCGAGCGGTGGACTGTTCATACGGGAACATTCCCATTTCTA 10902
Qy 5703 TTGACATCCCTGATGCAGCTTTTGTGAGATCATCAGAATCACCAACAATTTTAGAAGTTA 5762
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Qy 5763 GCTGCACAGTAGCAGACTGCATTTATTCTGCAGACTTTGGTGGTTCTCTAACATTACAGT 5822
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Qy 5823 ACAAAGCTGACAGGGAGGGACATTGTCCAGTTCACTCCCACTCCACGACAGCTGTTTTGA 5882
Db 11023 ATGTATCCGACCGCGAAGGTCAATGCCCCGTACATTCGCATTCGAGCACAGCAACTCTCC 11082
Qy 5883 AGGAAGCGACCACACATGTGACTGCCGTAGGCAGCATAACACTACATTTTAGCACATCGA 5942
Db 11083 AAGAGTCGACAGTACATGTCCTGGAGAAAGGAGCGGTGACAGTACACTTTAGCACCGCGA 11142

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Qy       5943 GCCCACAAGCAAATTTTATAGTTTCGCTATGCGGCAAGAAGTCCACCTGCAATGCTGAAT 6002
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Qy       6003 GTAAACCACCGGCCGACCACATAATTGGAGAACCACATAAAGTCGACCAAGAATTCCAGG 6062
Db      11203 GTAAACCACCAGCTGACCATATCGTGAGCACCCCGCACAAAAATGACCAAGAATTTCAAG 11262

Qy       6063 CGGCAGTTTCCAAAACATCTTGGAACTGGCTGCTTGCACTGTTTGGGGGAGCATCATCCC 6122
Db      11263 CCGCCATCTCAAAAACATCATGGAGTTGGCTGTTTGCCCTTTTCGGCGGCGCCTCGTCGC 11322

Qy       6123 TCATTGTTGTAGGACTTATAGTGTTGGTCTGCAGCTCTATGCTTATAAACACACGTAGAT 6182
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Qy       6183 GACTGAGCGCGGACACTGA-CATAGCGGTAAAACTCGATGTACTTCCGAGGAAGCGTGGT 6241
Db      11383 GACCGCTACGCCCCAATGATCCGACCAGCAAAACTCGATGTACTTCCGAGGAACTGATGT 11442

Qy       6242 GCATAATGCCACGCGCCGCT 6261
Db      11443 GCATAATGCATCAGGCTGGT 11462
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RESULT 7
AAC64507
ID AAC64507 standard; DNA; 11703 BP.
XX
AC AAC64507;
XX
DT 14-FEB-2001 (first entry)
XX
DE Alphavirus SinChironLP virus nucleotide sequence.
XX
KW Alphavirus; SinDCChiron virus; SinChironLP virus; immune response;
KW infection; human dendritic cell; immunostimulatory; cytostatic;
KW virucide; fungicide; antibacterial; antiparasitic; vaccine; cancer;
KW pathogen; antigen presenting cell; ds.
XX
OS Alphavirus.
XX
PN WO200061772-A2.
XX
PD 19-OCT-2000.
XX
PF 14-APR-2000; 2000WO-US10722.
XX
PR 14-APR-1999; 99US-0129498.
PR 09-AUG-1999; 99US-0148086.
PR 22-MAR-2000; 2000US-0191363.
XX
PA (CHIR) CHIRON CORP.
XX
PI Polo JM, Dubensky TW, Frolov I, Gardner JP, Otten G, Barnett S;
PI Driver DA;
XX
DR WPI; 2000-619231/59.
XX
PT New alphavirus that infects human dendritic cells for use in generating
PT an immune response to pathogenic agents such as bacteria, viruses,
PT fungi, parasites and cancer and for biological assays -
XX
PS Claim 10; Fig 2C; 83pp; English.
XX
CC The present invention describes an isolated alphavirus (AV) which
CC infects human dendritic cells and is not of American Type Culture
CC Collection (ATCC) number VR-2526. AAC64506 and AAC64507 represent the
CC nucleotide sequence of the specifically claimed SinDCChiron virus and
CC SinChironLP virus. The new AVs have immunostimulatory, cytostatic,
CC virucide, fungicide, antibacterial and antiparasitic activities and
CC can be used in vaccines. The AVs are used to infect dendritic cells,
CC preferably human cells. A heterologous sequence can be introduced and
CC expressed in human macrophages or antigen presenting cells in vivo and
CC in vitro, for use in biological assays. The AV-based vector systems
CC are used to generate an immune response to cancer or a pathogenic
CC agent, such as, bacteria, fungi, parasites or viruses. The AV can be
CC used to infect human dendritic cells, macrophages or antigen
CC presenting cells that previously could not be infected using an AV or
CC AV variant. The AV vectors are targeted directly to antigen presenting
CC cells.
XX
SQ Sequence 11703 BP; 3308 A; 3050 C; 2911 G; 2434 T; 0 other;

Query Match 36.7%; Score 2382; DB 21; Length 11703;
Best Local Similarity 64.6%; Pred. No. 0;
Matches 3694; Conservative 0; Mismatches 1985; Indels 41; Gaps 8;

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Qy        640 AACAGAAATCAGTACGTCAATGTAAACTACAAGAACCTATATTGGATCGGGCCGTCCATG 699
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Qy        700 AGAAGTATTACGCCCCGCGCCTCGATCTCGAAAGAGAGAAAATGTTACAGAAGAAACTGC 759
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Qy       1060 ACGGCGCATCGTGCTGTCTAGATACAGCCACTTTTTGTCCGGCTAAACTGAGAAGCTACC 1119
Db       6223 ACGGGACAGTCGCCTGCCTGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACC 6282

Qy       1120 CAAAGAAGCATAGCTATTTGCAGCCAGAGATAAGATCAGCCGTCCCATCGCCTATACAGA 1179
Db       6283 CGAAAAAACATGAGTATAGAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGA 6342

Qy       1180 ATACATTACAAAATGTATTGGCTGCAGCTACTAAAAGGAATTGCAACGTTACCCAAATGC 1239
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Db       6403 GTGAACTGCCAACACTGGACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCAT 6462

Qy       1300 GCAATGATGAGTACTGGGATACCTTTCGCGATAACCCTATTCGGCTAACTACAGAGAACG 1359
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Qy       1360 TTACGCAATATGTGACAAAGCTGAAAGGGCCGAAAGCAGCAGCATTGTTTGCGAATACTC 1419
Db       6523 TCACCGCATATGTAGCTAGACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGT 6582

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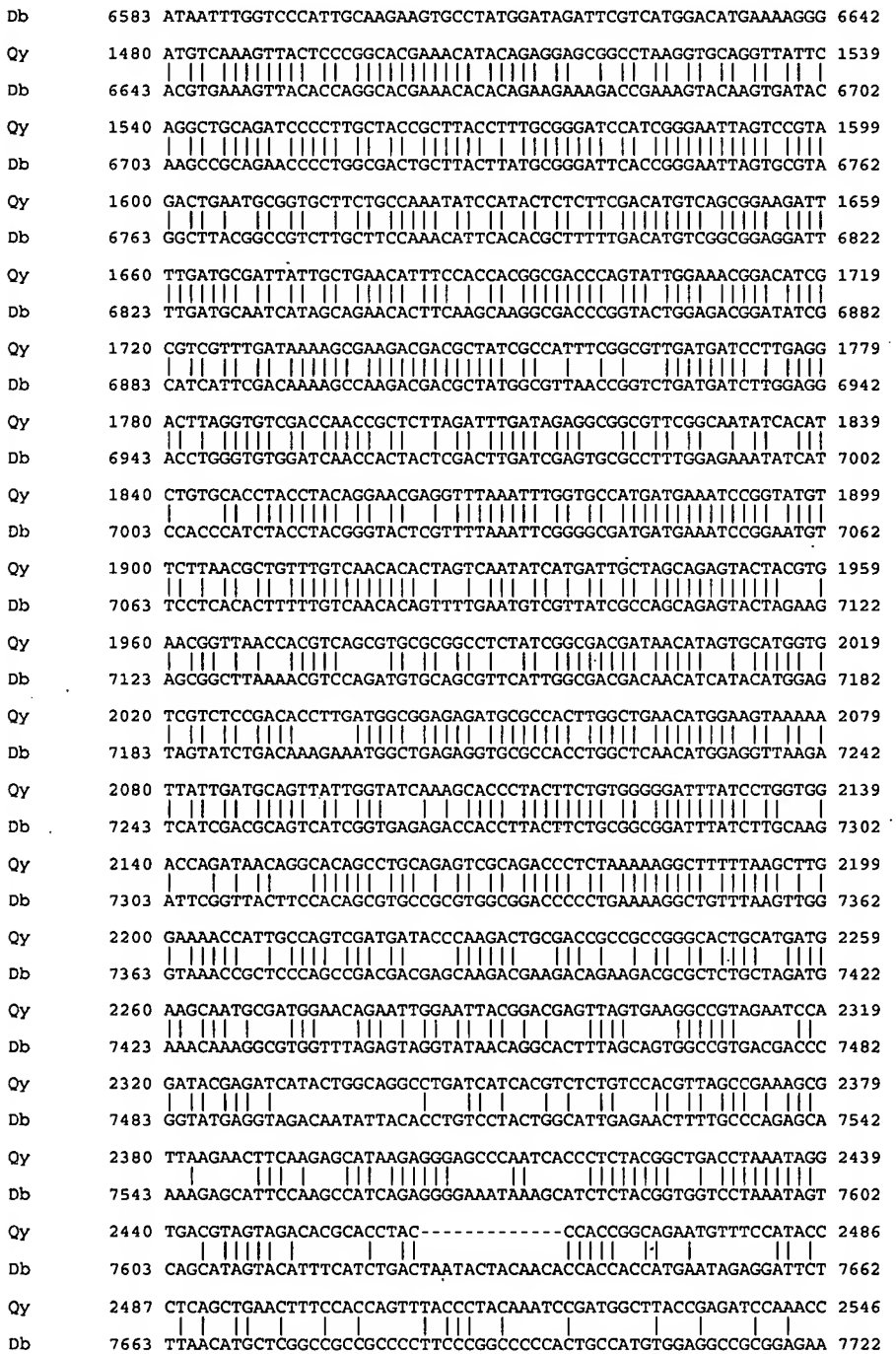
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Qy 1900 TCTTAACGCTGTTTGTCAACACACTAGTCAATATCATGATTGCTAGCAGAGTACTACGTG 1959
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Qy 3075 CGAGAGGAGTGGGCGGGAAAGGCGACAGCGGAAGACCGATCCTGGACAACAGAGGCAGAG 3134
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Qy 3483 ATTGCAGACACTCAACGCCGTGTTTCAGCCCAATAAAAATTGAGAACGTGTGGGACGAAT 3542
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Qy 3543 CTGATGATGGATCGATTAGAATCCAGGTCTCGGCACAATTCGGCTACAATCAGGCAGGCA 3602
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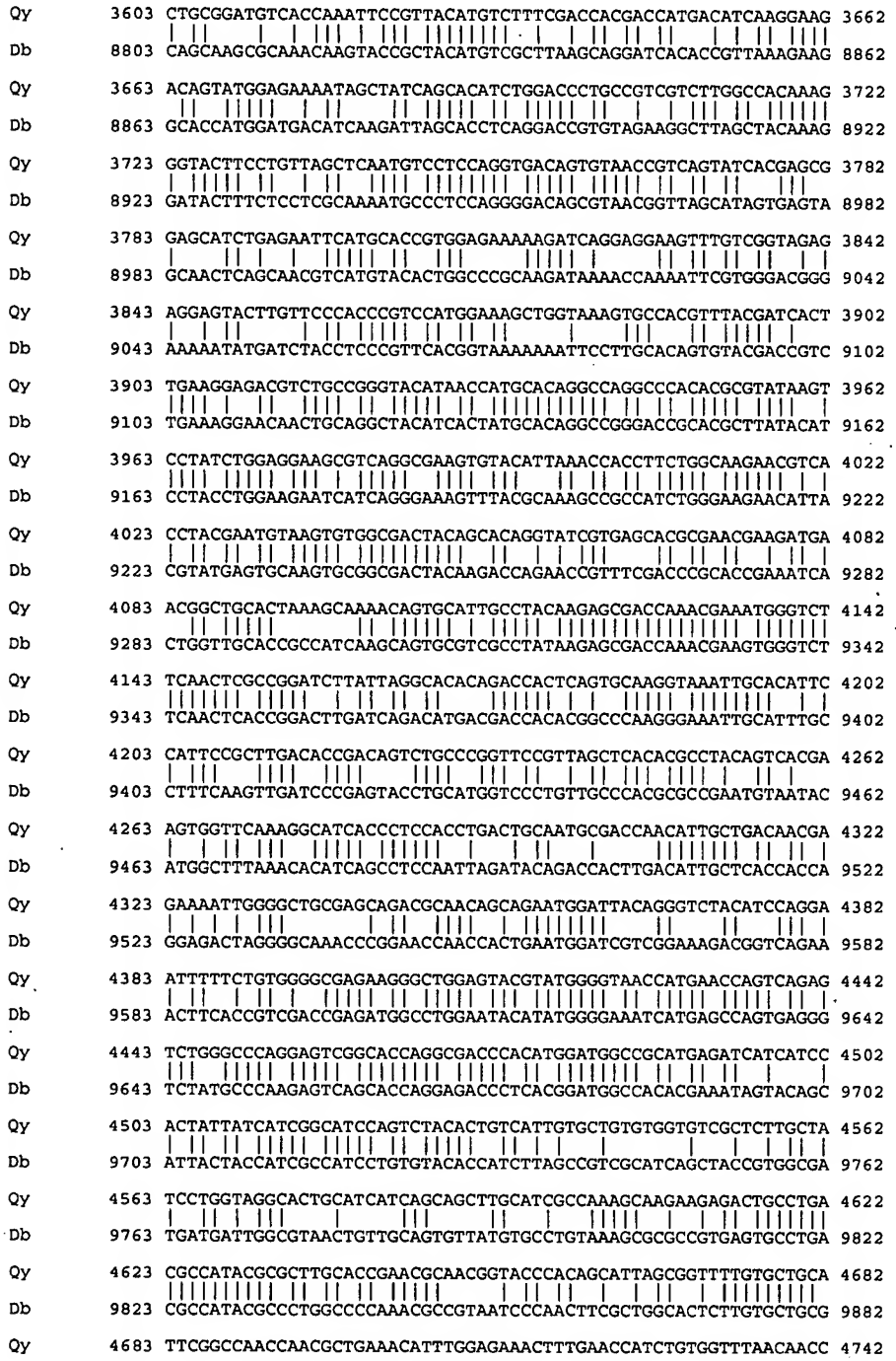

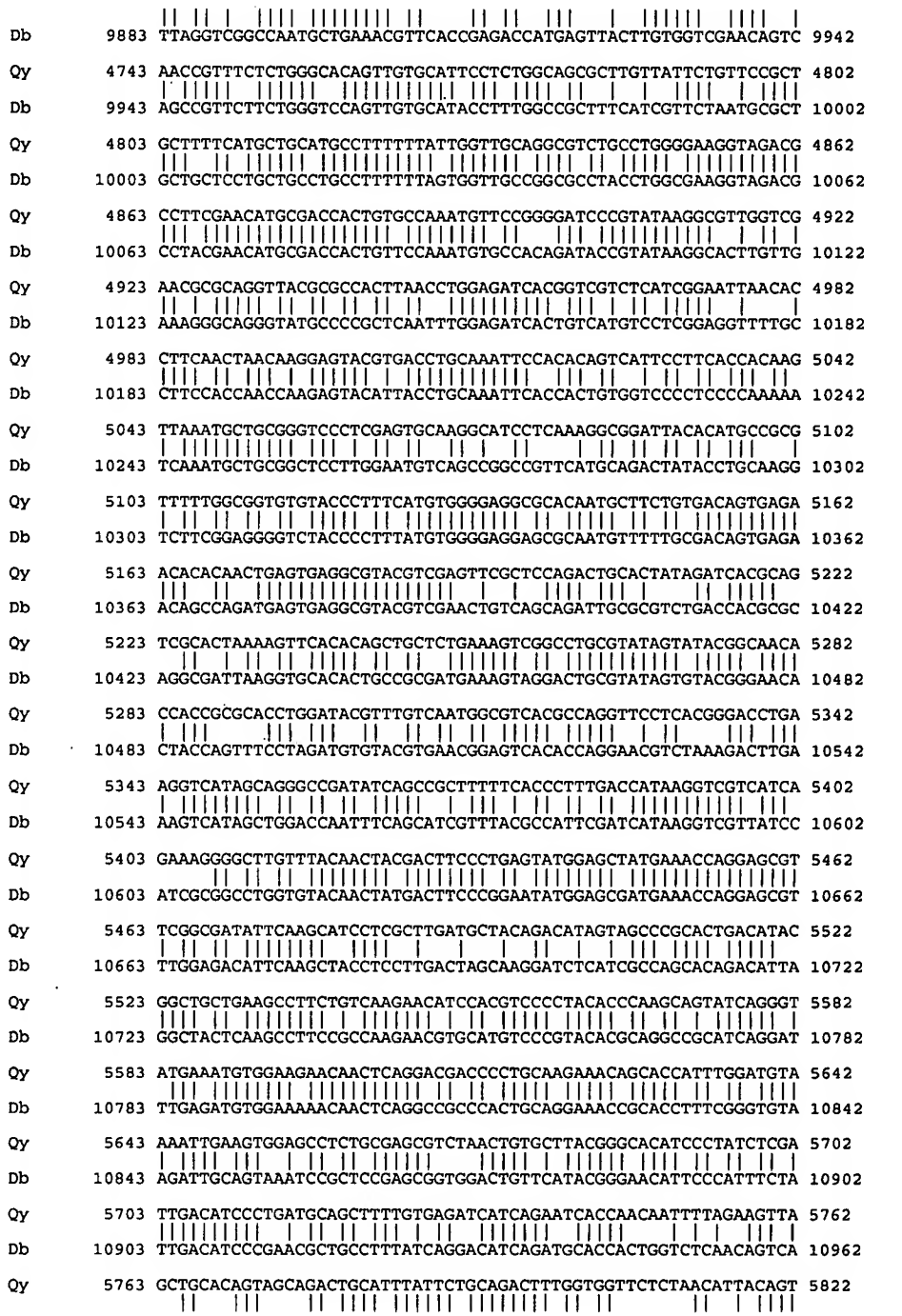

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Db      11443 GCATAATGCATCAGGCTGGT 11462
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RESULT 8
AAT47668
ID   AAT47668 standard; cDNA; 11663 BP.
XX
AC   AAT47668;
XX
DT   19-MAY-1997  (first entry)
XX
DE   South African Arbovirus 86 RNA transcript cDNA.
XX
KW   S.A.AR86; Sindbis virus; attenuation; vaccine; diagnosis; antibody;
KW   vector; Ockelbo; polyarthritis; ss.
XX
OS   South African Arbovirus No. 86.
XX
FH   Key             Location/Qualifiers
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FT                   /note= "a guanine for adenine substn. at nucleotide
FT                          215 is a preferred silent mutation used in
FT                          recombinant DNA constructs of the
FT                          invention"
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FT                          nucleotide 3863 is a preferred silent
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FT                          5984 is a preferred silent mutation used in
FT                          recombinant DNA constructs of the
FT                          invention"
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XX
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XX
PD   28-NOV-1996.
XX
PF   22-MAY-1996;   96WO-US07457.
XX
PR   23-MAY-1995;   95US-0446932.
XX
PA   (UYNC-) UNIV NORTH CAROLINA.
XX
PI   Davis NL,  Johnston RE,  Simpson DA;
XX
DR   WPI; 1997-020937/02.
XX
PT   New recombinant DNA encoding infectious South African Arbovirus 86
PT   RNA transcript and related mutants - under control of heterologous
PT   promoter, useful in prodn. of attenuated vaccines and to generate
PT   diagnostic antibodies
XX
PS   Claim 2; Page 13-19; 27pp; English.
XX
CC   A cDNA clone (AAT47668) codes for an infectious South African
CC   Arbovirus No. 86 (S.A.AR86) virus RNA transcript.  Novel
CC   recombinant DNA constructs comprise the cDNA, pref. mutated to
CC   include attenuating and silent mutations, and an upstream
CC   heterologous promoter (pref. T3, T7 or SP6).  Infectious
CC   attenuated viral particles produced from cells transfected with the
CC   RNA transcripts encoded by such cDNA clones are useful in live
CC   attenuated vaccines, e.g. against diseases caused by related
CC   viruses such as Ockelbo, and can also be used as vectors to express
CC   antigens of other viruses.  The cDNA clone can be administered to
CC   animals to raise antibodies for diagnosis of S.A.AR86 infection.
XX
SQ   Sequence 11663 BP; 3297 A; 3104 C; 2903 G; 2359 T; 0 other;
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Query Match 36.7%; Score 2381.6; DB 18; Length 11663;
Best Local Similarity 64.4%; Pred. No. 0;
Matches 3742; Conservative 0; Mismatches 1994; Indels 74; Gaps 9;

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Qy        700 AGAAGTATTACGCCCCGCGCCTCGATCTCGAAAGAGAGAAAATGTTACAGAAGAAACTGC 759

Db       5827 AAAGAATCTACGCCCCGGTGCTCGACACGTCGAAAGAGGAACAGCTCAAACTCAGGTACC 5886

Qy        760 AATTATGCGCCTCTGAAGGAAATAGAAGCAGGTATCAATCACGAAAAGTAGAAAATATGA 819

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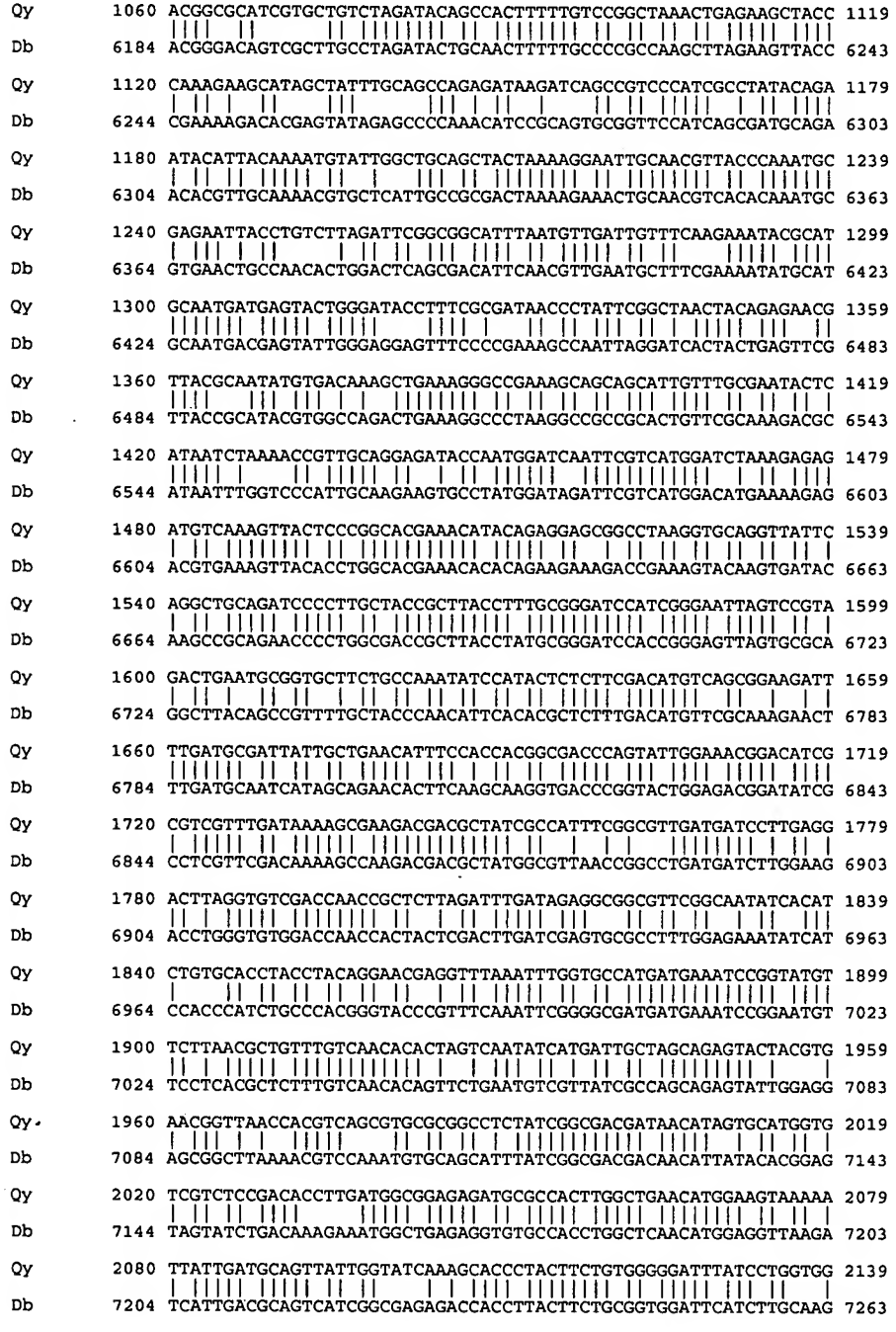
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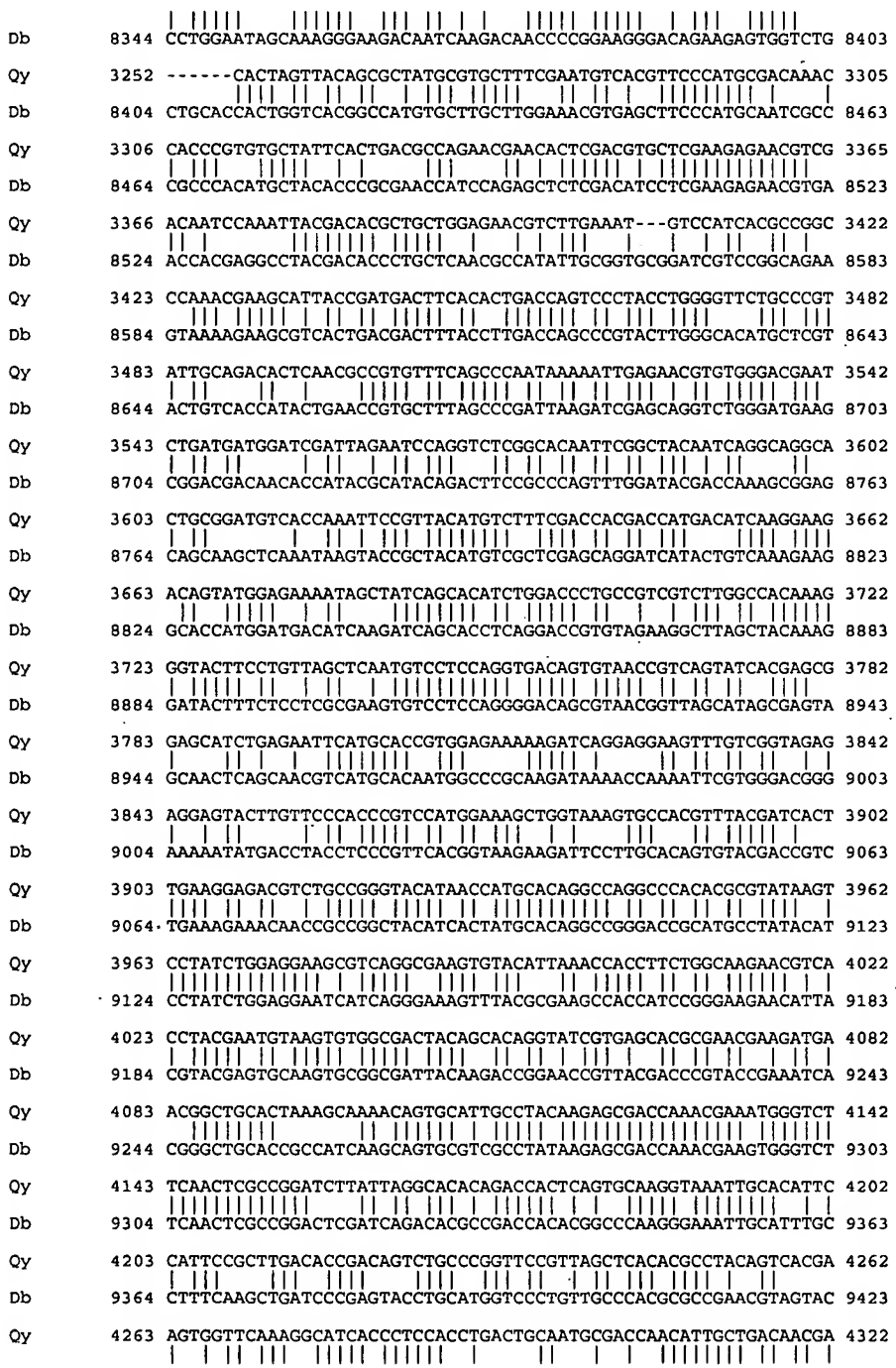
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RESULT 9
ABX81526
ID   ABX81526 standard; cDNA; 11740 BP.
XX
AC   ABX81526;
XX
DT   23-APR-2003  (first entry)
XX
DE   Sindbis virus cDNA #3.
XX
KW   Eukaryotic layered vector initiation system; cytopathic effect; gene; ss;
KW   alphaviral nonstructural protein 2; RNA vector replicon; alphavirus RNA;
KW   macromolecular synthesis; alphavirus RNA polymerase recognition sequence;
KW   3' polyadenylate tract; cellular macromolecular synthesis; cell death;
KW   Sindbis virus.
XX
OS   Sindbis virus.
XX
PN   US6465634-B1.
XX
PD   15-OCT-2002.
XX
PF   08-OCT-1999;   99US-0415900.
XX
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PR   04-APR-1997;   97US-0833148.
XX
PA   (CHIR ) CHIRON CORP.
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Dubensky TW,  Polo JM,  Belli BA,  Schlesinger S,  Dryga SA,  Frolov I;
XX
DR   WPI; 2003-147073/14.
XX
PT   Eukaryotic layered vector initiation system, for gene therapy, has
PT   alphaviral nonstructural protein gene having mutant nonstructural
PT   protein 2 gene, which reduces host-cell directed macromolecular
PT   synthesis -
XX
PS   Example 1; Fig 8A-8E; 161pp; English.
XX
CC   The invention relates to a eukaryotic layered vector initiation system,
CC   comprising a nucleic acid sequence encoding all four alphaviral
CC   nonstructural proteins and including an altered sequence encoding for
CC   nonstructural protein 2, such that when the altered sequence is operably
CC   incorporated into an RNA vector replicon, the time required to reach 50%
CC   inhibition of cellular macromolecular synthesis in cells is increased, as
CC   compared to an RNA vector replicon having a wild-type alphavirus
CC   nonstructural protein 2. The initiation system comprises a 5' promoter
CC   which directs synthesis of alphavirus RNA in vivo from cDNA, a 5'
CC   sequence which directs transcription of alphavirus RNA, a nucleic acid
CC   sequence which operably encodes all four alphaviral nonstructural
CC   proteins, an alphavirus RNA polymerase recognition sequence and a 3'
CC   polyadenylate tract. The eukaryotic layered vector initiation system is
CC   useful for stimulating an immune response within a vertebrate, for
CC   protein expression and gene therapy. The system exhibits reduced, delayed
CC   or no inhibition of cellular macromolecular synthesis, thus permitting
CC   its use for protein expression and gene therapy with reduced, delayed or
CC   no development of cytopathic effects or cell death. This sequence
CC   represents Sindbis virus cDNA, used in the scope of the invention.
XX
SQ   Sequence 11740 BP; 3345 A; 3049 C; 2908 G; 2438 T; 0 other;

  Query Match           36.7%;  Score 2380.4;  DB 25;  Length 11740;
  Best Local Similarity   64.6%;  Pred. No. 0;
  Matches 3693;  Conservative    0;  Mismatches 1986;  Indels   41;  Gaps    8;

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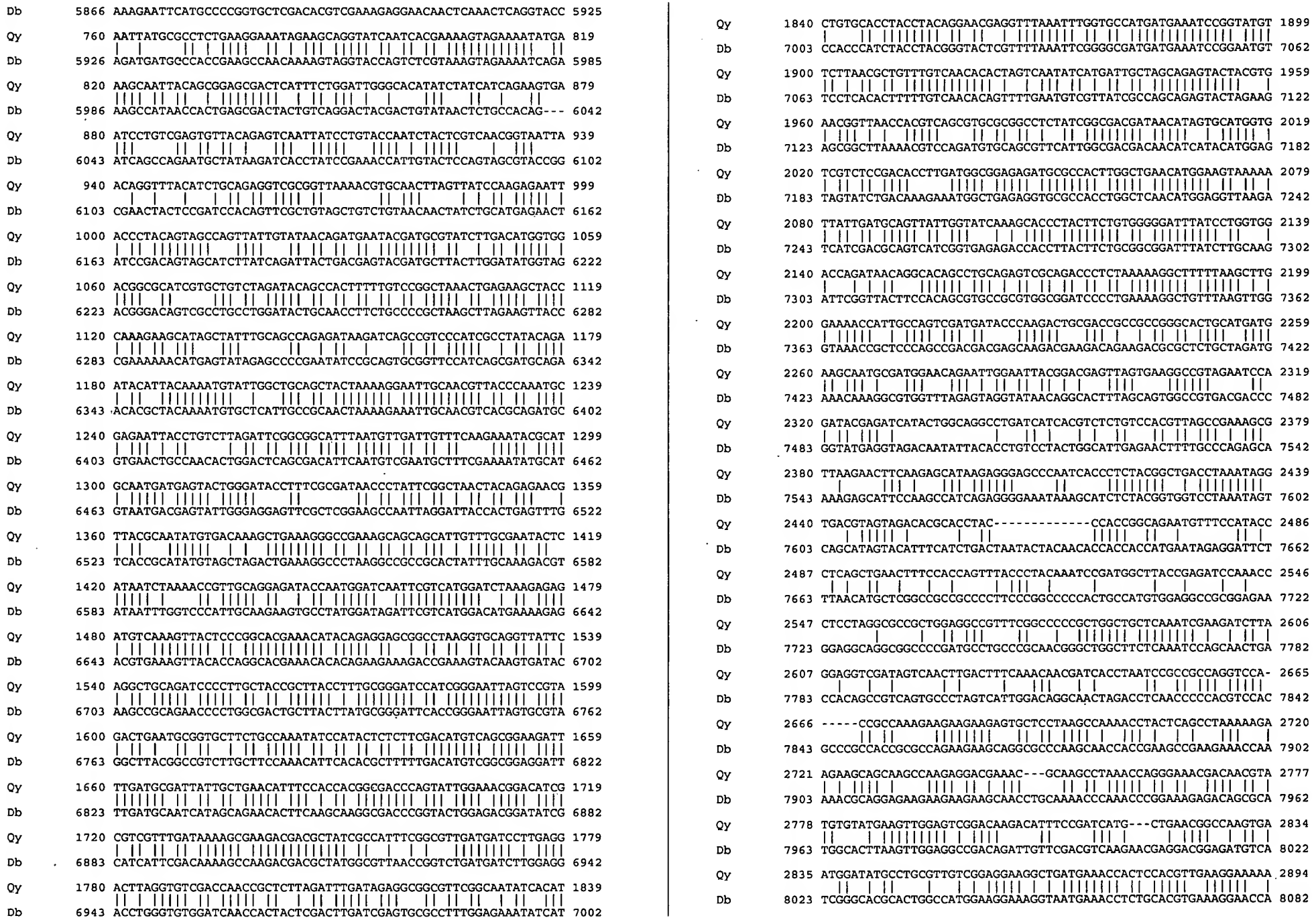

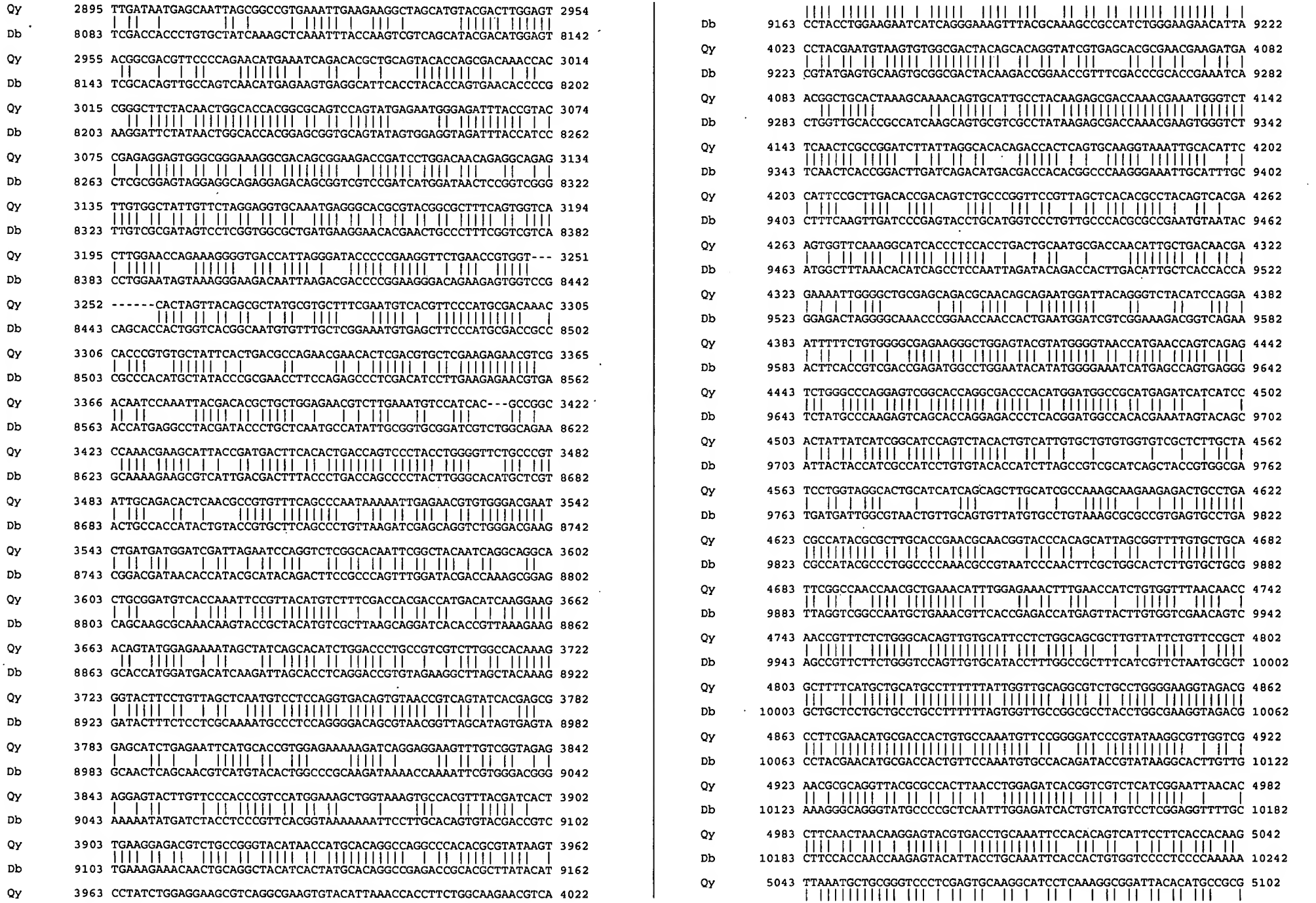

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Qy       5163 ACACACAACTGAGTGAGGCGTACGTCGAGTTCGCTCCAGACTGCACTATAGATCACGCAG 5222

Db      10363 ACAGCCAGATGAGTGAGGCGTACGTCGAATTGTCAGCAGATTGCGCGTCTGACCACGCGC 10422

Qy       5223 TCGCACTAAAAGTTCACACAGCTGCTCTGAAAGTCGGCCTGCGTATAGTATACGGCAACA 5282

Db      10423 AGGCGATTAAGGTGCACACTGCCGCGATGAAAGTAGGACTGCGTATTGTGTACGGGAACA 10482

Qy       5283 CCACCGCGCACCTGGATACGTTTGTCAATGGCGTCACGCCAGGTTCCTCACGGGACCTGA 5342

Db      10483 CTACCAGTTTCCTAGATGTGTACGTGAACGGAGTCACACCAGGAACGTCTAAAGACTTGA 10542

Qy       5343 AGGTCATAGCAGGGCCGATATCAGCCGCTTTTTCACCCTTTGACCATAAGGTCGTCATCA 5402

Db      10543 AAGTCATAGCTGGACCAATTTCAGCATCGTTTACGCCATTCGATCATAAGGTCGTTATCC 10602

Qy       5403 GAAAGGGGCTTGTTTACAACTACGACTTCCCTGAGTATGGAGCTATGAAACCAGGAGCGT 5462

Db      10603 ATCGCGGCCTGGTGTACAACTATGACTTCCCGGAATATGGAGCGATGAAACCAGGAGCGT 10662

Qy       5463 TCGGCGATATTCAAGCATCCTCGCTTGATGCTACAGACATAGTAGCCCGCACTGACATAC 5522

Db      10663 TTGGAGACATTCAAGCTACCTCCTTGACTAGCAAGGATCTCATCGCCAGCACAGACATTA 10722

Qy       5523 GGCTGCTGAAGCCTTCTGTCAAGAACATCCACGTCCCCTACACCCAAGCAGTATCAGGGT 5582

Db      10723 GGCTACTCAAGCCTTCCGCCAAGAACGTGCATGTCCCGTACACGCAGGCCTCATCAGGAT 10782

Qy       5583 ATGAAATGTGGAAGAACAACTCAGGACGACCCCTGCAAGAAACAGCACCATTTGGATGTA 5642

Db      10783 TTGAGATGTGGAAAAACAACTCAGGCCGCCCACTGCAGGAAACCGCACCTTTCGGGTGTA 10842

Qy       5643 AAATTGAAGTGGAGCCTCTGCGAGCGTCTAACTGTGCTTACGGGCACATCCCTATCTCGA 5702

Db      10843 AGATTGCAGTAAATCCGCTCCGAGCGGTGGACTGTTCATACGGGAACATTCCCATTTCTA 10902

Qy       5703 TTGACATCCCTGATGCAGCTTTTGTGAGATCATCAGAATCACCAACAATTTTAGAAGTTA 5762

Db      10903 TTGACATCCCGAACGCTGCCTTTATCAGGACATCAGATGCACCACTGGTCTCAACAGTCA 10962

Qy       5763 GCTGCACAGTAGCAGACTGCATTTATTCTGCAGACTTTGGTGGTTCTCTAACATTACAGT 5822

Db      10963 AATGTGAAGTCAGTGAGTGCACTTATTCAGCAGACTTCGGCGGGATGGCCACCCTGCAGT 11022

Qy       5823 ACAAAGCTGACAGGGAGGGACATTGTCCAGTTCACTCCCACTCCACGACAGCTGTTTTGA 5882

Db      11023 ATGTATCCGACCGCGAAGGTCAATGCCCCGTACATTCGCATTCGAGCACAGCAACTCTCC 11082

Qy       5883 AGGAAGCGACCACACATGTGACTGCCGTAGGCAGCATAACACTACATTTTAGCACATCGA 5942

Db      11083 AAGAGTCGACAGTACATGTCCTGGAGAAAGGAGCGGTGACAGTACACTTTAGCACCGCGA 11142

Qy       5943 GCCCACAAGCAAATTTTATAGTTTCGCTATGCGGCAAGAAGTCCACCTGCAATGCTGAAT 6002

Db      11143 GTCCACAGGCGAACTTTATCGTATCGCTGTGTGGGAAGAAGACAACATGCAATGCAGAAT 11202

Qy       6003 GTAAACCACCGGCCGACCACATAATTGGAGAACCACATAAAGTCGACCAAGAATTCCAGG 6062

Db      11203 GTAAACCACCAGCTGACCATATCGTGAGCACCCCGCACAAAAATGACCAAGAATTTCAAG 11262

Qy       6063 CGGCAGTTTCCAAAACATCTTGGAACTGGCTGCTTGCACTGTTTGGGGGAGCATCATCCC 6122

Db      11263 CCGCCATCTCAAAAACATCATGGAGTTGGCTGTTTGCCCTTTTCGGCGGCGCCTCGTCGC 11322

Qy       6123 TCATTGTTGTAGGACTTATAGTGTTGGTCTGCAGCTCTATGCTTATAAACACACGTAGAT 6182

Db      11323 TATTAATTATAGGACTTATGATTTTGCTTGCAGCATGATGCTGACTAGCACACGAAGAT 11382

Qy       6183 GACTGAGCGCGGACACTGA-CATAGCGGTAAAACTCGATGTACTTCCGAGGAAGCGTGGT 6241

Db      11383 GACCGCTACGCCCCAATGATCCGACCAGCAAAACTCGATGTACTTCCGAGGAACTGATGT 11442

Qy       6242 GCATAATGCCACGCGCCGCT 6261

Db      11443 GCATAATGCATCAGGCTGGT 11462
```

RESULT 10
AAT30787
ID AAT30787 standard; DNA; 16656 BP.
XX
AC AAT30787;
XX
DT 12-SEP-1996 (first entry)
XX
DE Alphavirus-based eukaryotic layered vector pVGELVIS.
XX
KW Alphavirus; Sindbis virus; vector; gene therapy; vaccine;
KW pVGELVIS; ss.
XX
OS Chimeric Sindbis virus;
OS Chimeric synthetic.
XX

FH	Key	Location/Qualifiers
FT	promoter	1..60
FT		/*tag= a
FT		/note= "wild-type Sindbis virus sequence
FT		capable of initiating transcription"
FT	CDS	60..5750
FT		/*tag= b
FT		/product= non-structural proteins NSP 1-3
FT	CDS	5928..7579
FT		/*tag= c
FT		/product= non-structural protein NSP 4
FT	misc_feature	7579..7602
FT		/*tag= d
FT		/function= minimal junction region core
FT	misc_feature	11647..11703
FT		/*tag= e
FT		/function= Sindbis polymerase recognition
FT		sequence

XX
PN WO9617072-A2.
XX
PD 06-JUN-1996.
XX
PF 30-NOV-1995; 95WO-US15490.
XX
PR 15-MAR-1995; 95US-0405827.
PR 30-NOV-1994; 94US-0348472.
PR 18-JAN-1995; 95US-0376184.
XX
PA (CHIR) CHIRON VIAGENE INC.
XX
PI Belli BA, Chang SMW, Driver DA, Dubensky TW, Ibanez CE;
PI Jolly DJ, Polo JM;
XX
DR WPI; 1996-277785/28.
XX
PT New recombinant alpha-virus vectors - used to develop prods and
PT methods for use in gene therapy and in the prodn. of vaccines
XX
PS Example 2; Page 186-194; 256pp; English.
XX
CC A eukaryotic layered vector initiation system, pVGELVIS (AAT30787),
CC is based on the Sindbis alphavirus. It is obtd. by inserting
CC the Sindbis clone pVGSP6GENrep into vector pCDNA3. The construct
CC can be used in the prodn. of Sindbis virus-based vectors used
CC to develop products and methods for use in gene therapy and in
CC vaccine prodn. pVGELVIS is capable of initiating alphavirus

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CC   infection; inactivation of the viral junction region (see also
CC   AAT30810) will prevent viral transcription of the subgenomic
CC   fragment.  The efficiency of pVGELVIS in generating wild-type
CC   Sindbis virus after transfection of BHK cells was approx. 1,000
CC   pfu/mg plasmid DNA.
XX
SQ   Sequence 16656 BP; 4469 A; 4352 C; 4179 G; 3656 T; 0 other;

  Query Match            36.6%;  Score 2370.8;  DB 17;  Length 16656;
  Best Local Similarity  64.6%;  Pred. No. 0;
  Matches 3694;  Conservative    0;  Mismatches 1982;  Indels   44;  Gaps    9;

Qy        580 ACTGACGGTATGAAGCGGGAGCGTATATTTTCTCATCGGAAACAGGCCAAGGTCACCTTC 639
              ||||||     |  |  || | ||| || || ||  |||| |||||||  || ||| | |
Db       5746 ACTGACTAACCGGGGTAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGC 5805

Qy        640 AACAGAAATCAGTACGTCAATGTAAACTACAAGAACCTATATTGGATCGGGCCGTCCATG 699
              || |||| ||.|| |  ||      | ||   |||||| |  ||||| ||     ||||  |
Db       5806 AAAAGAAGTCCGTTCTGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGG 5865

Qy        700 AGAAGTATTACGCCCCGCGCCTCGATCTCGAAAGAGAGAAAATGTTACAGAAGAAACTGC 759
              | |   | | ||||||   |||||       | ||||  ||    |  |    |     |
Db       5866 AAAGAATTCATGCCCCGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACC 5925

Qy        760 AATTATGCGCCTCTGAAGGAAATAGAAGCAGGTATCAATCACGAAAAGTAGAAAATATGA 819
              |  |     || | |||||  || | ||| ||||| || || ||||||||||||||  ||
Db       5926 AGATGATGCCCACCGAAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGA 5985

Qy        820 AAGCAATTACAGCGGAGCGACTCATTTCTGGATTGGGCACATATCTATCATCAGAAGTGA 879
              |||| || ||  | ||||||||  | || ||| |  |    |||   ||  |   ||
Db       5986 AAGCCATAACCACTGAGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAG--- 6042

Qy        880 ATCCTGTCGAGTGTTACAGAGTCAATTATCCTGTACCAATCTACTCGTCAACGGTAATTA 939
              |||     || || || |   |||  |||||   |||| | |||||    |  |||
Db       6043 ATCAGCCAGAATGCTATAAGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGG 6102

Qy        940 ACAGGTTTACATCTGCAGAGGTCGCGGTTAAAACGTGCAACTTAGTTATCCAAGAGAATT 999
              |  |   |  | || || |||| ||       || |||     | | || ||||| |
Db       6103 CGAACTACTCCGATCCACAGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACT 6162

Qy       1000 ACCCTACAGTAGCCAGTTATTGTATAACAGATGAATACGATGCGTATCTTGACATGGTGG 1059
              | || ||||||||   ||||  || || || || |||||||| ||  | || |||||
Db       6163 ATCCGACAGTAGCATCTTATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAG 6222

Qy       1060 ACGGCGCATCGTGCTGTCTAGATACAGCCACTTTTTGTCCGGCTAAACTGAGAAGCTACC 1119
              ||||  ||     ||| || ||||| || || || || || ||||| || ||||| ||||
Db       6223 ACGGGACAGTCGCCTGCCTGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACC 6282

Qy       1120 CAAAGAAGCATAGCTATTTGCAGCCAGAGATAAGATCAGCCGTCCCATCGCCTATACAGA 1179
              | || || |||  |||  |  ||  |  ||  |    || || |||||  | || ||||
Db       6283 CGAAAAAACATGAGTATAGACCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGA 6342

Qy       1180 ATACATTACAAAATGTATTGGCTGCAGCTACTAAAAGGAATTGCAACGTTACCCAAATGC 1239
              | ||  |||||||||||  |   ||| || |||||||| |||||||||| || || ||||
Db       6343 ACACGCTACAAAATGTGCTCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGC 6402

Qy       1240 GAGAATTACCTGTCTTAGATTCGGCGGCATTTAATGTTGATTGTTTCAAGAAATACGCAT 1299
              | ||| | ||     | || || ||| ||||| ||||| || || ||    ||||| ||||
Db       6403 GTGAACTGCCAACACTGGACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCAT 6462

Qy       1300 GCAATGATGAGTACTGGGATACCTTTCGCGATAACCCTATTCGGCTAACTACAGAGAACG 1359
              | ||||| ||||| ||||     ||         || ||| || | || || |||   |
Db       6463 GTAATGACGAGTATTGGGAGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTG 6522

Qy       1360 TTACGCAATATGTGACAAAGCTGAAAGGGCCGAAAGCAGCAGCATTGTTTGCGAATACTC 1419
              | ||   ||||||  | |  |||||||| || || || ||  | ||||| || ||
Db       6523 TCACCGCATATGTAGCTAGACTGAAAGGCCCTAAGGCCGCCACACTATTTGCAAAGACGT 6582

Qy       1420 ATAATCTAAAACCGTTGCAGGAGATACCAATGGATCAATTCGTCATGGATCTAAAGAGAG 1479
              |||||.|    || ||||| ||  | || ||||||  ||||||||||||  | || ||||
Db       6583 ATAATTTGGTCCCATTGCAAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAG 6642

Qy       1480 ATGTCAAAGTTACTCCCGGCACGAAACATACAGAGGAGCGGCCTAAGGTGCAGGTTATTC 1539

Db       6643 ACGTGAAAGTTACACCAGGCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATAC 6702

Qy       1540 AGGCTGCAGATCCCCTTGCTACCGCTTACCTTTGCGGGATCCATCGGGAATTAGTCCGTA 1599
              | || ||||| ||||| || || |||||| | |||||||| || ||||||||||| ||||
Db       6703 AAGCCGCAGAACCCCTGGCGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTA 6762

Qy       1600 GACTGAATGCGGTGCTTCTGCCAAATATCCATACTCTCTTCGACATGTCAGCGGAAGATT 1659
              | || |  || ||  | || ||||| || || || || || |||||||| ||||| ||||
Db       6763 GGCTTACGGCCGTCTTGCTTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATT 6822

Qy       1660 TTGATGCGATTATTGCTGAACATTTCCACCACGGCGACCCAGTATTGGAAACGGACATCG 1719
              ||||||| || || || ||||| ||| | || |||||||| ||| |||| ||||| ||||
Db       6823 TTGATGCAATCATAGCAGAACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCG 6882

Qy       1720 CGTCGTTTGATAAAAGCGAAGACGACGCTATCGCCATTTCGGCGTTGATGATCCTTGAGG 1779
              | || || || |||||| ||||||||||||||  ||  |  | |  ||||||||  | ||||
Db       6883 CATCATTCGACAAAAGCCAAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGG 6942

Qy       1780 ACTTAGGTGTCGACCAACCGCTCTTAGATTTGATAGAGGCGGCGTTCGGCAATATCACAT 1839
              || | ||||| || ||||| ||  | || ||||| |||   || || ||  | ||  |||
Db       6943 ACCTGGGTGTGGATCAACCACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCAT 7002

Qy       1840 CTGTGCACCTACCTACAGGAACGAGGTTTAAATTTGGTGCCATGATGAAATCCGGTATGT 1899
              |    || |||||||| || ||  | |||||||| || || ||||||||||||||  ||||
Db       7003 CCACCCATCTACCTACGGGTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGT 7062

Qy       1900 TCTTAACGCTGTTTGTCAACACACTAGTCAATATCATGATTGCTAGCAGAGTACTACGTG 1959
              || | || || |||||||||| | | ||| || | || |||||||||||  |
Db       7063 TCCTCACACTTTTTGTCAACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAG 7122

Qy       1960 AACGGTTAACCACGTCAGCGTGCGCGGCCTCTATCGGCGACGATAACATAGTGCATGGTG 2019
              | ||| | |  |||||     || || || |  || |||||||| |||||  | |||||
Db       7123 AGCGGCTTAAAACGTCCAGATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAG 7182

Qy       2020 TCGTCTCCGACACCTTGATGGCGGAGAGATGCGCCACTTGGCTGAACATGGAAGTAAAAA 2079
              | || || ||||      ||||| ||||| |||||||| ||||| |||||||| || || |
Db       7183 TAGTATCTGACAAAGAAATGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGA 7242

Qy       2080 TTATTGATGCAGTTATTGGTATCAAAGCACCCTACTTCTGTGGGGGATTTATCCTGGTGG 2139
              | || || ||||| || |||  | | |||| |||||||| || |||||||||| ||    |
Db       7243 TCATCGACGCAGTCATCGGTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAG 7302

Qy       2140 ACCAGATAACAGGCACAGCCTGCAGAGTCGCAGACCCTCTAAAAAGGCTTTTTAAGCTTG 2199
              |   | | ||   |||||| ||| | || || || || || |||||||| |||||| | |
Db       7303 ATTCGGTTACTTCCACAGCGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGG 7362

Qy       2200 GAAAACCATTGCCAGTCGATGATACCCAAGACTGCGACCGCCGCCGGGCACTGCATGATG 2259
              | |||||  | |||| ||| ||     ||||||   ||| |  | || || |||| ||||
Db       7363 GTAAACCGCTCCCAGCCGACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATG 7422

Qy       2260 AAGCAATGCGATGGAACAGAATTGGAATTACGGACGAGTTAGTGAAGGCCGTAGAATCCA 2319
              || ||| |   |||   ||| | || || || | |  ||||   ||||||||||   ||
Db       7423 AAACAAAGGCGTGGTTTAGAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCC 7482

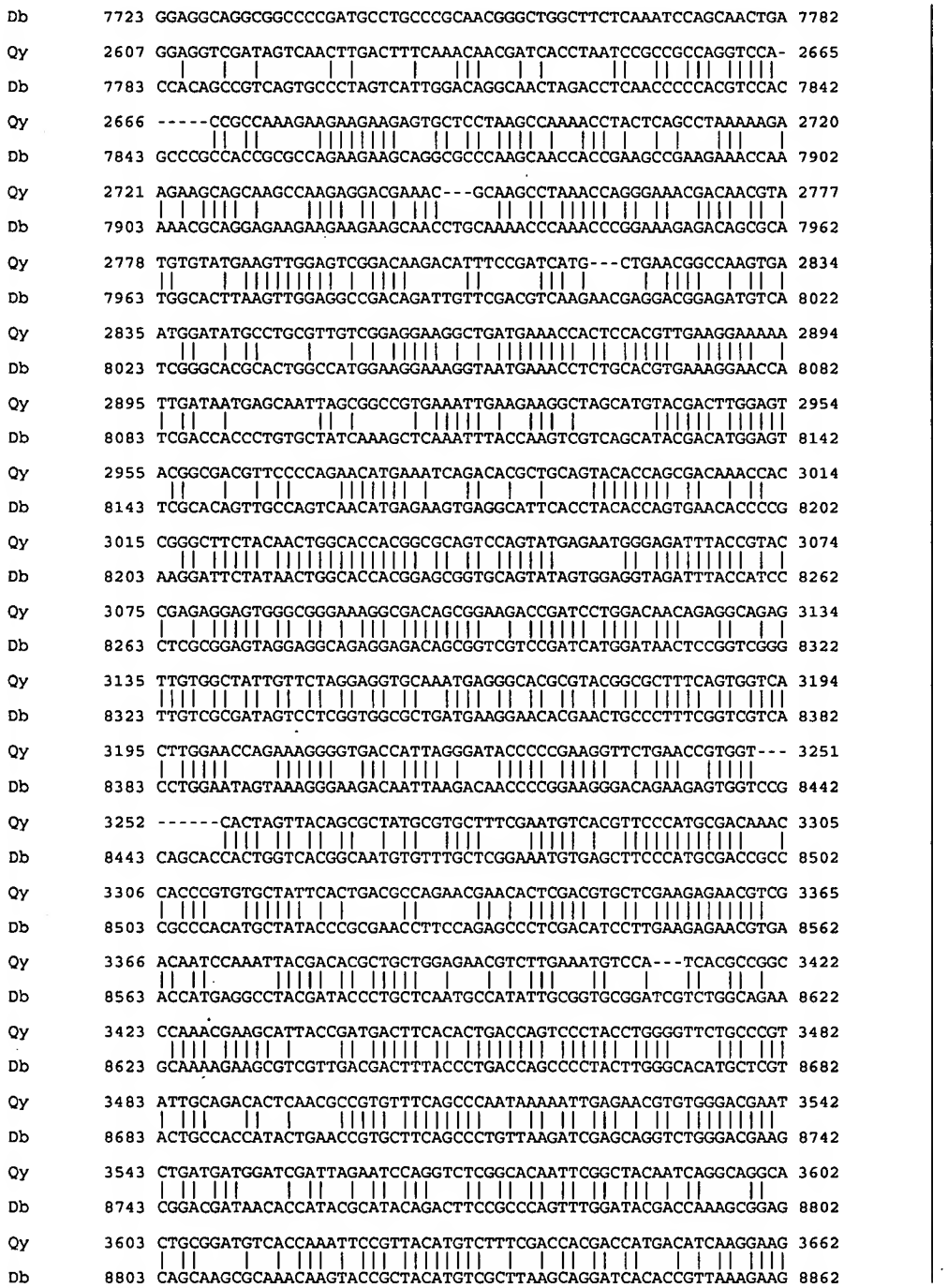
Qy       2320 GATACGAGATCATACTGGCAGGCCTGATCATCACGTCTCTGTCCACGTTAGCCGAAAGCG 2379
              | || ||| |                | || |  | |  ||  || || ||| | |||
Db       7483 GGTATGAGGTAGACAATATTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCA 7542

Qy       2380 TTAAGAACTTCAAGAGCATAAGAGGGAGCCCAATCACCCTCTACGGCTGACCTAAATAGG 2439
                |     ||| |  ||| ||||||     ||      ||||||||  | |||||||||
Db       7543 AAAGAGCATTCCAAGCCATCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGT 7602

Qy       2440 TGACGTAGTAGACACGCACCTAC------------CCACCGGCAGAATGTTTCCATACC 2486
              | |||||  |        | ||                |||||  ||  |      || |
Db       7603 CAGCATAGTACATTTCATCTGACTAATACTACAACACCACCACCATGAATAGAGGATTCT 7662

Qy       2487 CTCAGCTGAACTTTCCACCAGTTTACCCTACAAATCCGATGGCTTACCGAGATCCAAACC 2546
              | |  || | |  |  |     | |||  |  |  |  |  |  |  |  |  |  |
Db       7663 TTAACATGCTCGGCCGCCGCCCCTTCCCGGCCCCCACTGCCATGTGGAGGCCGCGGAGAA 7722

Qy       2547 CTCCTAGGCGCCGCTGGAGGCCGTTTCGGCCCCCGCTGGCTGCTCAAATCGAAGATCTTA 2606
                    |    | || |||    ||   | |||||| ||||||||  |  | || |
```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Db 7783 CCACAGCCGTCAGTGCCCTAGTCATTGGACAGGCAACTAGACCTCAACCCCCACGTCCAC 7842
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Qy 3075 CGAGAGGAGTGGGCGGGAAAGGCGACAGCGGAAGACCGATCCTGGACAACAGAGGCAGAG 3134
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Db 8383 CCTGGAATAGTAAAGGGAAGACAATTAAGACAACCCCGGAAGGGACAGAAGAGTGGTCCG 8442
Qy 3252 ------CACTAGTTACAGCGCTATGCGTGCTTTCGAATGTCACGTTCCCATGCGACAAAC 3305
Db 8443 CAGCACCACTGGTCACGGCAATGTGTTTGCTCGGAAATGTGAGCTTCCCATGCGACCGCC 8502
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Qy 3366 ACAATCCAAATTACGACACGCTGCTGGAGAACGTCTTGAAATGTCCA---TCACGCCGGC 3422
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Qy 3423 CCAAACGAAGCATTACCGATGACTTCACACTGACCAGTCCCTACCTGGGGTTCTGCCCGT 3482
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Qy 3483 ATTGCAGACACTCAACGCCGTGTTTCAGCCCAATAAAAATTGAGAACGTGTGGGACGAAT 3542
Db 8683 ACTGCCACCATACTGAACCGTGCTTCAGCCCTGTTAAGATCGAGCAGGTCTGGGACGAAG 8742
Qy 3543 CTGATGATGGATCGATTAGAATCCAGGTCTCGGCACAATTCGGCTACAATCAGGCAGGCA 3602
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Qy 4323 GAAAATTGGGGCTGCGAGCAGACGCAACAGCAGAATGGATTACAGGGTCTACATCCAGGA 4382
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Qy 4383 ATTTTTCTGTGGGGCGAGAAGGGCTGGAGTACGTATGGGGTAACCATGAACCAGTCAGAG 4442
Db 9580 ACTTCACCGTCGACCGAGATGGCCTGGAATACATATGGGGAAATCATGAGCCAGTGAGGG 9639
Qy 4443 TCTGGGCCCAGGAGTCGGCACCAGGCGACCCACATGGATGGCCGCATGAGATCATCATCC 4502
Db 9640 TCTATGCCCAAGAGTCAGCACCAGGAGACCCTCACGGATGGCCACACGAAATAGTACAGC 9699
Qy 4503 ACTATTATCATCGGCATCCAGTCTACACTGTCATTGTGCTGTGTGGTGTCGCTCTTGCTA 4562
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Qy 4563 TCCTGGTAGGCACTGCATCATCAGCAGCTTGCATCGCCAAAGCAAGAAGAGACTGCCTGA 4622
Db 9760 TGATGATTGGCGTAACTGTTGCAGTGTTATGTGCCTGTAAAGCGCGCCGTGAGTGCCTGA 9819
Qy 4623 CGCCATACGCGCTTGCACCGAACGCAACGGTACCCACAGCATTAGCGGTTTTGTGCTGCA 4682
Db 9820 CGCCATACGCCCTGGCCCCAAACGCCGTAATCCCAACTTCGCTGGCACTCTTGTGCTGCG 9879
Qy 4683 TTCGGCCAACCAACGCTGAAACATTTGGAGAAACTTTGAACCATCTGTGGTTTAACAACC 4742
Db 9880 TTAGGTCGGCCAATGCTGAAACGTTCACCGAGACCATGAGTTACTTGTGGTCGAACAGTC 9939

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Qy       4743 AACCGTTTCTCTGGGCACAGTTGTGCATTCCTCTGGCAGCGCTTGTTATTCTGTTCCGCT 4802
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Qy       4803 GCTTTTCATGCTGCATGCCTTTTTTATTGGTTGCAGGCGTCTGCCTGGGGAAGGTAGACG 4862
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Qy       4863 CCTTCGAACATGCGACCACTGTGCCAAATGTTCCGGGGATCCCGTATAAGGCGTTGGTCG 4922
              ||| ||||||||||||||||| ||||||| ||   ||| ||||||||||  | || |
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Qy       4923 AACGCGCAGGTTACGCGCCACTTAACCTGGAGATCACGGTCGTCTCATCGGAATTAACAC 4982
              || | ||||| || || || || ||  |||||||||| ||| |.|| |||||  |    |
Db      10120 AAAGGGCAGGGTATGCCCCGCTCAATTTGGAGATCACTGTCATGTCCTCGGAGGTTTTGC 10179

Qy       4983 CTTCAACTAACAAGGAGTACGTGACCTGCAAATTCCACACAGTCATTCCTTCACCACAAG 5042
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Qy       5103 TTTTTGGCGGTGTGTACCCTTTCATGTGGGGAGGCGCACAATGCTTCTGTGACAGTGAGA 5162
              | || || || || ||||| || |||||||||||| || ||||| || || ||||||||||
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Qy       5163 ACACACAACTGAGTGAGGCGTACGTCGAGTTCGCTCCAGACTGCACTATAGATCACGCAG 5222
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Qy       5223 TCGCACTAAAAGTTCACACAGCTGCTCTGAAAGTCGGCCTGCGTATAGTATACGGCAACA 5282
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Qy       5283 CCACCGCGCACCTGGATACGTTTGTCAATGGCGTCACGCCAGGTTCCTCACGGGACCTGA 5342
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               || || || |||||||| |||||||| || |||||||| ||||||||||||||||
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              |||| || |||||||| | ||||||| | || ||||| ||||| || || | |||||| |
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Qy       5583 ATGAAATGTGGAAGAACAACTCAGGACGACCCCTGCAAGAAACAGCACCATTTGGATGTA 5642
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Qy       5823 ACAAAGCTGACAGGGAGGGACATTGTCCAGTTCACTCCCACTCCACGACAGCTGTTTTGA 5882
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             |  | | ||| | || || || || || || || || || || |  |||||   | |
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Qy       5883 AGGAAGCGACCACACATGTGACTGCCGTAGGCAGCATAACACTACATTTTAGCACATCGA 5942
              | ||  |||| ||||||    |    |||      | ||| |||| ||||||||  |||
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Qy       5943 GCCCACAAGCAAATTTTATAGTTTCGCTATGCGGCAAGAAGTCCACCTGCAATGCTGAAT 6002
              | ||||| || || ||||| || ||||| || || |||||| | || ||||||||  ||||
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Qy       6003 GTAAACCACCGGCCGACCACATAATTGGAGAACCACATAAAGTCGACCAAGAATTCCAGG 6062
              |||||||||| || ||||| ||  |  |    || || |||   |||||||||| || |
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Qy       6063 CGGCAGTTTCCAAAACATCTTGGAACTGGCTGCTTGCACTGTTTGGGGGAGCATCATCCC 6122
              | ||  | || |||||||| |||| |||||| |||| || || || || || || || |
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              |  |  || ||||||||||  | || |  ||||||   ||||| |  | ||||||  ||||
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              ||| |          || ||| |  | | | ||||||||||||||||||||||  |  ||
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Qy       6242 GCATAATGCCACGCGCCGCT 6261
              |||||||||  |  || | |
Db      11440 GCATAATGCATCAGGCTGGT 11459
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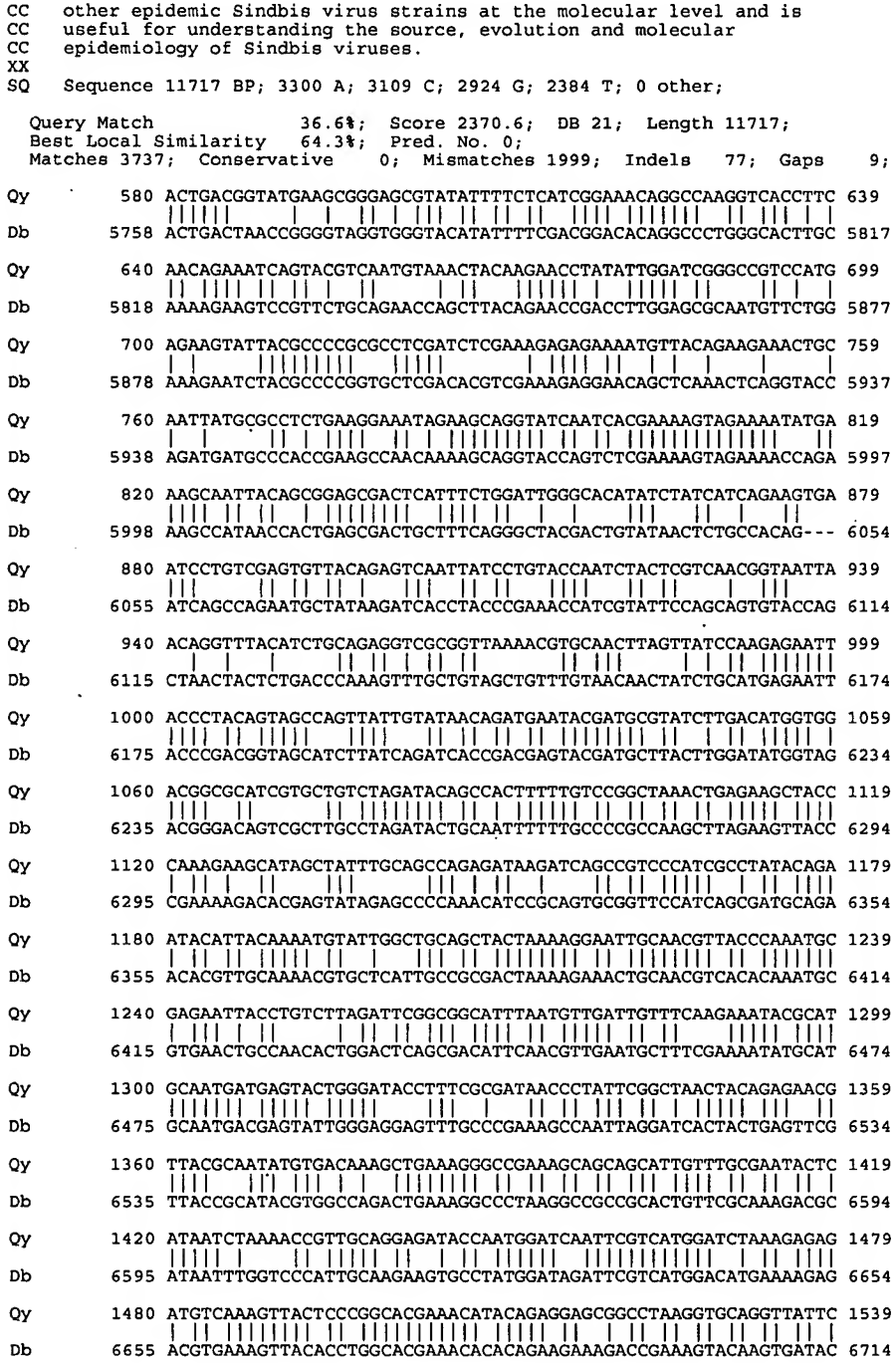
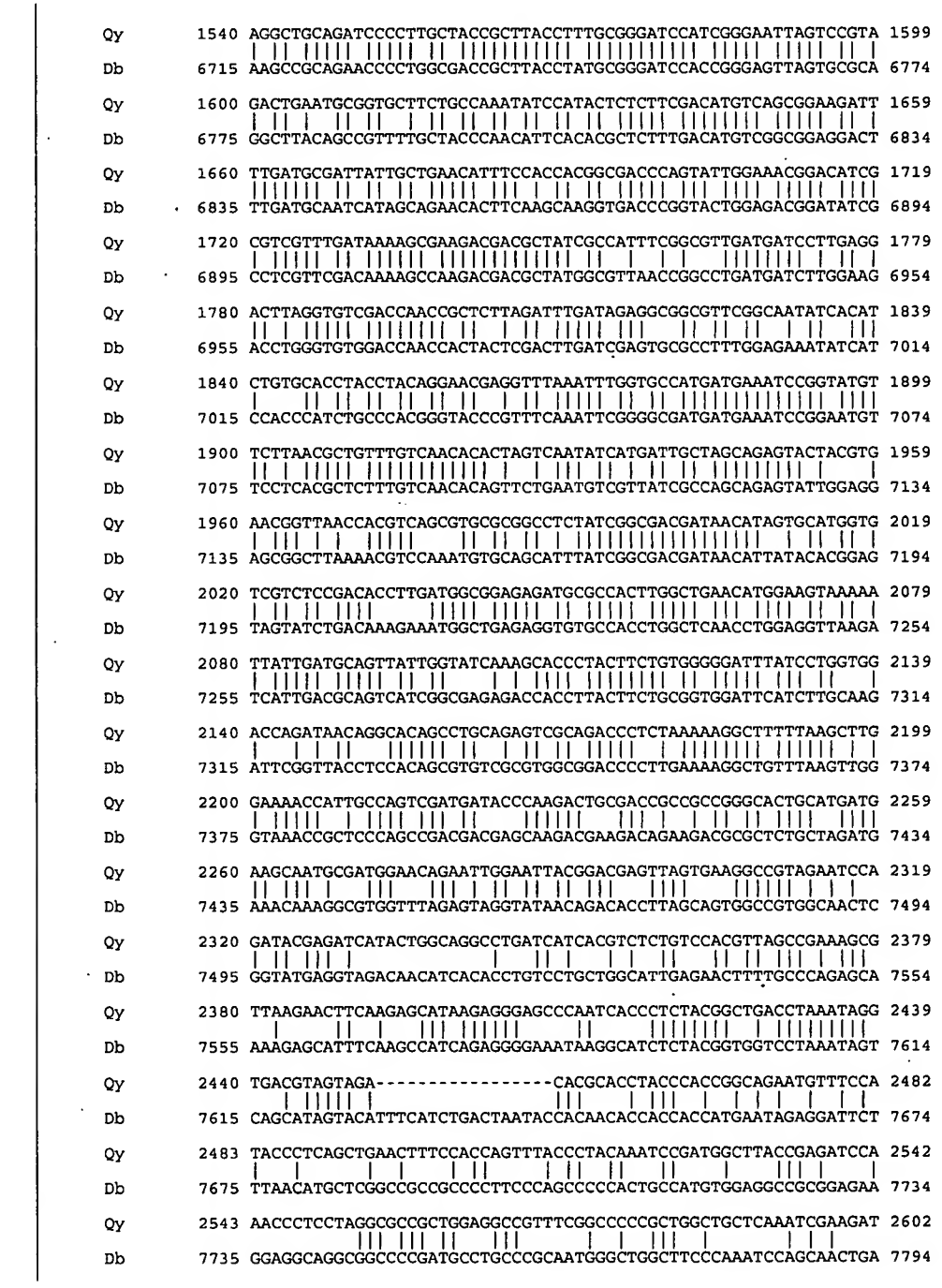
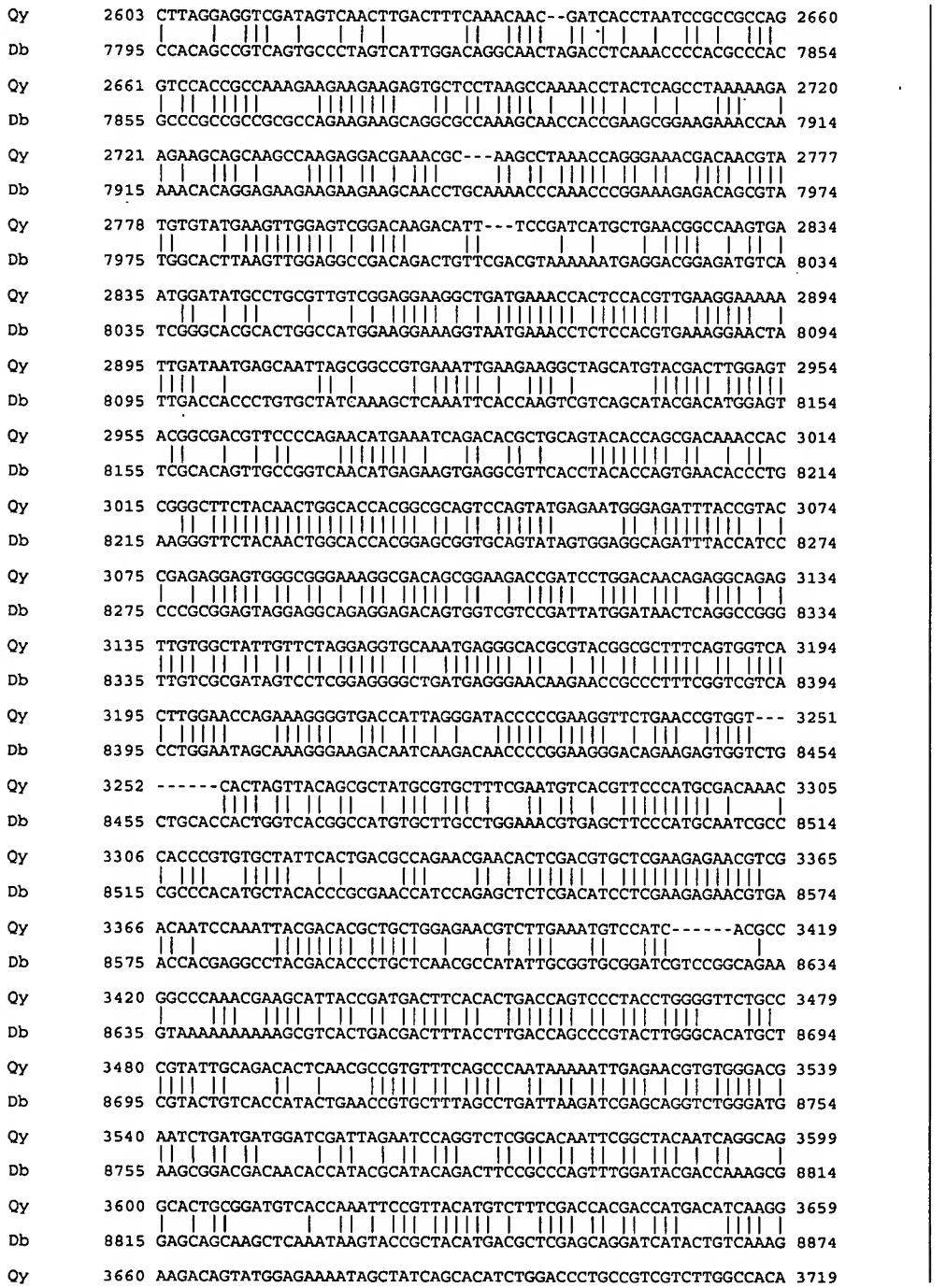
RESULT 11
AAA70577
ID AAA70577 standard; cDNA; 11717 BP.
XX
AC AAA70577;
XX
DT 06-DEC-2000 (first entry)
XX
DE Sindbis-like virus strain YN87448 complete genome.
XX
KW Genome; Sindbis-like virus strain YN87448; primer; RT-PCR; vaccine;
KW epidemic; Sindbis encephalitis; evolution; epidemiology; ds.
XX
OS Sindbis-like virus strain YN87448.
XX
PN CN1252445-A.
XX
PD 10-MAY-2000.
XX
PF 27-OCT-1998; 98CN-0120694.
XX
PR 27-OCT-1998; 98CN-0120694.
XX
PA (VIRO-) INST VIROLOGY CHINESE ACAD PREVENTIVE ME.
XX
PI Liang G, Zhou G, Li L;
XX
DR WPI; 2000-443226/39.
XX
PT Whole genome sequence of YN87448 virus strain and its cloning method -
XX
PS Claim 1; Page 2-9; 24pp; Chinese.
XX
CC This sequence represents the complete genome of the Sindbis-like virus
CC strain YN87448. The genome was cloned as 15 fragments using the PCR
CC primers AAA70578-A70603 into the plasmid pGEM-T. The invention relates
CC to the isolation and method of cloning the complete genome for the
CC Sindbis-like virus strain YN87448 by a RT-PCR process. The YN87448
CC strain virus appears to be the optimal candidate for a vaccine to
CC prevent epidemics of Sindbis encephalitis. The sequence of this
CC strain's genome shows the difference between this viral strain and

CC other epidemic Sindbis virus strains at the molecular level and is
CC useful for understanding the source, evolution and molecular
CC epidemiology of Sindbis viruses.
XX
SQ Sequence 11717 BP; 3300 A; 3109 C; 2924 G; 2384 T; 0 other;

Query Match 36.6%; Score 2370.6; DB 21; Length 11717;
Best Local Similarity 64.3%; Pred. No. 0;
Matches 3737; Conservative 0; Mismatches 1999; Indels 77; Gaps 9;



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Db 7795 CCACAGCCGTCAGTGCCCTAGTCATTGGACAGGCAACTAGACCTCAAACCCCACGCCCAC 7854
Qy 2661 GTCCACCGCCAAAGAAGAAGAAGAGTGCTCCTAAGCCAAAACCTACTCAGCCTAAAAAGA 2720
Db 7855 GCCCGCCGCCGCGCCAGAAGAAGCAGGCGCCAAAGCAACCACCGAAGCGGAAGAAACCAA 7914
Qy 2721 AGAAGCAGCAAGCCAAGAGGACGAAACGC---AAGCCTAAACCAGGGAAACGACAACGTA 2777
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Qy 2778 TGTGTATGAAGTTGGAGTCGGACAAGACATT---TCCGATCATGCTGAACGGCCAAGTGA 2834
Db 7975 TGGCACTTAAGTTGGAGGCCGACAGACTGTTCGACGTAAAAAATGAGGACGGAGATGTCA 8034
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Db 8395 CCTGGAATAGCAAAGGGAAGACAATCAAGACAACCCCGGAAGGGACAGAAGAGTGGTCTG 8454
Qy 3252 ------CACTAGTTACAGCGCTATGCGTGCTTTCGAATGTCACGTTCCCATGCGACAAAC 3305
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Db      10555 TGAAAGTCATAGCTGGACCAATTTCAGCATTGTTTACACCATTCGATCACAAGGTCGTTA 10614

Qy       5400 TCAGAAAGGGGCTTGTTTACAACTACGACTTCCCTGAGTATGGAGCTATGAAACCAGGAG 5459

Db      10615 TCCATCGCGGCCTGGTGTACAACTATGACTTTCCGGAATACGGAGCGATGAAACCAGGAG 10674

Qy       5460 CGTTCGGCGATATTCAAGCATCCTCGCTTGATGCTACAGACATAGTAGCCCGCACTGACA 5519

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Qy       5520 TACGGCTGCTGAAGCCTTCTGTCAAGAACATCCACGTCCCCTACACCCAAGCAGTATCAG 5579

Db      10735 TTAGGCTACTCAAGCCTTCCGCCAAGAACGTGCATGTCCCGTACACGCAGGCCGCATCTG 10794

Qy       5580 GGTATGAAATGTGGAAGAACAACTCAGGACGACCCCTGCAAGAAACAGCACCATTTGGAT 5639

Db      10795 GATTCGAGATGTGGAAAAACAACTCAGGCCGCCCACTGCAGGAAACCGCCCCTTTTGGGC 10854

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Db      10855 GCAAGATTGCAGTCAATCCGCTTCAGGCGGTGGACTGCTCATACGGGAACATTCCCATCT 10914

Qy       5700 CGATTGACATCCCTGATGCAGCTTTTGTGAGATCATCAGAATCACCAACAATTTTAGAAG 5759

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Qy       5760 TTAGCTGCACAGTAGCAGACTGCATTTATTCTGCAGACTTTGGTGGTTCTCTAACATTAC 5819

Db      10975 TCAAATGTGATGTCAGTGAGTGCACTTATTCAGCGGACTTCGGCGGGATGGCTACCCTGC 11034

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Db      11095 TCCAAGAGTCGACAGTTCATGTCCTGGAGAAAGGAGCGGTGACAGTACACTTCAGCACCG 11154

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Db      11215 AATGCAAACCACCAGCTGATCATATCGTGAGCACCCCGCACAAAAATGACCAAGAATTCC 11274

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Db      11275 AAGCCGCCATCTCAAAAACTTCATGGAGTTGGCTGTTTGCCCTTTTCGGCGGCGCCTCGT 11334

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Db      11395 GATGACCGCTACGCCCCAATGACCCGACCAGCAAAACTCGATGTACTTCCGAGGAACTGA 11454

Qy       6239 GGTGCATAATGCCACGCGCCGCT--------------------------------TGAC 6265

Db      11455 TGTGCATAATGCATCAGGCTGGTATATTAGATCCCCGCTTACCGCGGGCAATATAGCAAC 11514

Qy       6266 ACTAAAACTCGATGTATTTCCGAGGAAGCACAGTGCATAATGCTGTGCAGTGT 6318

Db      11515 ACCAAAACTCGACGTATTTCCGAGGAAGCGCAGTGCATAATGCTGCGCAGTGT 11567
```

RESULT 12
AAV60125
ID AAV60125 standard; DNA; 16656 BP.
XX
AC AAV60125;
XX
DT 25-MAR-2003 (updated)
DT 04-DEC-1998 (first entry)
XX
DE Representative eukaryotic layered vector initiation system.
XX
KW Eukaryotic layered vector initiation system; stimulate; immune response;
KW ss.
XX
OS Synthetic.
OS Sindbis virus.
XX
PN US5814482-A.
XX
PD 29-SEP-1998.
XX
PF 30-OCT-1996; 96US-0739158.
XX
PR 14-SEP-1994; 94WO-US10469.
PR 15-MAR-1995; 95US-0404796.
PR 15-SEP-1993; 93US-0122791.
PR 18-FEB-1994; 94US-0198450.
PR 30-NOV-1994; 94US-0348472.
PR 18-JAN-1995; 95US-0376184.
XX
PA (DRIV/) DRIVER D A.
PA (DUBE/) DUBENSKY T W.
PA (JOLL/) JOLLY D J.
PA (POLO/) POLO J M.
XX
PI Driver DA, Dubensky TW, Jolly DJ, Polo JM;
XX
DR WPI; 1998-541753/46.
XX

PT Eukaryotic layered vector initiation system - containing eukaryotic
PT promoter and heterologous antigen coding sequence, useful for
PT stimulating immune response
XX
PS Example 1; Fig 3A-H; 144pp; English.
XX
CC The present sequence is a representative eukaryotic layered vector
CC initiation system, based on Sindbis. The eukaryotic layered vector
CC initiation system comprises a eukaryotic promoter 5' of viral cDNA
CC which initiates, in a susceptible target cell, 5' to 3' synthesis of
CC RNA from the viral cDNA. The RNA comprises a vector construct which
CC autonomously amplifies in the cell and expresses a heterologous nucleic
CC acid sequence which encodes an antigen or modified form that stimulates
CC an immune response within an animal. The system is useful for stimulating
CC an immune response to an antigen by introducing the vector into target
CC cells, preferably by infection in vivo, especially where the immune
CC response is a cell mediated, HLA class I-restricted or an HLA class
CC II-restricted immune response.
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 16656 BP; 4467 A; 4349 C; 4183 G; 3657 T; 0 other;

Query Match 36.5%; Score 2369.2; DB 19; Length 16656;
Best Local Similarity 64.6%; Pred. No. 0;
Matches 3693; Conservative 0; Mismatches 1983; Indels 44; Gaps 9;

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Qy       580 ACTGACGGTATGAAGCGGGAGCGTATATTTTCTCATCGGAAACAGGCCAAGGTCACCTTC 639
Db      5746 ACTGACTAACCGGGGTAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGC 5805

Qy       640 AACAGAAATCAGTACGTCAATGTAAACTACAAGAACCTATATTGGATCGGGCCGTCCATG 699
Db      5806 AAAAGAAGTCCGTTCTGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGG 5865

Qy       700 AGAAGTATTACGCCCCGCGCCTCGATCTCGAAAGAGAGAAAATGTTACAGAAGAAACTGC 759
Db      5866 AAAGAATTCATGCCCCGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACC 5925

Qy       760 AATTATGCGCCTCTGAAGGAAATAGAAGCAGGTATCAATCACGAAAAGTAGAAAATATGA 819
Db      5926 AGATGATGCCCACCGAAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGA 5985

Qy       820 AAGCAATTACAGCGGAGCGACTCATTTCTGGATTGGGCACATATCTATCATCAGAAGTGA 879
Db      5986 AAGCCATAACCACTGAGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAG--- 6042

Qy       880 ATCCTGTCGAGTGTTACAGAGTCAATTATCCTGTACCAATCTACTCGTCAACGGTAATTA 939
Db      6043 ATCAGCCAGAATGCTATAAGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGG 6102

Qy       940 ACAGGTTTACATCTGCAGAGGTCGCGGTTAAAACGTGCAACTTAGTTATCCAAGAGAATT 999
Db      6103 CGAACTACTCCGATCCACAGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACT 6162

Qy      1000 ACCCTACAGTAGCCAGTTATTGTATAACAGATGAATACGATGCGTATCTTGACATGGTGG 1059
Db      6163 ATCCGACAGTAGCATCTTATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAG 6222

Qy      1060 ACGGCGCATCGTGCTGTCTAGATACAGCCACTTTTTGTCCGGCTAAACTGAGAAGCTACC 1119
Db      6223 ACGGGACAGTCGCCTGCCTGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACC 6282

Qy      1120 CAAAGAAGCATAGCTATTTGCAGCCAGAGATAAGATCAGCCGTCCCATCGCCTATACAGA 1179
Db      6283 CGAAAAAACATGAGTATAGAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGA 6342

Qy      1180 ATACATTACAAAATGTATTGGCTGCAGCTACTAAAAGGAATTGCAACGTTACCCAAATGC 1239
Db      6343 ACACGCTACAAAATGTGCTCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGC 6402

Qy      1240 GAGAATTACCTGTCTTAGATTCGGCGGCATTTAATGTTGATTGTTTCAAGAAATACGCAT 1299
Db      6403 GTGAACTGCCAACACTGGACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCAT 6462

Qy      1300 GCAATGATGAGTACTGGGATACCTTTCGCGATAACCCTATTCGGCTAACTACAGAGAACG 1359
Db      6463 GTAATGACGAGTATTGGGAGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTG 6522

Qy      1360 TTACGCAATATGTGACAAAGCTGAAAGGGCCGAAAGCAGCAGCATTGTTTGCGAATACTC 1419
Db      6523 TCACCGCATATGTAGCTAGACTGAAAGGCCCTAAGGCCGCCACACTATTTGCAAAGACGT 6582

Qy      1420 ATAATCTAAAACCGTTGCAGGAGATACCAATGGATCAATTCGTCATGGATCTAAAGAGAG 1479
Db      6583 ATAATTTGGTCCCATTGCAAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAG 6642

Qy      1480 ATGTCAAAGTTACTCCCGGCACGAAACATACAGAGGAGCGGCCTAAGGTGCAGGTTATTC 1539
Db      6643 ACGTGAAAGTTACACCAGGCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATAC 6702

Qy      1540 AGGCTGCAGATCCCCTTGCTACCGCTTACCTTTGCGGGATCCATCGGGAATTAGTCCGTA 1599
Db      6703 AAGCCGCAGAACCCCTGGCGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTA 6762

Qy      1600 GACTGAATGCGGTGCTTCTGCCAAATATCCATACTCTCTTCGACATGTCAGCGGAAGATT 1659
Db      6763 GGCTTACGGCCGTCTTGCTTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATT 6822

Qy      1660 TTGATGCGATTATTGCTGAACATTTCCACCACGGCGACCCAGTATTGGAAACGGACATCG 1719
Db      6823 TTGATGCAATCATAGCAGAACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCG 6882

Qy      1720 CGTCGTTTGATAAAAGCGAAGACGACGCTATCGCCATTTCGGCGTTGATGATCCTTGAGG 1779
Db      6883 CATCATTCGACAAAAGCCAAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGG 6942

Qy      1780 ACTTAGGTGTCGACCAACCGCTCTTAGATTTGATAGAGGCGGCGTTCGGCAATATCACAT 1839
Db      6943 ACCTGGGTGTGGATCAACCACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCAT 7002

Qy      1840 CTGTGCACCTACCTACAGGAACGAGGTTTAAATTTGGTGCCATGATGAAATCCGGTATGT 1899
Db      7003 CCACCCATCTACCTACGGGTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGT 7062

Qy      1900 TCTTAACGCTGTTTGTCAACACACTAGTCAATATCATGATTGCTAGCAGAGTACTACGTG 1959
Db      7063 TCCTCACACTTTTTGTCAACACAGTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAG 7122

Qy      1960 AACGGTTAACCACGTCAGCGTGCGCGGCCTCTATCGGCGACGATAACATAGTGCATGGTG 2019
Db      7123 AGCGGCTTAAAACGTCCAGATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAG 7182

Qy      2020 TCGTCTCCGACACCTTGATGGCGGAGAGATGCGCCACTTGGCTGAACATGGAAGTAAAAA 2079
Db      7183 TAGTATCTGACAAAGAAATGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGA 7242

Qy      2080 TTATTGATGCAGTTATTGGTATCAAAGCACCCTACTTCTGTGGGGGATTTATCCTGGTGG 2139
Db      7243 TCATCGACGCAGTCATCGGTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAG 7302

Qy      2140 ACCAGATAACAGGCACAGCCTGCAGAGTCGCAGACCCTCTAAAAAGGCTTTTTAAGCTTG 2199
Db      7303 ATTCGGTTACTTCCACAGCGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGG 7362

Qy      2200 GAAAACCATTGCCAGTCGATGATACCCAAGACTGCGACCGCCGCCGGGCACTGCATGATG 2259
Db      7363 GTAAACCGCTCCCAGCCGACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATG 7422

Qy      2260 AAGCAATGCGATGGAACAGAATTGGAATTACGGACGAGTTAGTGAAGGCCGTAGAATCCA 2319
Db      7423 AAACAAAGGCGTGGTTTAGAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCC 7482

Qy      2320 GATACGAGATCATACTGGCAGGCCTGATCATCACGTCTCTGTCCACGTTAGCCGAAAGCG 2379
Db      7483 GGTATGAGGTAGACAATATTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCA 7542
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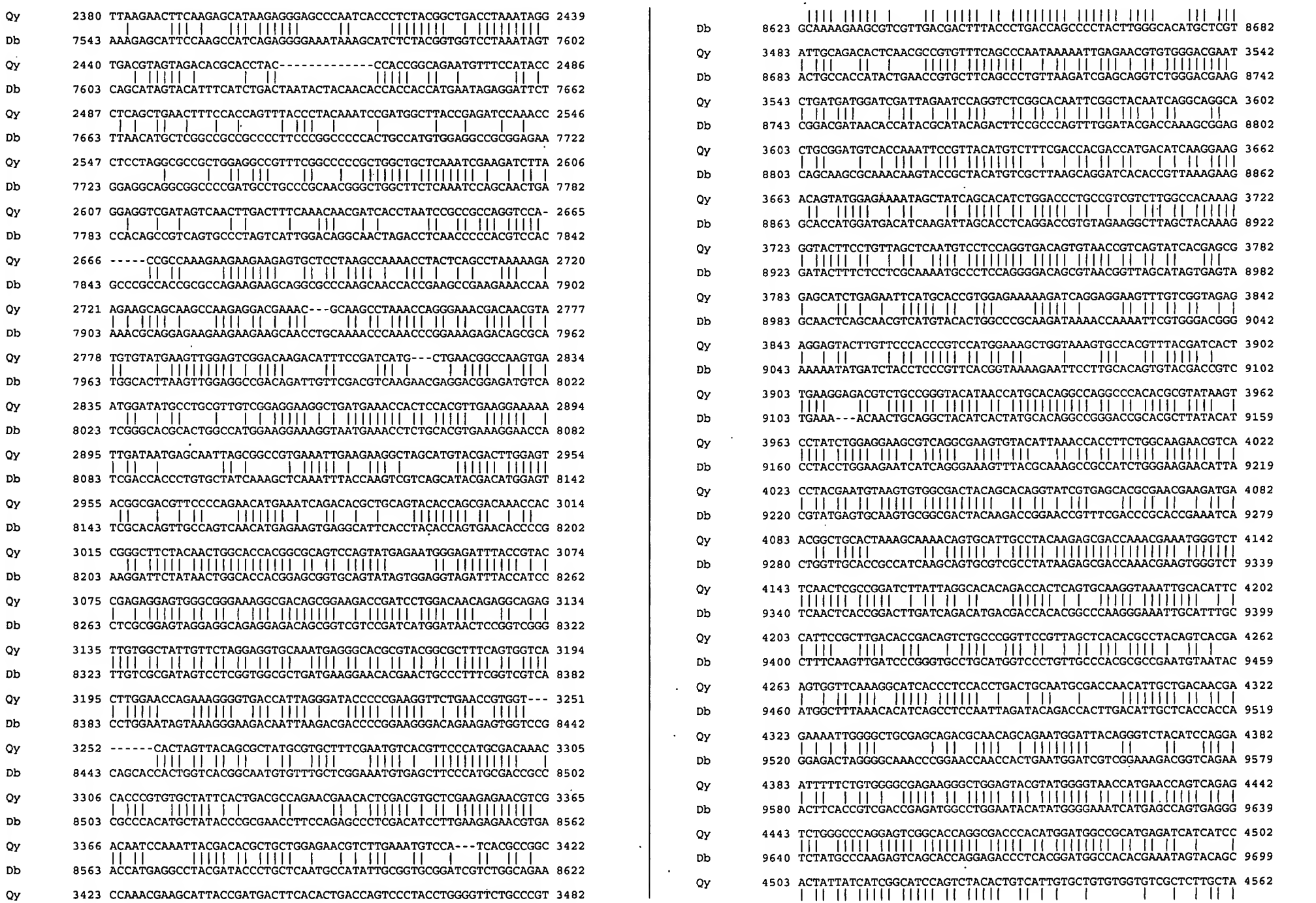

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Db      9700 ATTACTACCATCGCCATCCTGTGTACACCATCTTAGCCGTCGCATCAGCTACCGTGGCGA 9759

Qy      4563 TCCTGGTAGGCACTGCATCATCAGCAGCTTGCATCGCCAAAGCAAGAAGAGACTGCCTGA 4622

Db      9760 TGATGATTGGCGTAACTGTTGCAGTGTTATGTGCCTGTAAAGCGCGCCGTGAGTGCCTGA 9819

Qy      4623 CGCCATACGCGCTTGCACCGAACGCAACGGTACCCACAGCATTAGCGGTTTTGTGCTGCA 4682

Db      9820 CGCCATACGCCCTGGCCCCAAACGCCGTAATCCCAACTTCGCTGGCACTCTTGTGCTGCG 9879

Qy      4683 TTCGGCCAACCAACGCTGAAACATTTGGAGAAACTTTGAACCATCTGTGGTTTAACAACC 4742

Db      9880 TTAGGTCGGCCAATGCTGAAACGTTCACCGAGACCATGAGTTACTTGTGGTCGAACAGTC 9939

Qy      4743 AACCGTTTCTCTGGGCACAGTTGTGCATTCCTCTGGCAGCGCTTGTTATTCTGTTCCGCT 4802

Db      9940 AGCCGTTCTTCTGGGTCCAGTTGTGCATACCTTTGGCCGCGTTCATCGTTCTAATGCGCT 9999

Qy      4803 GCTTTTCATGCTGCATGCCTTTTTTATTGGTTGCAGGCGTCTGCCTGGGGAAGGTAGACG 4862

Db     10000 ACTGCTCCTGCTGCCTGCCTTTTTTAGTGGTTGCCGGCGCCTACCTGGCGAAGGTAGACG 10059

Qy      4863 CCTTCGAACATGCGACCACTGTGCCAAATGTTCCGGGGATCCCGTATAAGGCGTTGGTCG 4922

Db     10060 CCTACGAACATGCGACCACTGTTCCAAATGTGCCACAGATACCGTATAAGGCACTTGTTG 10119

Qy      4923 AACGCGCAGGTTACGCGCCACTTAACCTGGAGATCACGGTCGTCTCATCGGAATTAACAC 4982

Db     10120 AAAGGGCAGGGTATGCCCCGCTCAATTTGGAGATCACTGTCATGTCCTCGGAGGTTTTGC 10179

Qy      4983 CTTCAACTAACAAGGAGTACGTGACCTGCAAATTCCACACAGTCATTCCTTCACCACAAG 5042

Db     10180 CTTCCACCAACCAAGAGTACATTACCTGCAAATTCACCACTGTGGTCCCCTCCCCAAAAA 10239

Qy      5043 TTAAATGCTGCGGGTCCCTCGAGTGCAAGGCATCCTCAAAGGCGGATTACACATGCCGCG 5102

Db     10240 TCAAATGCTGCGGCTCCTTGGAATGTCAGCCGGCCGCTCATGCAGACTATACCTGCAAGG 10299

Qy      5103 TTTTTGGCGGTGTGTACCCTTTCATGTGGGGAGGCGCACAATGCTTCTGTGACAGTGAGA 5162

Db     10300 TCTTCGGAGGGGTCTACCCCTTTATGTGGGGAGGAGCGCAATGTTTTTGCGACAGTGAGA 10359

Qy      5163 ACACACAACTGAGTGAGGCGTACGTCGAGTTCGCTCCAGACTGCACTATAGATCACGCAG 5222

Db     10360 ACAGCCAGATGAGTGAGGCGTACGTCGAATTGTCAGCAGATTGCGCGTCTGACCACGCGC 10419

Qy      5223 TCGCACTAAAAGTTCACACAGCTGCTCTGAAAGTCGGCCTGCGTATAGTATACGGCAACA 5282

Db     10420 AGGCGATTAAGGTGCACACTGCCGCGATGAAAGTAGGACTGCGTATAGTGTACGGGAACA 10479

Qy      5283 CCACCGCGCACCTGGATACGTTTGTCAATGGCGTCACGCCAGGTTCCTCACGGGACCTGA 5342

Db     10480 CTACCAGTTTCCTAGATGTGTACGTGAACGGAGTCACACCAGGAACGTCTAAAGACTTGA 10539

Qy      5343 AGGTCATAGCAGGGCCGATATCAGCCGCTTTTTCACCCTTTGACCATAAGGTCGTCATCA 5402

Db     10540 AAGTCATAGCTGGACCAATTTCAGCATCGTTTACGCCATTCGATCATAAGGTCGTTATCC 10599

Qy      5403 GAAAGGGGCTTGTTTACAACTACGACTTCCCTGAGTATGGAGCTATGAAACCAGGAGCGT 5462

Db     10600 ATCGCGGCCTGGTGTACAACTATGACTTCCCGGAATATGGAGCGATGAAACCAGGAGCGT 10659

Qy      5463 TCGGCGATATTCAAGCATCCTCGCTTGATGCTACAGACATAGTAGCCCGCACTGACATAC 5522

Db     10660 TCGGAGACATTCAAGCTACCTCCTTGACTAGCAAGGATCTCATCGCCAGCACAGACATTA 10719

Qy      5523 GGCTGCTGAAGCCTTCTGTCAAGAACATCCACGTCCCCTACACCCAAGCAGTATCAGGGT 5582

Db     10720 GGCTACTCAAGCCTTCCGCCAAGAACGTGCATGTCCCGTACACGCAGGCCGCATCAGGAT 10779

Qy      5583 ATGAAATGTGGAAGAACAACTCAGGACGACCCCTGCAAGAAACAGCACCATTTGGATGTA 5642

Db     10780 TTGAGATGTGGAAAAACAACTCAGGCCGCCCACTGCAGGAAACCGCACCTTTCGGGTGTA 10839

Qy      5643 AAATTGAAGTGGAGCCTCTGCGAGCGTCTAACTGTGCTTACGGGCACATCCCTATCTCGA 5702

Db     10840 AGATTGCAGTAAATCCGCTCCGAGCGGTGGACTGTTCATACGGGAACATTCCCATTTCTA 10899

Qy      5703 TTGACATCCCTGATGCAGCTTTTGTGAGATCATCAGAATCACCAACAATTTTAGAAGTTA 5762

Db     10900 TTGACATCCCGAACGCTGCCTTTATCAGGACATCAGATGCACCACTGGTCTCAACAGTCA 10959

Qy      5763 GCTGCACAGTAGCAGACTGCATTTATTCTGCAGACTTTGGTGGTTCTCTAACATTACAGT 5822

Db     10960 AATGTGAAGTCAGTGAGTGCACTTATTCAGCAGACTTCGGCGGGATGGCCACCCTGCAGT 11019

Qy      5823 ACAAAGCTGACAGGGAGGGACATTGTCCAGTTCACTCCCACTCCACGACAGCTGTTTTGA 5882

Db     11020 ATGTATCCGACCGCGAAGGTCAATGCCCCGTACATTCGCATTCGAGCACAGCAACTCTCC 11079

Qy      5883 AGGAAGCGACCACACATGTGACTGCCGTAGGCAGCATAACACTACATTTTAGCACATCGA 5942

Db     11080 AAGAGTCGACAGTACATGTCCTGGAGAAAGGAGCGGTGACAGTACACTTTAGCACCGCGA 11139

Qy      5943 GCCCACAAGCAAATTTTATAGTTTCGCTATGCGGCAAGAAGTCCACCTGCAATGCTGAAT 6002

Db     11140 GTCCACAGGCGAACTTTATCGTATCGCTGTGTGGGAAGAAGACAACATGCAATGCAGAAT 11199

Qy      6003 GTAAACCACCGGCCGACCACATAATTGGAGAACCACATAAAGTCGACCAAGAATTCCAGG 6062

Db     11200 GTAAACCACCAGCTGACCATATCGTGAGCACCCCGCACAAAAATGACCAAGAATTTCAAG 11259

Qy      6063 CGGCAGTTTCCAAAACATCTTGGAACTGGCTGCTTGCACTGTTTGGGGGAGCATCATCCC 6122

Db     11260 CCGCCATCTCAAAAACATCATGGAGTTGGCTGTTTGCCCTTTTCGGCGGCGCCTCGTCGC 11319

Qy      6123 TCATTGTTGTAGGACTTATAGTGTTGGTCTGCAGCTCTATGCTTATAAACACACGTAGAT 6182

Db     11320 TATTAATTATAGGACTTATGATTTTTGCTTGCAGCATGATGCTGACTAGCACACGAAGAT 11379

Qy      6183 GACTGAGCGCGGACACTGA-CATAGCGGTAAAACTCGATGTACTTCCGAGGAAGCGTGGT 6241

Db     11380 GACCGCTACGCCCCAATGATCCGACCAGCAAAACTCGATGTACTTCCGAGGAACTGATGT 11439

Qy      6242 GCATAATGCCACGCGCCGCT 6261

Db     11440 GCATAATGCATCAGGCTGGT 11459
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RESULT 13
AAV42364
ID AAV42364 standard; DNA; 16656 BP.
XX
AC AAV42364;
XX
DT 02-OCT-1998 (first entry)
XX
DE Representative eukaryotic layered vector initiation system sequence.
XX
KW Representative eukaryotic layered vector initiation system;
KW DNA alphavirus; structural protein expression; inhibit; pathogen;
KW immune response; stimulate; ss.
XX
OS Sindbis virus.
XX
PN US5789245-A.
XX
PD 04-AUG-1998.
XX
PF 30-OCT-1996; 96US-0741881.
XX
PR 15-MAR-1995; 95US-0404796.
PR 15-SEP-1993; 93US-0122791.
PR 18-FEB-1994; 94US-0198450.
PR 30-NOV-1994; 94US-0348472.
PR 20-JAN-1995; 95US-0376184.

PR 30-OCT-1996; 96US-0741881.
XX
PA (CHIR) CHIRON CORP.
XX
PI Chang SMW, Driver DA, Dubensky TW, Ibanez CE, Jolly DJ;
PI Polo JM;
XX
DR WPI; 1998-446089/38.
XX
PT DNA alpha:virus structural protein expression cassettes - for
PT producing recombinant alpha:virus particles
XX
PS Disclosure; Fig 3A-H; 140pp; English.
XX
CC The present sequence is a representative eukaryotic layered vector
CC initiation system derived from Sindbis virus. The specification describes
CC a DNA alphavirus structural protein expression cassette which comprises
CC an inducible promoter and an alphavirus structural protein gene, where
CC the promoter directs the expression of the alphavirus structural protein
CC gene upon induction of the promoter within a cell, and where prior to
CC induction within the cell, the expression cassette does not express
CC sufficient quantities of structural proteins to be cytotoxic to a BHK
CC cell containing the expression cassette. The products may be used to
CC inhibit pathogens and stimulate an immune response.
XX
SQ Sequence 16656 BP; 4467 A; 4349 C; 4183 G; 3657 T; 0 other;

Query Match 36.5%; Score 2369.2; DB 19; Length 16656;
Best Local Similarity 64.6%; Pred. No. 0;
Matches 3693; Conservative 0; Mismatches 1983; Indels 44; Gaps 9;

```
Qy        580 ACTGACGGTATGAAGCGGGAGCGTATATTTTCTCATCGGAAACAGGCCAAGGTCACCTTC 639
              ||||||     |  |  || | ||| || || ||  |||| |||||||  || ||| | |
Db       5746 ACTGACTAACCGGGGTAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGC 5805

Qy        640 AACAGAAATCAGTACGTCAATGTAAACTACAAGAACCTATATTGGATCGGGCCGTCCATG 699
              || |||| || || |  ||      | ||   ||||||  |  |||||  ||    ||||  |
Db       5806 AAAAGAAGTCCGTTCTGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGG 5865

Qy        700 AGAAGTATTACGCCCCGCGCCTCGATCTCGAAAGAGAGAAAATGTTACAGAAGAAACTGC 759
              | |    | | ||||||   |||||        | |||| ||     |  |      |
Db       5866 AAAGAATTCATGCCCCGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACC 5925

Qy        760 AATTATGCGCCTCTGAAGGAAATAGAAGCAGGTATCAATCACGAAAAGTAGAAAATATGA 819
              |  |     || | ||||  || | ||| |||||  || || || ||||||||||||  ||
Db       5926 AGATGATGCCCACCGAAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGA 5985

Qy        820 AAGCAATTACAGCGGAGCGACTCATTTCTGGATTGGGCACATATCTATCATCAGAAGTGA 879
              |||| || ||  | |||||||  | || ||| |  |    |||   ||  |   ||
Db       5986 AAGCCATAACCACTGAGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAG--- 6042

Qy        880 ATCCTGTCGAGTGTTACAGAGTCAATTATCCTGTACCAATCTACTCGTCAACGGTAATTA 939
              |||     || || |   |||  |||||   |||| | |||||     |  |||
Db       6043 ATCAGCCAGAATGCTATAAGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGG 6102

Qy        940 ACAGGTTTACATCTGCAGAGGTCGCGGTTAAAACGTGCAACTTAGTTATCCAAGAGAATT 999
                |  |   |  | || || |||| ||       || |||     | | || |||||  |
Db       6103 CGAACTACTCCGATCCACAGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACT 6162

Qy       1000 ACCCTACAGTAGCCAGTTATTGTATAACAGATGAATACGATGCGTATCTTGACATGGTGG 1059
              | || ||||||||   ||||   || || || || |||||||| ||  | || |||||  |
Db       6163 ATCCGACAGTAGCATCTTATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAG 6222

Qy       1060 ACGGCGCATCGTGCTGTCTAGATACAGCCACTTTTTGTCCGGCTAAACTGAGAAGCTACC 1119
              ||||  ||     ||| || ||||| || || || || || ||||| || |||||  ||||
Db       6223 ACGGGACAGTCGCCTGCCTGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACC 6282

Qy       1120 CAAAGAAGCATAGCTATTTGCAGCCAGAGATAAGATCAGCCGTCCCATCGCCTATACAGA 1179
              | || || |||   |||     ||  | ||  |    || || |||||  | || ||||
Db       6283 CGAAAAAACATGAGTATAGAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGA 6342

Qy       1180 ATACATTACAAAATGTATTGGCTGCAGCTACTAAAAGGAATTGCAACGTTACCCAAATGC 1239
              | ||  ||||||||||  |   ||| || |||||||| |||||||||| || || ||||
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Db       6343 ACACGCTACAAAATGTGCTCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGC 6402

Qy       1240 GAGAATTACCTGTCTTAGATTCGGCGGCATTTAATGTTGATTGTTTCAAGAAATACGCAT 1299
              | ||| | ||     | || || ||| |||| ||||| || || ||    ||||| ||||
Db       6403 GTGAACTGCCAACACTGGACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCAT 6462

Qy       1300 GCAATGATGAGTACTGGGATACCTTTCGCGATAACCCTATTCGGCTAACTACAGAGAACG 1359
              | ||||| ||||| |||||     ||         || || ||| || | || || |||   |
Db       6463 GTAATGACGAGTATTGGGAGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTG 6522

Qy       1360 TTACGCAATATGTGACAAAGCTGAAAGGGCCGAAAGCAGCAGCATTGTTTGCGAATACTC 1419
              | ||    ||||||  | |  |||||||| || || || ||  || | ||||| || ||
Db       6523 TCACCGCATATGTAGCTAGACTGAAAGGCCCTAAGGCCGCCACACTATTTGCAAAGACGT 6582

Qy       1420 ATAATCTAAAACCGTTGCAGGAGATACCAATGGATCAATTCGTCATGGATCTAAAGAGAG 1479
              |||||  |    || ||||| ||  | || ||||||  |||||||||||  | || ||||
Db       6583 ATAATTTGGTCCCATTGCAAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAG 6642

Qy       1480 ATGTCAAAGTTACTCCCGGCACGAAACATACAGAGGAGCGGCCTAAGGTGCAGGTTATTC 1539
              | || |||||||| || ||||||||||| ||||| ||  | || || || || || || | |
Db       6643 ACGTGAAAGTTACACCAGGCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATAC 6702

Qy       1540 AGGCTGCAGATCCCCTTGCTACCGCTTACCTTTGCGGGATCCATCGGGAATTAGTCCGTA 1599
              | || ||||| ||||| || || |||||| | |||||||| || ||||||||||| ||||
Db       6703 AAGCCGCAGAACCCCTGGCGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTA 6762

Qy       1600 GACTGAATGCGGTGCTTCTGCCAAATATCCATACTCTCTTCGACATGTCAGCGGAAGATT 1659
              | || |  || ||  | || ||||| || || || || || |||||||| ||||| ||||
Db       6763 GGCTTACGGCCGTCTTGCTTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATT 6822

Qy       1660 TTGATGCGATTATTGCTGAACATTTCCACCACGGCGACCCAGTATTGGAAACGGACATCG 1719
              ||||||| || || || |||| | || |||||||| ||| |||| ||||| ||||
Db       6823 TTGATGCAATCATAGCAGAACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCG 6882

Qy       1720 CGTCGTTTGATAAAAGCGAAGACGACGCTATCGCCATTTCGGCGTTGATGATCCTTGAGG 1779
              | || || || |||||| ||||||||||||| ||  |  | |  |||||||| | ||||
Db       6883 CATCATTCGACAAAAGCCAAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGG 6942

Qy       1780 ACTTAGGTGTCGACCAACCGCTCTTAGATTTGATAGAGGCGGCGTTCGGCAATATCACAT 1839
              || | ||||| || ||||| ||  | || ||||| |||   || || ||  | ||  |||
Db       6943 ACCTGGGTGTGGATCAACCACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCAT 7002

Qy       1840 CTGTGCACCTACCTACAGGAACGAGGTTTAAATTTGGTGCCATGATGAAATCCGGTATGT 1899
              |    || |||||||| || ||  | |||||||| || || ||||||||||||||| ||||
Db       7003 CCACCCATCTACCTACGGGTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGT 7062

Qy       1900 TCTTAACGCTGTTTGTCAACACACTAGTCAATATCATGATTGCTAGCAGAGTACTACGTG 1959
              || | || || ||||||||||||  |  | ||| || | || || ||||||||||||  |
Db       7063 TCCTCACACTTTTTGTCAACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAG 7122

Qy       1960 AACGGTTAACCACGTCAGCGTGCGCGGCCTCTATCGGCGACGATAACATAGTGCATGGTG 2019
              | ||| | |  |||||     || || || |  || |||||||| |||||  | |||||  |
Db       7123 AGCGGCTTAAAACGTCCAGATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAG 7182

Qy       2020 TCGTCTCCGACACCTTGATGGCGGAGAGATGCGCCACTTGGCTGAACATGGAAGTAAAAA 2079
              | || || ||||     ||||| ||||| |||||||| ||||| |||||||| || || |
Db       7183 TAGTATCTGACAAAGAAATGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGA 7242

Qy       2080 TTATTGATGCAGTTATTGGTATCAAAGCACCCTACTTCTGTGGGGGATTTATCCTGGTGG 2139
              | || || ||||| || |||   | | |||| |||||||| || ||||||||| ||   |
Db       7243 TCATCGACGCAGTCATCGGTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAG 7302

Qy       2140 ACCAGATAACAGGCACAGCCTGCAGAGTCGCAGACCCTCTAAAAAGGCTTTTTAAGCTTG 2199
              |   | | ||   |||||| ||| | || || || || || ||||||||| ||||||  | |
Db       7303 ATTCGGTTACTTCCACAGCGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGG 7362

Qy       2200 GAAAACCATTGCCAGTCGATGATACCCAAGACTGCGACCGCCGCCGGGCACTGCATGATG 2259
              | ||||| | |||| ||| ||  |||||||   ||| |  | || || ||||  ||||
Db       7363 GTAAACCGCTCCCAGCCGACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATG 7422

Qy       2260 AAGCAATGCGATGGAACAGAATTGGAATTACGGACGAGTTAGTGAAGGCCGTAGAATCCA 2319
              || ||| |   |||   ||| | || || || | |   ||||    ||||||      ||
Db       7423 AAACAAAGGCGTGGTTTAGAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCC 7482
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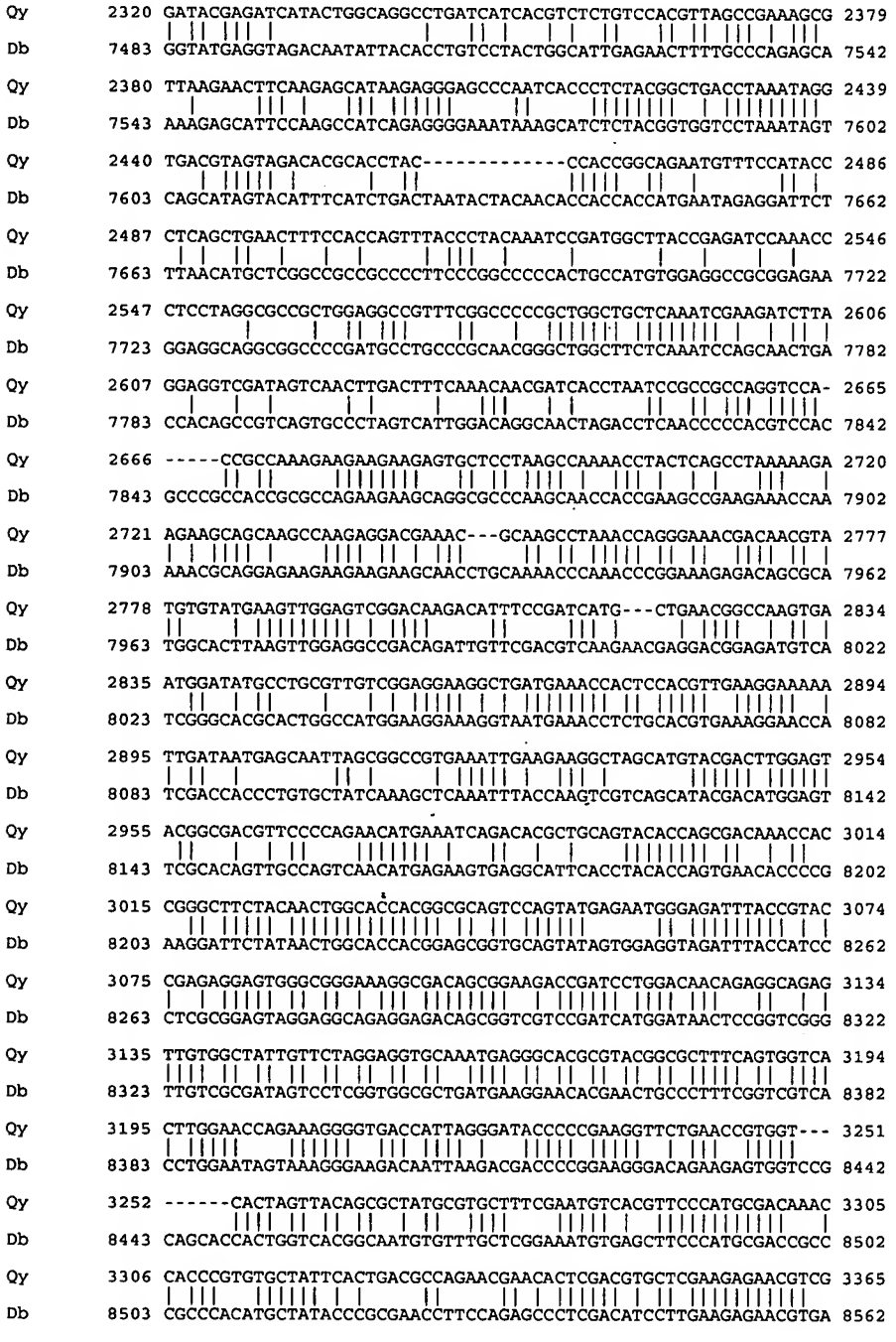
Qy 2320 GATACGAGATCATACTGGCAGGCCTGATCATCACGTCTCTGTCCACGTTAGCCGAAAGCG 2379
Db 7483 GGTATGAGGTAGACAATATTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCA 7542
Qy 2380 TTAAGAACTTCAAGAGCATAAGAGGGAGCCCAATCACCCTCTACGGCTGACCTAAATAGG 2439
Db 7543 AAAGAGCATTCCAAGCCATCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGT 7602
Qy 2440 TGACGTAGTAGACACGCACCTAC----------CCACCGGCAGAATGTTTCCATACC 2486
Db 7603 CAGCATAGTACATTTCATCTGACTAATACTACAACACCACCACCATGAATAGAGGATTCT 7662
Qy 2487 CTCAGCTGAACTTTCCACCAGTTTACCCTACAAATCCGATGGCTTACCGAGATCCAAACC 2546
Db 7663 TTAACATGCTCGGCCGCCGCCCCTTCCCGGCCCCCACTGCCATGTGGAGGCCGCGGAGAA 7722
Qy 2547 CTCCTAGGCGCCGCTGGAGGCCGTTTCGGCCCCCGCTGGCTGCTCAAATCGAAGATCTTA 2606
Db 7723 GGAGGCAGGCGGCCCCGATGCCTGCCCGCAACGGGCTGGCTTCTCAAATCCAGCAACTGA 7782
Qy 2607 GGAGGTCGATAGTCAACTTGACTTTCAAACAACGATCACCTAATCCGCCGCCAGGTCCA- 2665
Db 7783 CCACAGCCGTCAGTGCCCTAGTCATTGGACAGGCAACTAGACCTCAACCCCCACGTCCAC 7842
Qy 2666 -----CCGCCAAAGAAGAAGAAGAGTGCTCCTAAGCCAAAACCTACTCAGCCTAAAAAGA 2720
Db 7843 GCCCGCCACCGCGCCAGAAGAAGCAGGCGCCCAAGCAACCACCGAAGCCGAAGAAACCAA 7902
Qy 2721 AGAAGCAGCAAGCCAAGAGGACGAAAC---GCAAGCCTAAACCAGGGAAACGACAACGTA 2777
Db 7903 AAACGCAGGAGAAGAAGAAGAAGCAACCTGCAAAACCCAAACCCGGAAAGAGACAGCGCA 7962
Qy 2778 TGTGTATGAAGTTGGAGTCGGACAAGACATTTCCGATCATG---CTGAACGGCCAAGTGA 2834
Db 7963 TGGCACTTAAGTTGGAGGCCGACAGATTGTTCGACGTCAAGAACGAGGACGGAGATGTCA 8022
Qy 2835 ATGGATATGCCTGCGTTGTCGGAGGAAGGCTGATGAAACCACTCCACGTTGAAGGAAAAA 2894
Db 8023 TCGGGCACGCACTGGCCATGGAAGGAAAGGTAATGAAACCTCTGCACGTGAAAGGAACCA 8082
Qy 2895 TTGATAATGAGCAATTAGCGGCCGTGAAATTGAAGAAGGCTAGCATGTACGACTTGGAGT 2954
Db 8083 TCGACCACCCTGTGCTATCAAAGCTCAAATTTACCAAGTCGTCAGCATACGACATGGAGT 8142
Qy 2955 ACGGCGACGTTCCCCAGAACATGAAATCAGACACGCTGCAGTACACCAGCGACAAACCAC 3014
Db 8143 TCGCACAGTTGCCAGTCAACATGAGAAGTGAGGCATTCACCTACACCAGTGAACACCCCG 8202
Qy 3015 CGGGCTTCTACAACTGGCACCACGGCGCAGTCCAGTATGAGAATGGGAGATTTACCGTAC 3074
Db 8203 AAGGATTCTATAACTGGCACCACGGAGCGGTGCAGTATAGTGGAGGTAGATTTACCATCC 8262
Qy 3075 CGAGAGGAGTGGGCGGGAAAGGCGACAGCGGAAGACCGATCCTGGACAACAGAGGCAGAG 3134
Db 8263 CTCGCGGAGTAGGAGGCAGAGGAGACAGCGGTCGTCCGATCATGGATAACTCCGGTCGGG 8322
Qy 3135 TTGTGGCTATTGTTCTAGGAGGTGCAAATGAGGGCACGCGTACGGCGCTTTCAGTGGTCA 3194
Db 8323 TTGTCGCGATAGTCCTCGGTGGCGCTGATGAAGGAACACGAACTGCCCTTTCGGTCGTCA 8382
Qy 3195 CTTGGAACCAGAAAGGGGTGACCATTAGGGATACCCCCGAAGGTTCTGAACCGTGGT--- 3251
Db 8383 CCTGGAATAGTAAAGGGAAGACAATTAAGACGACCCCGGAAGGGACAGAAGAGTGGTCCG 8442
Qy 3252 ------CACTAGTTACAGCGCTATGCGTGCTTTCGAATGTCACGTTCCCATGCGACAAAC 3305
Db 8443 CAGCACCACTGGTCACGGCAATGTGTTTGCTCGGAAATGTGAGCTTCCCATGCGACCGCC 8502
Qy 3306 CACCCGTGTGCTATTCACTGACGCCAGAACGAACACTCGACGTGCTCGAAGAGAACGTCG 3365
Db 8503 CGCCCACATGCTATACCCGCGAACCTTCCAGAGCCCTCGACATCCTTGAAGAGAACGTGA 8562
Qy 3366 ACAATCCAAATTACGACACGCTGCTGGAGAACGTCTTGAAATGTCCA---TCACGCCGGC 3422
Db 8563 ACCATGAGGCCTACGATACCCTGCTCAATGCCATATTGCGGTGCGGATCGTCTGGCAGAA 8622
Qy 3423 CCAAACGAAGCATTACCGATGACTTCACACTGACCAGTCCCTACCTGGGGTTCTGCCCGT 3482
Db 8623 GCAAAAGAAGCGTCGTTGACGACTTTACCCTGACCAGCCCCTACTTGGGCACATGCTCGT 8682
Qy 3483 ATTGCAGACACTCAACGCCGTGTTTCAGCCCAATAAAAATTGAGAACGTGTGGGACGAAT 3542
Db 8683 ACTGCCACCATACTGAACCGTGCTTCAGCCCTGTTAAGATCGAGCAGGTCTGGGACGAAG 8742
Qy 3543 CTGATGATGGATCGATTAGAATCCAGGTCTCGGCACAATTCGGCTACAATCAGGCAGGCA 3602
Db 8743 CGGACGATAACACCATACGCATACAGACTTCCGCCCAGTTTGGATACGACCAAAGCGGAG 8802
Qy 3603 CTGCGGATGTCACCAAATTCCGTTACATGTCTTTCGACCACGACCATGACATCAAGGAAG 3662
Db 8803 CAGCAAGCGCAAACAAGTACCGCTACATGTCGCTTAAGCAGGATCACACCGTTAAAGAAG 8862
Qy 3663 ACAGTATGGAGAAAATAGCTATCAGCACATCTGGACCCTGCCGTCGTCTTGGCCACAAAG 3722
Db 8863 GCACCATGGATGACATCAAGATTAGCACCTCAGGACCGTGTAGAAGGCTTAGCTACAAAG 8922
Qy 3723 GGTACTTCCTGTTAGCTCAATGTCCTCCAGGTGACAGTGTAACCGTCAGTATCACGAGCG 3782
Db 8923 GATACTTTCTCCTCGCAAAATGCCCTCCAGGGGACAGCGTAACGGTTAGCATAGTGAGTA 8982
Qy 3783 GAGCATCTGAGAATTCATGCACCGTGGAGAAAAAGATCAGGAGGAAGTTTGTCGGTAGAG 3842
Db 8983 GCAACTCAGCAACGTCATGTACACTGGCCCGCAAGATAAAACCAAAATTCGTGGGACGGG 9042
Qy 3843 AGGAGTACTTGTTCCCACCCGTCCATGGAAAGCTGGTAAAGTGCCACGTTTACGATCACT 3902
Db 9043 AAAAATATGATCTACCTCCCGTTCACGGTAAAAGAATTCCTTGCACAGTGTACGACCGTC 9102
Qy 3903 TGAAGGAGACGTCTGCCGGGTACATAACCATGCACAGGCCAGGCCCACACGCGTATAAGT 3962
Db 9103 TGAAA---ACAACTGCAGGCTACATCACTATGCACAGGCCGGGACCGCACGCTTATACAT 9159
Qy 3963 CCTATCTGGAGGAAGCGTCAGGCGAAGTGTACATTAAACCACCTTCTGGCAAGAACGTCA 4022
Db 9160 CCTACCTGGAAGAATCATCAGGGAAAGTTTACGCAAAGCCGCCATCTGGGAAGAACATTA 9219
Qy 4023 CCTACGAATGTAAGTGTGGCGACTACAGCACAGGTATCGTGAGCACGCGAACGAAGATGA 4082
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Qy 4083 ACGGCTGCACTAAAGCAAAACAGTGCATTGCCTACAAGAGCGACCAAACGAAATGGGTCT 4142
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Qy 4143 TCAACTCGCCGGATCTTATTAGGCACACAGACCACTCAGTGCAAGGTAAATTGCACATTC 4202
Db 9340 TCAACTCACCGGACTTGATCAGACATGACGACCACACGGCCCAAGGGAAATTGCATTTGC 9399
Qy 4203 CATTCCGCTTGACACCGACAGTCTGCCCGGTTCCGTTAGCTCACACGCCTACAGTCACGA 4262
Db 9400 CTTTCAAGTTGATCCCGGGTGCCTGCATGGTCCCTGTTGCCCACGCGCCGAATGTAATAC 9459
Qy 4263 AGTGGTTCAAAGGCATCACCCTCCACCTGACTGCAATGCGACCAACATTGCTGACAACGA 4322
Db 9460 ATGGCTTTAAACACATCAGCCTCCAATTAGATACAGACCACTTGACATTGCTCACCACCA 9519
Qy 4323 GAAAATTGGGGCTGCGAGCAGACGCAACAGCAGAATGGATTACAGGGTCTACATCCAGGA 4382
Db 9520 GGAGACTAGGGGCAAACCCGGAACCAACCACTGAATGGATCGTCGGAAAGACGGTCAGAA 9579
Qy 4383 ATTTTTCTGTGGGGCGAGAAGGGCTGGAGTACGTATGGGGTAACCATGAACCAGTCAGAG 4442
Db 9580 ACTTCACCGTCGACCGAGATGGCCTGGAATACATATGGGGAAATCATGAGCCAGTGAGGG 9639
Qy 4443 TCTGGGCCCAGGAGTCGGCACCAGGCGACCCACATGGATGGCCGCATGAGATCATCATCC 4502

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Db       9640 TCTATGCCCAAGAGTCAGCACCAGGAGACCCTCACGGATGGCCACACGAAATAGTACAGC 9699

Qy       4503 ACTATTATCATCGGCATCCAGTCTACACTGTCATTGTGCTGTGTGGTGTCGCTCTTGCTA 4562

Db       9700 ATTACTACCATCGCCATCCTGTGTACACCATCTTAGCCGTCGCATCAGCTACCGTGGCGA 9759

Qy       4563 TCCTGGTAGGCACTGCATCATCAGCAGCTTGCATCGCCAAAGCAAGAAGAGACTGCCTGA 4622

Db       9760 TGATGATTGGCGTAACTGTTGCAGTGTTATGTGCCTGTAAAGCGCGCCGTGAGTGCCTGA 9819

Qy       4623 CGCCATACGCGCTTGCACCGAACGCAACGGTACCCACAGCATTAGCGGTTTTGTGCTGCA 4682

Db       9820 CGCCATACGCCCTGGCCCCAAACGCCGTAATCCCAACTTCGCTGGCACTCTTGTGCTGCG 9879

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Db       9880 TTAGGTCGGCCAATGCTGAAACGTTCACCGAGACCATGAGTTACTTGTGGTCGAACAGTC 9939

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Db       9940 AGCCGTTCTTCTGGGTCCAGTTGTGCATACCTTTGGCCGCGTTCATCGTTCTAATGCGCT 9999

Qy       4803 GCTTTTCATGCTGCATGCCTTTTTTATTGGTTGCAGGCGTCTGCCTGGGGAAGGTAGACG 4862

Db      10000 ACTGCTCCTGCTGCCTGCCTTTTTTAGTGGTTGCCGGCGCCTACCTGGCGAAGGTAGACG 10059

Qy       4863 CCTTCGAACATGCGACCACTGTGCCAAATGTTCCGGGGATCCCGTATAAGGCGTTGGTCG 4922

Db      10060 CCTACGAACATGCGACCACTGTTCCAAATGTGCCACAGATACCGTATAAGGCACTTGTTG 10119

Qy       4923 AACGCGCAGGTTACGCGCCACTTAACCTGGAGATCACGGTCGTCTCATCGGAATTAACAC 4982

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Db      10180 CTTCCACCAACCAAGAGTACATTACCTGCAAATTCACCACTGTGGTCCCCTCCCCAAAAA 10239

Qy       5043 TTAAATGCTGCGGGTCCCTCGAGTGCAAGGCATCCTCAAAGGCGGATTACACATGCCGCG 5102

Db      10240 TCAAATGCTGCGGCTCCTTGGAATGTCAGCCGGCCGCTCATGCAGACTATACCTGCAAGG 10299

Qy       5103 TTTTTGGCGGTGTGTACCCTTTCATGTGGGGAGGCGCACAATGCTTCTGTGACAGTGAGA 5162

Db      10300 TCTTCGGAGGGGTCTACCCCTTTATGTGGGGAGGAGCGCAATGTTTTTGCGACAGTGAGA 10359

Qy       5163 ACACACAACTGAGTGAGGCGTACGTCGAGTTCGCTCCAGACTGCACTATAGATCACGCAG 5222

Db      10360 ACAGCCAGATGAGTGAGGCGTACGTCGAATTGTCAGCAGATTGCGCGTCTGACCACGCGC 10419

Qy       5223 TCGCACTAAAAGTTCACACAGCTGCTCTGAAAGTCGGCCTGCGTATAGTATACGGCAACA 5282

Db      10420 AGGCGATTAAGGTGCACACTGCCGCGATGAAAGTAGGACTGCGTATAGTGTACGGGAACA 10479

Qy       5283 CCACCGCGCACCTGGATACGTTTGTCAATGGCGTCACGCCAGGTTCCTCACGGGACCTGA 5342

Db      10480 CTACCAGTTTCCTAGATGTGTACGTGAACGGAGTCACACCAGGAACGTCTAAAGACTTGA 10539

Qy       5343 AGGTCATAGCAGGGCCGATATCAGCCGCTTTTTCACCCTTTGACCATAAGGTCGTCATCA 5402

Db      10540 AAGTCATAGCTGGACCAATTTCAGCATCGTTTACGCCATTCGATCATAAGGTCGTTATCC 10599

Qy       5403 GAAAGGGGCTTGTTTACAACTACGACTTCCCTGAGTATGGAGCTATGAAACCAGGAGCGT 5462

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Qy       5463 TCGGCGATATTCAAGCATCCTCGCTTGATGCTACAGACATAGTAGCCCGCACTGACATAC 5522

Db      10660 TCGGAGACATTCAAGCTACCTCCTTGACTAGCAAGGATCTCATCGCCAGCACAGACATTA 10719

Qy       5523 GGCTGCTGAAGCCTTCTGTCAAGAACATCCACGTCCCCTACACCCAAGCAGTATCAGGGT 5582

Db      10720 GGCTACTCAAGCCTTCCGCCAAGAACGTGCATGTCCCGTACACGCAGGCCGCATCAGGAT 10779

Qy       5583 ATGAAATGTGGAAGAACAACTCAGGACGACCCCTGCAAGAAACAGCACCATTTGGATGTA 5642

Db      10780 TTGAGATGTGGAAAAACAACTCAGGCCGCCCACTGCAGGAAACCGCACCTTTCGGGTGTA 10839

Qy       5643 AAATTGAAGTGGAGCCTCTGCGAGCGTCTAACTGTGCTTACGGGCACATCCCTATCTCGA 5702

Db      10840 AGATTGCAGTAAATCCGCTCCGAGCGGTGGACTGTTCATACGGGAACATTCCCATTTCTA 10899

Qy       5703 TTGACATCCCTGATGCAGCTTTTGTGAGATCATCAGAATCACCAACAATTTTAGAAGTTA 5762

Db      10900 TTGACATCCCGAACGCTGCCTTTATCAGGACATCAGATGCACCACTGGTCTCAACAGTCA 10959

Qy       5763 GCTGCACAGTAGCAGACTGCATTTATTCTGCAGACTTTGGTGGTTCTCTAACATTACAGT 5822

Db      10960 AATGTGAAGTCAGTGAGTGCACTTATTCAGCAGACTTCGGCGGGATGGCCACCCTGCAGT 11019

Qy       5823 ACAAAGCTGACAGGGAGGGACATTGTCCAGTTCACTCCCACTCCACGACAGCTGTTTTGA 5882

Db      11020 ATGTATCCGACCGCGAAGGTCAATGCCCCGTACATTCGCATTCGAGCACAGCAACTCTCC 11079

Qy       5883 AGGAAGCGACCACACATGTGACTGCCGTAGGCAGCATAACACTACATTTTAGCACATCGA 5942

Db      11080 AAGAGTCGACAGTACATGTCCTGGAGAAAGGAGCGGTGACAGTACACTTTAGCACCGCGA 11139

Qy       5943 GCCCACAAGCAAATTTTATAGTTTCGCTATGCGGCAAGAAGTCCACCTGCAATGCTGAAT 6002

Db      11140 GTCCACAGGCGAACTTTATCGTATCGCTGTGTGGGAAGAAGACAACATGCAATGCAGAAT 11199

Qy       6003 GTAAACCACCGGCCGACCACATAATTGGAGAACCACATAAAGTCGACCAAGAATTCCAGG 6062

Db      11200 GTAAACCACCAGCTGACCATATCGTGAGCACCCCGCACAAAAATGACCAAGAATTTCAAG 11259

Qy       6063 CGGCAGTTTCCAAAACATCTTGGAACTGGCTGCTTGCACTGTTTGGGGGAGCATCATCCC 6122

Db      11260 CCGCCATCTCAAAAACATCATGGAGTTGGCTGTTTGCCCTTTTCGGCGGCGCCTCGTCGC 11319

Qy       6123 TCATTGTTGTAGGACTTATAGTGTTGGTCTGCAGCTCTATGCTTATAAACACACGTAGAT 6182

Db      11320 TATTAATTATAGGACTTATGATTTTTGCTTGCAGCATGATGCTGACTAGCACACGAAGAT 11379

Qy       6183 GACTGAGCGCGGACACTGA-CATAGCGGTAAAACTCGATGTACTTCCGAGGAAGCGTGGT 6241

Db      11380 GACCGCTACGCCCCAATGATCCGACCAGCAAAACTCGATGTACTTCCGAGGAACTGATGT 11439

Qy       6242 GCATAATGCCACGCGCCGCT 6261

Db      11440 GCATAATGCATCAGGCTGGT 11459
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RESULT 14
AAV70684
ID   AAV70684 standard; DNA; 16656 BP.
XX
AC   AAV70684;
XX
DT   20-MAR-2003  (updated)
DT   02-FEB-1999  (first entry)
XX
DE   Representative eukaryotic layered vector initiation system.
XX
KW   Eukaryotic layered vector initiation system;
KW   alphavirus vector construct; gene therapy; ss.
XX
OS   Synthetic.
OS   Sindbis virus.
XX
PN   US5843723-A.
XX
PD   01-DEC-1998.
XX
PF   30-OCT-1996;   96US-0739167.
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XX
PR 15-MAR-1995; 95US-0404796.
PR 15-SEP-1993; 93US-0122791.
PR 18-FEB-1994; 94US-0198450.
PR 30-NOV-1994; 94US-0348472.
PR 20-JAN-1995; 95US-0376184.
XX
PA (CHIR) CHIRON CORP.
XX
PI Belli BA, Chang SMW, Driver DA, Dubensky TW, Ibanez CE;
PI Jolly DJ, Polo JM;
XX
DR WPI; 1999-044581/04.
XX
PT Alphavirus vectors constructs containing a 5' promoter of viral cDNA
PT by in vitro transcription - used in gene therapy
XX
PS Disclosure; Fig 3A-H; 140pp; English.
XX
CC The present sequence represents a representative eukaryotic layered
CC vector initiation system derived from Sindbis. The sequence exemplifies
CC the invention. The specification describes alphavirus vector constructs.
CC These constructs comprise a promoter 5' of viral cDNA which initiates
CC the synthesis of RNA from the viral cDNA by in vitro transcription,
CC followed by a 5' sequence which initiates transcription of alphavirus
CC RNA, followed by a nucleotide sequence encoding alphavirus nonstructural
CC proteins, a viral junction region which has been inactivated such that
CC viral transcription of a subgenomic fragment is prevented, an internal
CC ribosome entry site or a sequence which promotes ribosome read through
CC between adjacent reading frames, and an alphavirus RNA polymerase
CC recognition sequence. The recombinant alphavirus vectors can be used
CC for gene therapy.
CC (Updated on 20-MAR-2003 to correct PR field.)
XX
SQ Sequence 16656 BP; 4467 A; 4349 C; 4183 G; 3657 T; 0 other;

Query Match 36.5%; Score 2369.2; DB 20; Length 16656;
Best Local Similarity 64.6%; Pred. No. 0;
Matches 3693; Conservative 0; Mismatches 1983; Indels 44; Gaps 9;

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Qy        580 ACTGACGGTATGAAGCGGGAGCGTATATTTTCTCATCGGAAACAGGCCAAGGTCACCTTC 639
              ||||||     |  |  || | ||| || || ||  |||| |||||||  || ||| | |
Db       5746 ACTGACTAACCGGGGTAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGC 5805

Qy        640 AACAGAAATCAGTACGTCAATGTAAACTACAAGAACCTATATTGGATCGGGCCGTCCATG 699
              || |||| || || |  ||     | ||   |||||| |  ||||| ||    ||||  |
Db       5806 AAAAGAAGTCCGTTCTGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGG 5865

Qy        700 AGAAGTATTACGCCCCGCGCCTCGATCTCGAAAGAGAGAAAATGTTACAGAAGAAACTGC 759
              | |    | | ||||||   |||||        | |||| ||    |  |    |     |
Db       5866 AAAGAATTCATGCCCCGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACC 5925

Qy        760 AATTATGCGCCTCTGAAGGAAATAGAAGCAGGTATCAATCACGAAAAGTAGAAAATATGA 819
              |  |      || | ||||  || | ||| |||||  || || || ||||||||||||  ||
Db       5926 AGATGATGCCCACCGAAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGA 5985

Qy        820 AAGCAATTACAGCGGAGCGACTCATTTCTGGATTGGGCACATATCTATCATCAGAAGTGA 879
              |||| || ||  | |||||||||  | || ||| |  |    |||   ||  |   ||
Db       5986 AAGCCATAACCACTGAGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAG--- 6042

Qy        880 ATCCTGTCGAGTGTTACAGAGTCAATTATCCTGTACCAATCTACTCGTCAACGGTAATTA 939
              |||      || || |  |||  |||||   |||| | |||||     |  |||
Db       6043 ATCAGCCAGAATGCTATAAGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGG 6102

Qy        940 ACAGGTTTACATCTGCAGAGGTCGCGGTTAAAACGTGCAACTTAGTTATCCAAGAGAATT 999
                |  |   |  | || || |||| ||      || |||    | | || |||||  |
Db       6103 CGAACTACTCCGATCCACAGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACT 6162

Qy       1000 ACCCTACAGTAGCCAGTTATTGTATAACAGATGAATACGATGCGTATCTTGACATGGTGG 1059
              | || ||||||||   ||||  || || || || |||||||| ||  | || |||||  |
Db       6163 ATCCGACAGTAGCATCTTATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAG 6222

Qy       1060 ACGGCGCATCGTGCTGTCTAGATACAGCCACTTTTTGTCCGGCTAAACTGAGAAGCTACC 1119
              |||| ||     ||| || ||||| || || || || || ||||| || ||||| ||||
Db       6223 ACGGGACAGTCGCCTGCCTGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACC 6282

Qy       1120 CAAAGAAGCATAGCTATTTGCAGCCAGAGATAAGATCAGCCGTCCCATCGCCTATACAGA 1179
              | || || |||   |||       ||  | ||  |    || || |||||  | || ||||
Db       6283 CGAAAAAACATGAGTATAGAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGA 6342

Qy       1180 ATACATTACAAAATGTATTGGCTGCAGCTACTAAAAGGAATTGCAACGTTACCCAAATGC 1239
              | ||  |||||||||  |   ||| || |||||||| |||||||||| || || ||||
Db       6343 ACACGCTACAAAATGTGCTCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGC 6402

Qy       1240 GAGAATTACCTGTCTTAGATTCGGCGGCATTTAATGTTGATTGTTTCAAGAAATACGCAT 1299
              | ||| | ||      | || || ||| |||| ||||| || || ||    ||||| ||||
Db       6403 GTGAACTGCCAACACTGGACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCAT 6462

Qy       1300 GCAATGATGAGTACTGGGATACCTTTCGCGATAACCCTATTCGGCTAACTACAGAGAACG 1359
              | ||||| |||||  |||||     ||         || || ||| || | || ||  |
Db       6463 GTAATGACGAGTATTGGGAGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTG 6522

Qy       1360 TTACGCAATATGTGACAAAGCTGAAAGGGCCGAAAGCAGCAGCATTGTTTGCGAATACTC 1419
              | ||   ||||||  | |  |||||||| || || || ||  || | ||||| || ||
Db       6523 TCACCGCATATGTAGCTAGACTGAAAGGCCCTAAGGCCGCCACACTATTTGCAAAGACGT 6582

Qy       1420 ATAATCTAAAACCGTTGCAGGAGATACCAATGGATCAATTCGTCATGGATCTAAAGAGAG 1479
              |||||  |    || ||||| ||  | || ||||||  |||||||||||  | || ||||
Db       6583 ATAATTTGGTCCCATTGCAAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAG 6642

Qy       1480 ATGTCAAAGTTACTCCCGGCACGAAACATACAGAGGAGCGGCCTAAGGTGCAGGTTATTC 1539
              | || |||||||| || |||||||||| ||||| ||  | || || || || || || |
Db       6643 ACGTGAAAGTTACACCAGGCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATAC 6702

Qy       1540 AGGCTGCAGATCCCCTTGCTACCGCTTACCTTTGCGGGATCCATCGGGAATTAGTCCGTA 1599
              | || ||||| ||||| || || |||||| | |||||||| || ||||||||||| ||||
Db       6703 AAGCCGCAGAACCCCTGGCGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTA 6762

Qy       1600 GACTGAATGCGGTGCTTCTGCCAAATATCCATACTCTCTTCGACATGTCAGCGGAAGATT 1659
              | || |  || ||  | || ||||| || || || || || |||||||| ||||| ||||
Db       6763 GGCTTACGGCCGTCTTGCTTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATT 6822

Qy       1660 TTGATGCGATTATTGCTGAACATTTCCACCACGGCGACCCAGTATTGGAAACGGACATCG 1719
              |||||| || || || ||||| ||| | || |||||||| ||| |||| ||||| ||||
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Qy       1720 CGTCGTTTGATAAAAGCGAAGACGACGCTATCGCCATTTCGGCGTTGATGATCCTTGAGG 1779
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Qy       1840 CTGTGCACCTACCTACAGGAACGAGGTTTAAATTTGGTGCCATGATGAAATCCGGTATGT 1899
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Qy       2020 TCGTCTCCGACACCTTGATGGCGGAGAGATGCGCCACTTGGCTGAACATGGAAGTAAAAA 2079
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Qy       2080 TTATTGATGCAGTTATTGGTATCAAAGCACCCTACTTCTGTGGGGGATTTATCCTGGTGG 2139
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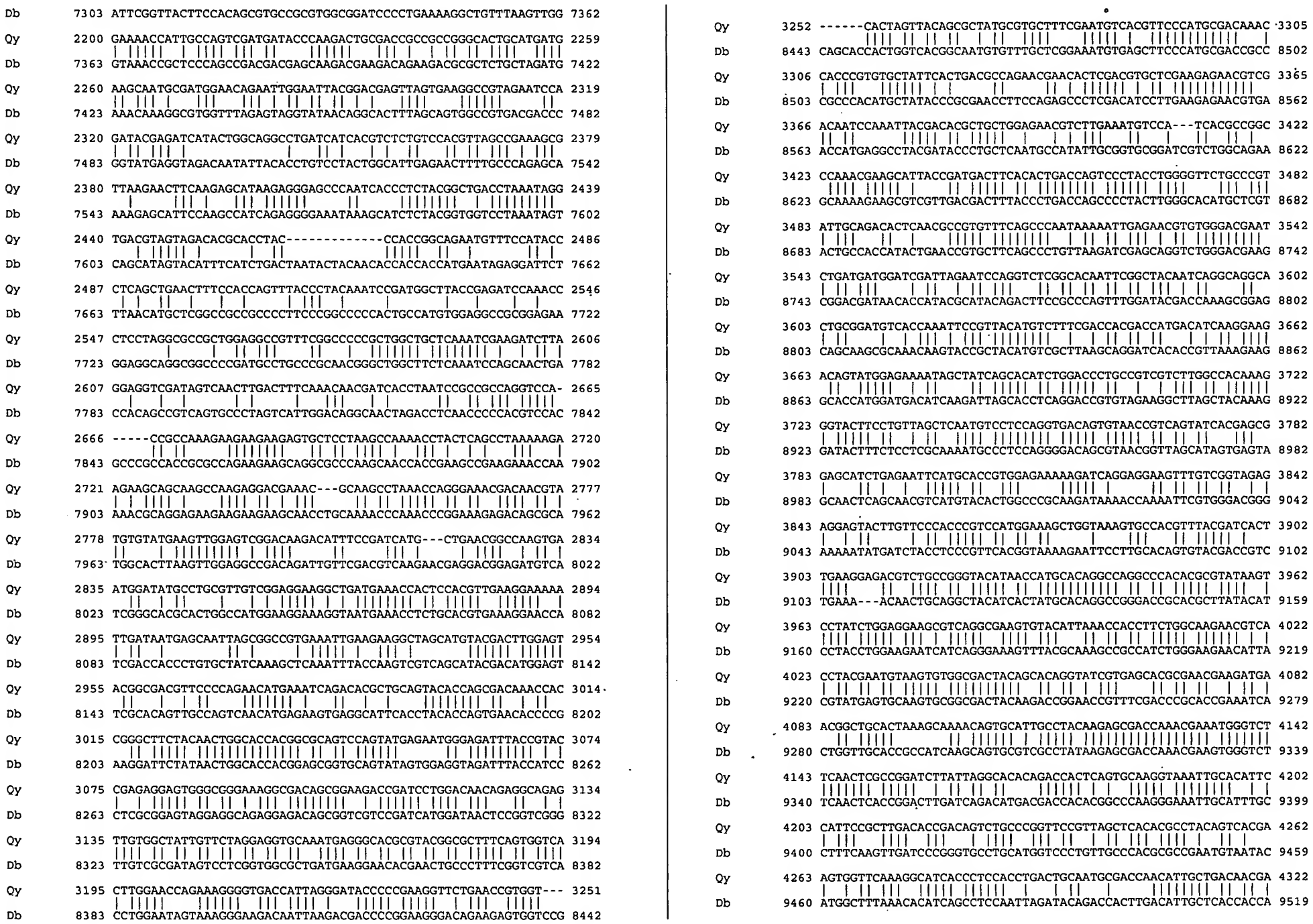

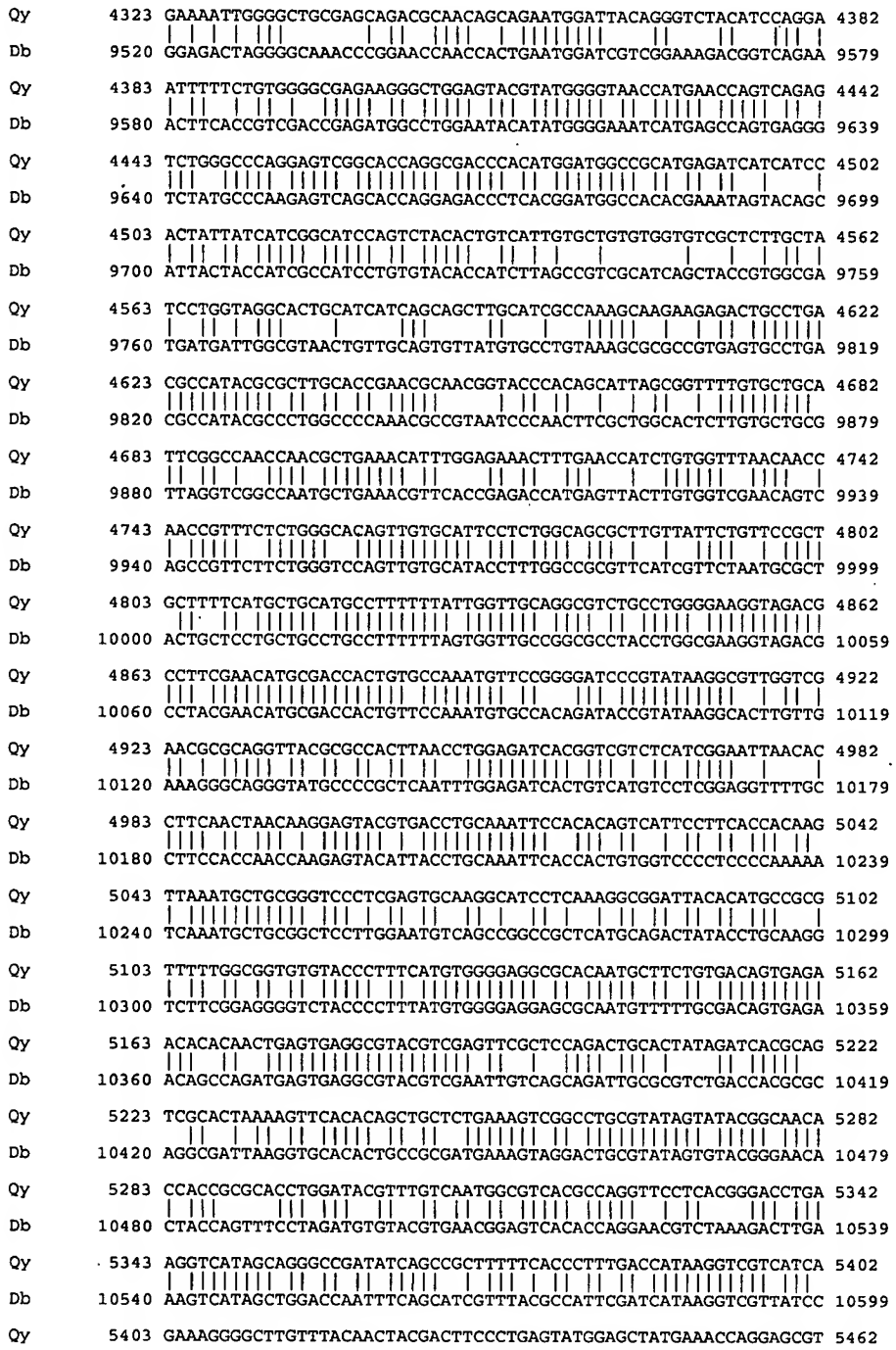

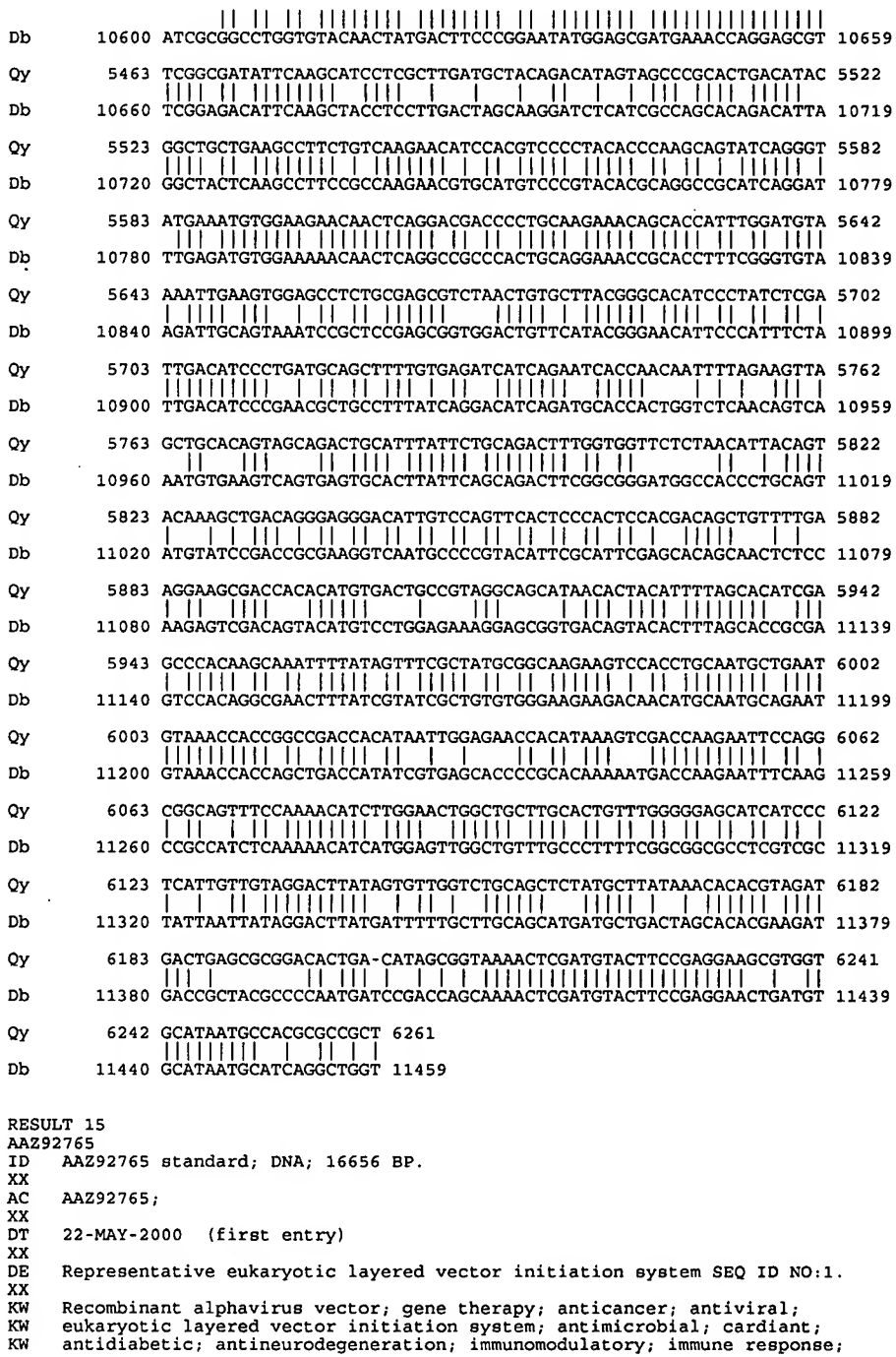

RESULT 15
AAZ92765
ID AAZ92765 standard; DNA; 16656 BP.
XX
AC AAZ92765;
XX
DT 22-MAY-2000 (first entry)
XX
DE Representative eukaryotic layered vector initiation system SEQ ID NO:1.
XX
KW Recombinant alphavirus vector; gene therapy; anticancer; antiviral;
KW eukaryotic layered vector initiation system; antimicrobial; cardiant;
KW antidiabetic; antineurodegeneration; immunomodulatory; immune response;

KW infection; melanoma; cancer; diabetes; autoimmune disorder;
KW graft versus host disease; Alzheimer's disease; heart disease;
KW haemophilia; cystic fibrosis; PCR primer; ss.
XX
OS Sindbis virus.
XX
PN US6015686-A.
XX
PD 18-JAN-2000.
XX
PF 15-MAR-1995; 95US-0404796.
XX
PR 15-SEP-1993; 93US-0122791.
PR 18-FEB-1994; 94US-0198450.
PR 30-NOV-1994; 94US-0348472.
PR 20-JAN-1995; 95US-0376184.
XX
PA (CHIR) CHIRON VIAGENE INC.
XX
PI Polo JM, Jolly DJ, Driver DA, Dubensky TW;
XX
DR WPI; 2000-181143/16.
XX
PT Eukaryotic layered vector initiation system useful for gene therapy and
PT production of recombinant protein, comprises promoter that directs
PT synthesis of RNA containing a vector construct -
XX
PS Example 2; Fig 3; 141pp; English.
XX
CC The present invention describes a eukaryotic layered vector initiation
CC system (A) comprising a eukaryotic promoter (EP), 5' of viral cDNA (I)
CC which initiates the 5' to 3' synthesis of RNA (II) from (I). (II)
CC comprises a vector construct (VC), expressing a heterologous nucleic
CC acid (III), which amplifies autonomously in a cell. (A) can have
CC anticancer, antiviral, antimicrobial, antidiabetic, immunomodulatory,
CC antineurodegeneration and cardiant activities. (A) are used to express
CC therapeutic proteins in cell cultures; in gene therapy (for humans or
CC animals), e.g. to induce a specific immune response; to inhibit
CC interaction of an agent with cellular receptors; to express a toxin;
CC to regulate the immune system or to express a replacement gene, e.g.
CC for treatment or prevention of infections (by viruses or other
CC pathogens), melanoma (or other cancers), diabetes (or other autoimmune
CC disorders), graft versus host disease, Alzheimer's disease, heart
CC disease, haemophilia, cystic fibrosis and many others; or for production
CC of packaged vector particles (also useful for gene therapy). (A) can
CC also be used to produce transgenic plants that express resistance or
CC growth promoting sequences. AAZ92765 to AAZ92891 and AAY80146 represent
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 16656 BP; 4467 A; 4349 C; 4183 G; 3657 T; 0 other;

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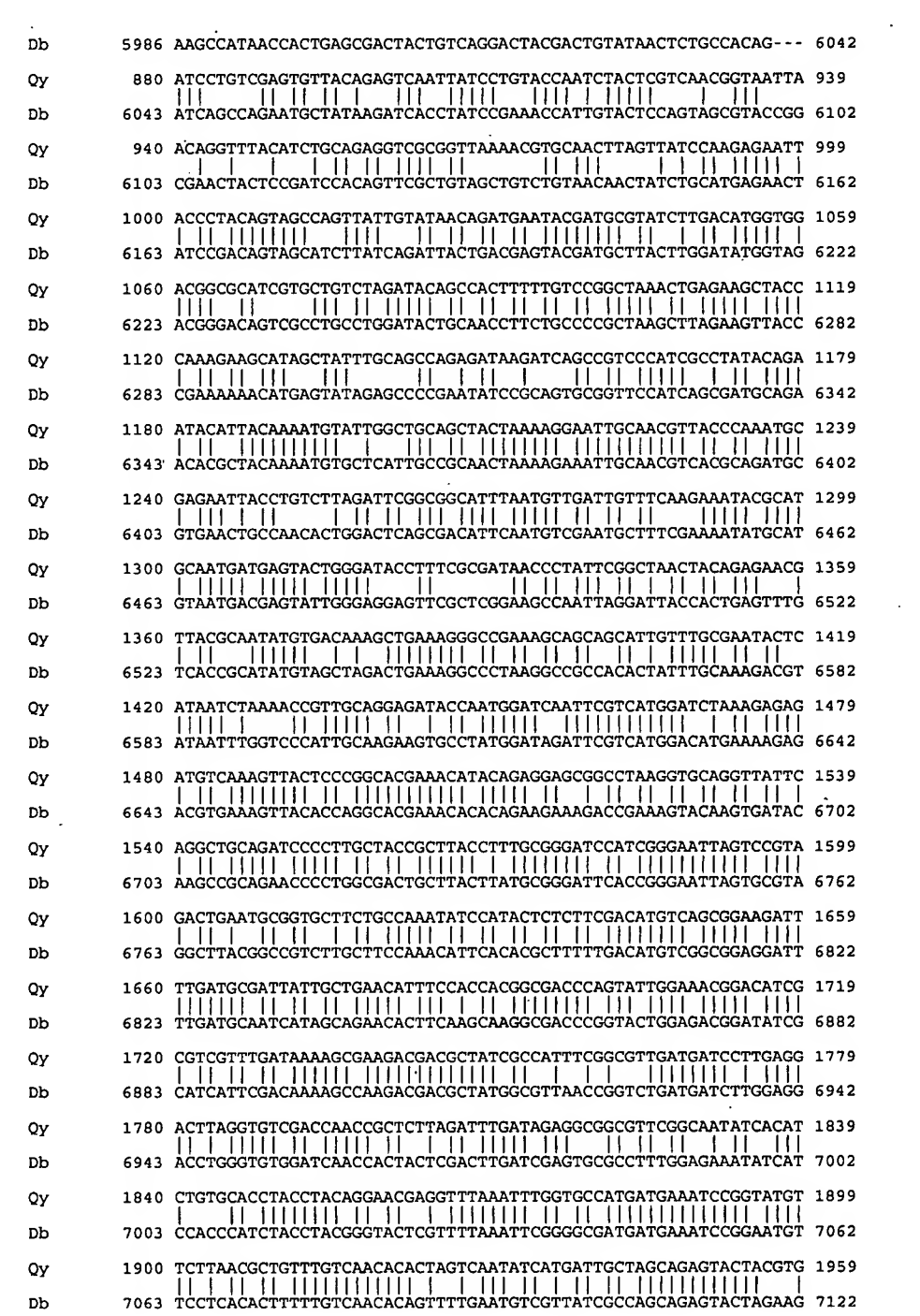

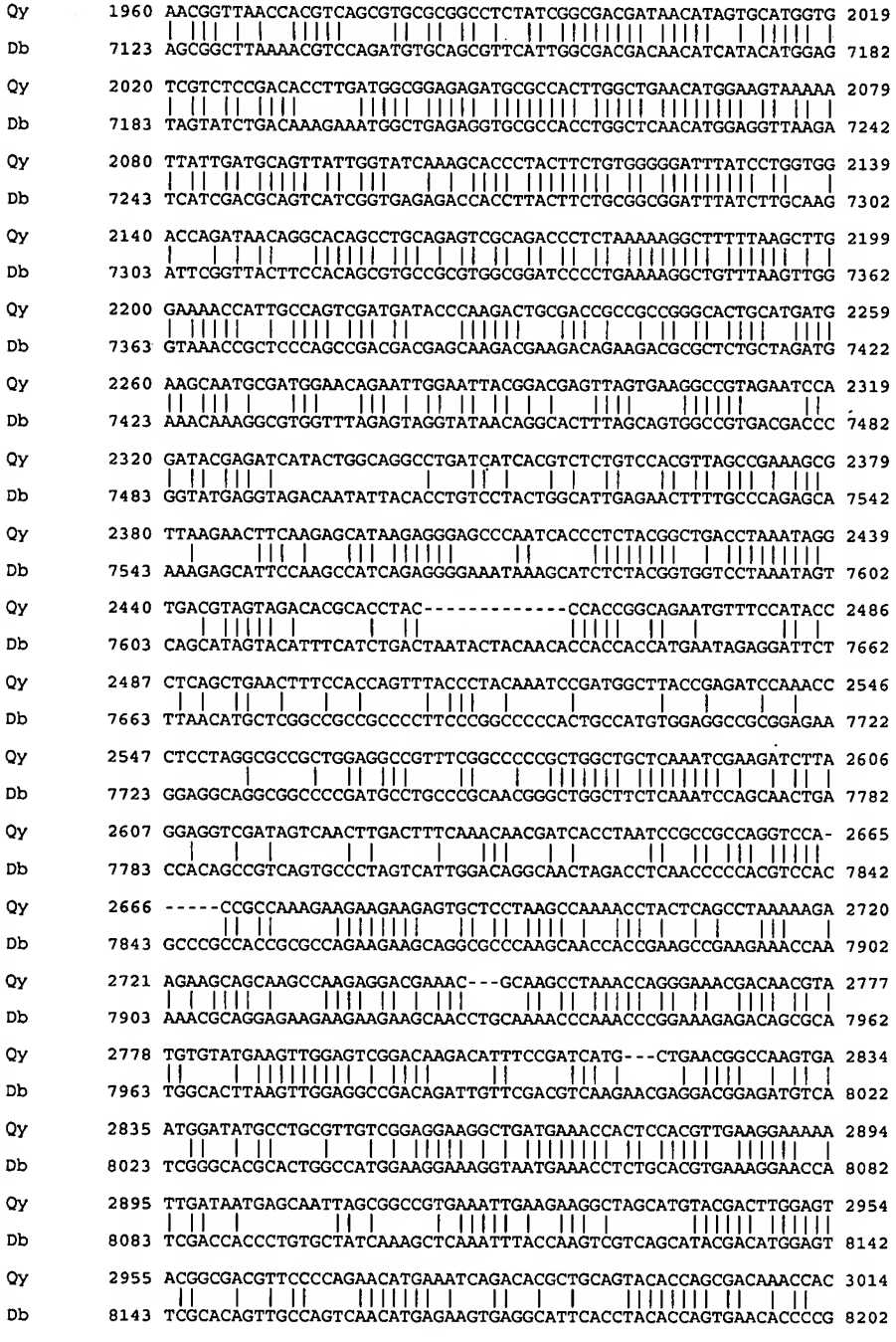
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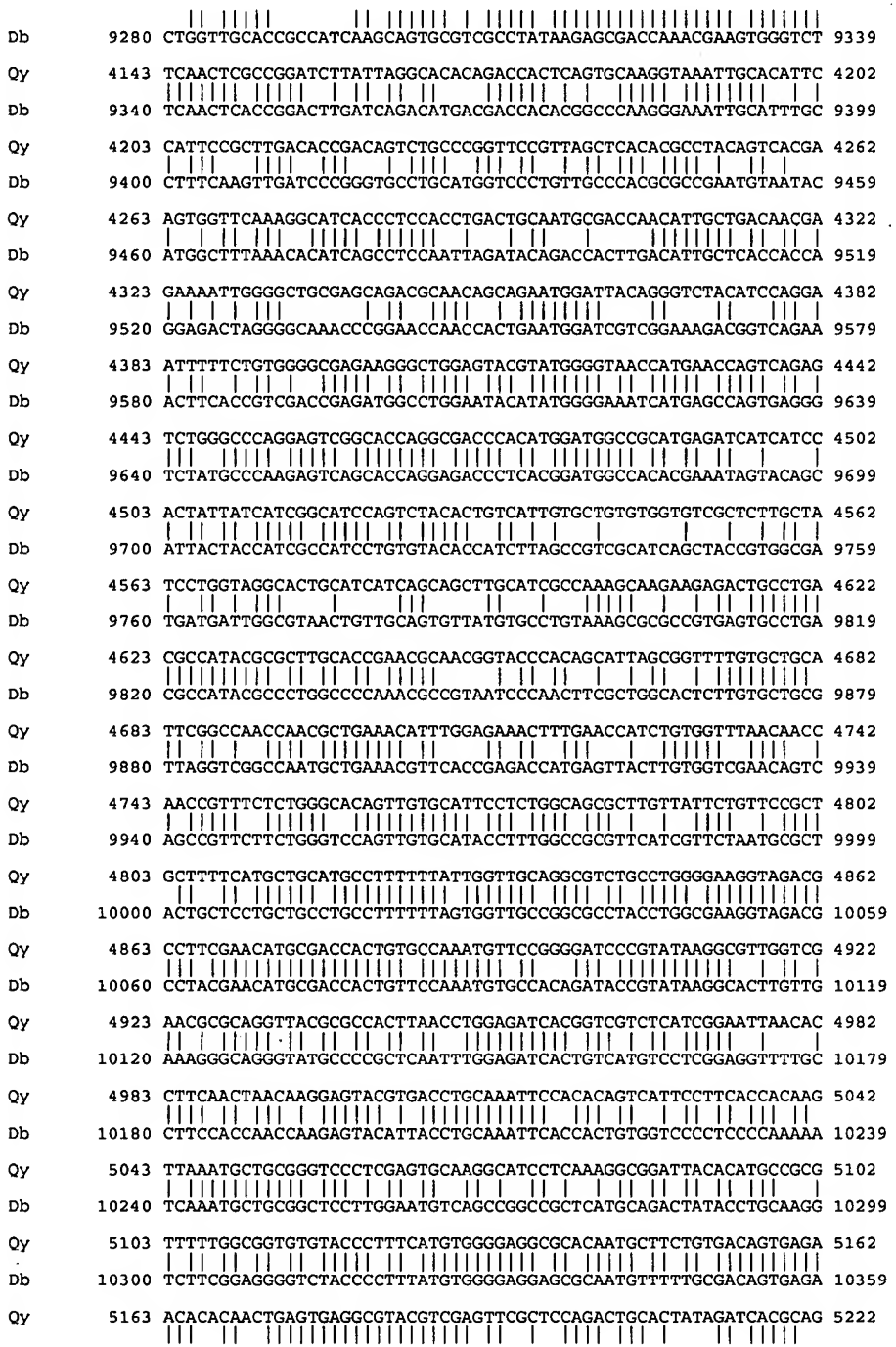
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6485	100.0	11484	12	US-10-023-649-1	Sequence 1, Appli
2	4137.2	63.8	4395	12	US-10-023-649-7	Sequence 7, Appli
3	4129.8	63.7	4150	12	US-10-023-649-5	Sequence 5, Appli
4	2380.4	36.7	11740	11	US-09-507-362-103	Sequence 103, App
5	1442.6	22.2	11517	10	US-09-901-106-1	Sequence 1, Appli
6	926.2	14.3	12523	10	US-09-991-258-1	Sequence 1, Appli
7	924.6	14.3	12379	10	US-09-991-258-14	Sequence 14, Appl
8	924.6	14.3	13584	10	US-09-991-258-17	Sequence 17, Appl
9	916.2	14.1	7479	10	US-09-991-258-2	Sequence 2, Appli
10	827.6	12.8	8000	11	US-09-507-362-102	Sequence 102, App
11	824.4	12.7	8000	11	US-09-507-362-101	Sequence 101, App
12	816	12.6	11282	10	US-09-733-042-1	Sequence 1, Appli
13	816	12.6	11282	11	US-09-275-883-1	Sequence 1, Appli
14	764	11.8	8100	12	US-09-190-246-4	Sequence 4, Appli
15	764	11.8	10610	11	US-09-994-412-3	Sequence 3, Appli
16	764	11.8	15538	12	US-09-190-246-1	Sequence 1, Appli
17	607.6	9.4	2943	10	US-09-991-258-12	Sequence 12, Appl
18	607.6	9.4	6989	10	US-09-991-258-11	Sequence 11, Appl
19	307.4	4.7	1026	10	US-09-991-258-9	Sequence 9, Appli
20	307.4	4.7	5076	10	US-09-991-258-8	Sequence 8, Appli
21	229.4	3.5	477	10	US-09-981-286A-12	Sequence 12, Appl
22	213.2	3.3	525	10	US-09-981-286A-6	Sequence 6, Appli
23	211.8	3.3	503	10	US-09-981-286A-31	Sequence 31, Appl
24	211.8	3.3	503	10	US-09-981-286A-32	Sequence 32, Appl
25	58.4	0.9	60	12	US-10-123-101-75	Sequence 75, Appl
c 26	46.8	0.7	3673778	12	US-10-312-841-1	Sequence 1, Appli
c 27	46.4	0.7	6239	12	US-10-311-455-1749	Sequence 1749, Ap
c 28	46.4	0.7	6239	12	US-10-240-453-171	Sequence 171, App
c 29	46.2	0.7	15767	12	US-10-311-455-1179	Sequence 1179, Ap
c 30	46.2	0.7	15767	12	US-10-240-485-105	Sequence 105, App
c 31	45	0.7	4057	12	US-10-240-453-261	Sequence 261, App
c 32	45	0.7	4057	14	US-10-239-676-181	Sequence 181, App
c 33	44.2	0.7	7201	12	US-10-311-455-1409	Sequence 1409, Ap
c 34	44	0.7	5930	12	US-10-311-455-1368	Sequence 1368, Ap
35	43.8	0.7	3341	10	US-09-764-868-1433	Sequence 1433, Ap
36	43.8	0.7	3342	10	US-09-764-868-1434	Sequence 1434, Ap
c 37	43.8	0.7	6640	12	US-10-311-455-1630	Sequence 1630, Ap
c 38	43.8	0.7	8238	12	US-10-311-455-1962	Sequence 1962, Ap
c 39	43.6	0.7	398	10	US-09-960-352-11930	Sequence 11930, A
c 40	43.6	0.7	271990	14	US-10-195-144-87	Sequence 87, Appl
c 41	43.4	0.7	7461	12	US-10-311-455-1757	Sequence 1757, Ap
42	43.2	0.7	11416	12	US-10-311-455-91	Sequence 91, Appl
43	43.2	0.7	3673778	12	US-10-312-841-2	Sequence 2, Appli
44	43	0.7	113515	12	US-10-311-455-2147	Sequence 2147, Ap
c 45	43	0.7	3673778	12	US-10-312-841-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-023-649-1
; Sequence 1, Application US/10023649
; Publication No. US20030143201A1
; GENERAL INFORMATION:
; APPLICANT: The Minister of National Defence, Government of Canada
; APPLICANT: Nagata, Leslie P
; APPLICANT: Wong, Jonathon P
; TITLE OF INVENTION: No. US20030143201A1el DNA-Based Vaccine Against the Encephalitis
; FILE REFERENCE: NEL-001
; CURRENT APPLICATION NUMBER: US/10/023,649
; CURRENT FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: 60/256,948
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 11484
; TYPE: DNA
; ORGANISM: Western equine encephalomyelitis virus - strain 71V-1658
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(7428)
; OTHER INFORMATION: 5' UTR <1 .. 24
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7473)..(11183)
; OTHER INFORMATION: encodes nucleocapsid, E3, E2, 6K and E1 proteins
US-10-023-649-1

Query Match 100.0%; Score 6485; DB 12; Length 11484;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      4861 CGCCTTCGAACATGCGACCACTGTGCCAAATGTTCCGGGGATCCCGTATAAGGCGTTGGT 4920
Db      9860 CGCCTTCGAACATGCGACCACTGTGCCAAATGTTCCGGGGATCCCGTATAAGGCGTTGGT 9919

Qy      4921 CGAACGCGCAGGTTACGCGCCACTTAACCTGGAGATCACGGTCGTCTCATCGGAATTAAC 4980
Db      9920 CGAACGCGCAGGTTACGCGCCACTTAACCTGGAGATCACGGTCGTCTCATCGGAATTAAC 9979

Qy      4981 ACCTTCAACTAACAAGGAGTACGTGACCTGCAAATTCCACACAGTCATTCCTTCACCACA 5040
Db      9980 ACCTTCAACTAACAAGGAGTACGTGACCTGCAAATTCCACACAGTCATTCCTTCACCACA 10039

Qy      5041 AGTTAAATGCTGCGGGTCCCTCGAGTGCAAGGCATCCTCAAAGGCGGATTACACATGCCG 5100
Db     10040 AGTTAAATGCTGCGGGTCCCTCGAGTGCAAGGCATCCTCAAAGGCGGATTACACATGCCG 10099

Qy      5101 CGTTTTTGGCGGTGTGTACCCTTTCATGTGGGGAGGCGCACAATGCTTCTGTGACAGTGA 5160
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Db     10160 GAACACACAACTGAGTGAGGCGTACGTCGAGTTCGCTCCAGACTGCACTATAGATCACGC 10219

Qy      5221 AGTCGCACTAAAAGTTCACACAGCTGCTCTGAAAGTCGGCCTGCGTATAGTATACGGCAA 5280
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Qy      5281 CACCACCGCGCACCTGGATACGTTTGTCAATGGCGTCACGCCAGGTTCCTCACGGGACCT 5340
Db     10280 CACCACCGCGCACCTGGATACGTTTGTCAATGGCGTCACGCCAGGTTCCTCACGGGACCT 10339

Qy      5341 GAAGGTCATAGCAGGGCCGATATCAGCCGCTTTTTCACCCTTTGACCATAAGGTCGTCAT 5400
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Qy      5401 CAGAAAGGGGCTTGTTTACAACTACGACTTCCCTGAGTATGGAGCTATGAAACCAGGAGC 5460
Db     10400 CAGAAAGGGGCTTGTTTACAACTACGACTTCCCTGAGTATGGAGCTATGAAACCAGGAGC 10459

Qy      5461 GTTCGGCGATATTCAAGCATCCTCGCTTGATGCTACAGACATAGTAGCCCGCACTGACAT 5520
Db     10460 GTTCGGCGATATTCAAGCATCCTCGCTTGATGCTACAGACATAGTAGCCCGCACTGACAT 10519

Qy      5521 ACGGCTGCTGAAGCCTTCTGTCAAGAACATCCACGTCCCCTACACCCAAGCAGTATCAGG 5580
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Db     10520 ACGGCTGCTGAAGCCTTCTGTCAAGAACATCCACGTCCCCTACACCCAAGCAGTATCAGG 10579

Qy      5581 GTATGAAATGTGGAAGAACAACTCAGGACGACCCCTGCAAGAAACAGCACCATTTGGATG 5640
Db     10580 GTATGAAATGTGGAAGAACAACTCAGGACGACCCCTGCAAGAAACAGCACCATTTGGATG 10639

Qy      5641 TAAAATTGAAGTGGAGCCTCTGCGAGCGTCTAACTGTGCTTACGGGCACATCCCTATCTC 5700
Db     10640 TAAAATTGAAGTGGAGCCTCTGCGAGCGTCTAACTGTGCTTACGGGCACATCCCTATCTC 10699

Qy      5701 GATTGACATCCCTGATGCAGCTTTTGTGAGATCATCAGAATCACCAACAATTTTAGAAGT 5760
Db     10700 GATTGACATCCCTGATGCAGCTTTTGTGAGATCATCAGAATCACCAACAATTTTAGAAGT 10759

Qy      5761 TAGCTGCACAGTAGCAGACTGCATTTATTCTGCAGACTTTGGTGGTTCTCTAACATTACA 5820
Db     10760 TAGCTGCACAGTAGCAGACTGCATTTATTCTGCAGACTTTGGTGGTTCTCTAACATTACA 10819

Qy      5821 GTACAAAGCTGACAGGGAGGGACATTGTCCAGTTCACTCCCACTCCACGACAGCTGTTTT 5880
Db     10820 GTACAAAGCTGACAGGGAGGGACATTGTCCAGTTCACTCCCACTCCACGACAGCTGTTTT 10879

Qy      5881 GAAGGAAGCGACCACACATGTGACTGCCGTAGGCAGCATAACACTACATTTTAGCACATC 5940
Db     10880 GAAGGAAGCGACCACACATGTGACTGCCGTAGGCAGCATAACACTACATTTTAGCACATC 10939

Qy      5941 GAGCCCACAAGCAAATTTTATAGTTTCGCTATGCGGCAAGAAGTCCACCTGCAATGCTGA 6000
Db     10940 GAGCCCACAAGCAAATTTTATAGTTTCGCTATGCGGCAAGAAGTCCACCTGCAATGCTGA 10999

Qy      6001 ATGTAAACCACCGGCCGACCACATAATTGGAGAACCACATAAAGTCGACCAAGAATTCCA 6060
Db     11000 ATGTAAACCACCGGCCGACCACATAATTGGAGAACCACATAAAGTCGACCAAGAATTCCA 11059

Qy      6061 GGCGGCAGTTTCCAAAACATCTTGGAACTGGCTGCTTGCACTGTTTGGGGGAGCATCATC 6120
Db     11060 GGCGGCAGTTTCCAAAACATCTTGGAACTGGCTGCTTGCACTGTTTGGGGGAGCATCATC 11119

Qy      6121 CCTCATTGTTGTAGGACTTATAGTGTTGGTCTGCAGCTCTATGCTTATAAACACACGTAG 6180
Db     11120 CCTCATTGTTGTAGGACTTATAGTGTTGGTCTGCAGCTCTATGCTTATAAACACACGTAG 11179

Qy      6181 ATGACTGAGCGCGGACACTGACATAGCGGTAAAACTCGATGTACTTCCGAGGAAGCGTGG 6240
Db     11180 ATGACTGAGCGCGGACACTGACATAGCGGTAAAACTCGATGTACTTCCGAGGAAGCGTGG 11239

Qy      6241 TGCATAATGCCACGCGCCGCTTGACACTAAAACTCGATGTATTTCCGAGGAAGCACAGTG 6300
Db     11240 TGCATAATGCCACGCGCCGCTTGACACTAAAACTCGATGTATTTCCGAGGAAGCACAGTG 11299

Qy      6301 CATAATGCTGTGCAGTGTCACATTAATCGTATATCACACTACATATTAACAACACTATAT 6360
Db     11300 CATAATGCTGTGCAGTGTCACATTAATCGTATATCACACTACATATTAACAACACTATAT 11359

Qy      6361 CACTTTTATGAGACTCACTATGGGTCTCTAATATACACTACACATATTTTACTTAAAAAC 6420
Db     11360 CACTTTTATGAGACTCACTATGGGTCTCTAATATACACTACACATATTTTACTTAAAAAC 11419

Qy      6421 ACTATACACACTTTATAAATTCTTTTATAATTTTTCTTTTGTTTTTATTTTGTTTTTAAA 6480
Db     11420 ACTATACACACTTTATAAATTCTTTTATAATTTTTCTTTTGTTTTTATTTTGTTTTTAAA 11479

Qy      6481 ATTTC 6485
Db     11480 ATTTC 11484
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RESULT 2
US-10-023-649-7
; Sequence 7, Application US/10023649
; Publication No. US20030143201A1
; GENERAL INFORMATION:
; APPLICANT: The Minister of National Defence, Government of Canada

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;  APPLICANT:  Nagata, Leslie P
;  APPLICANT:  Wong, Jonathon P
;  TITLE OF INVENTION: No. US20030143201A1el DNA-Based Vaccine Against the Encephalitis
;  FILE REFERENCE: NEL-001
;  CURRENT APPLICATION NUMBER: US/10/023,649
;  CURRENT FILING DATE:  2002-12-27
;  PRIOR APPLICATION NUMBER: 60/256,948
;  PRIOR FILING DATE: 2000-12-21
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 4395
;   TYPE: DNA
;   ORGANISM: Western equine encephalomyelitis virus - STRAIN 71v-1658
;   FEATURE:
;   NAME/KEY: CMV promoter
;   LOCATION: (1)..(1260)
;   OTHER INFORMATION: Pvax vector sequence: 1-196; CMV promoter: 1-115; CMV putative tr
;   OTHER INFORMATION: anscriptional start site: 125; T7 promoter: 48-167; pVAX multiclo
;   OTHER INFORMATION: ning region: 168-196; polyprotein (C-E3-E2-6K-E1): 214-4065; pcDW
;   OTHER INFORMATION: -HX45 nontranslated region: 4066-4348; pcDW-HX45 vector sequence:
;   OTHER INFORMATION: 4349-4385; pVAX vector sequence: 4386
US-10-023-649-7

  Query Match           63.8%;  Score 4137.2;  DB 12;  Length 4395;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 4139;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2324 CGAGATCATACTGGCAGGCCTGATCATCACGTCTCTGTCCACGTTAGCCGAAAGCGTTAA 2383
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Db        267 GAACTTCAAGAGCATAAGAGGGAGCCCAATCACCCTCTACGGCTGACCTAAATAGGTGAC 326

Qy       2444 GTAGTAGACACGCACCTACCCACCGGCAGAATGTTTCCATACCCTCAGCTGAACTTTCCA 2503
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
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Qy       2504 CCAGTTTACCCTACAAATCCGATGGCTTACCGAGATCCAAACCCTCCTAGGCGCCGCTGG 2563
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Db        387 CCAGTTTACCCTACAAATCCGATGGCTTACCGAGATCCAAACCCTCCTAGGCGCCGCTGG 446

Qy       2564 AGGCCGTTTCGGCCCCCGCTGGCTGCTCAAATCGAAGATCTTAGGAGGTCGATAGTCAAC 2623
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGGCCGTTTCGGCCCCCGCTGGCTGCTCAAATCGAAGATCTTAGGAGGTCGATAGTCAAC 506

Qy       2624 TTGACTTTCAAACAACGATCACCTAATCCGCCGCCAGGTCCACCGCCAAAGAAGAAGAAG 2683
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Db        507 TTGACTTTCAAACAACGATCACCTAATCCGCCGCCAGGTCCACCGCCAAAGAAGAAGAAG 566

Qy       2684 AGTGCTCCTAAGCCAAAACCTACTCAGCCTAAAAAGAAGAAGCAGCAAGCCAAGAGGACG 2743
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Db        567 AGTGCTCCTAAGCCAAAACCTACTCAGCCTAAAAAGAAGAAGCAGCAAGCCAAGAGGACG 626

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Db        627 AAACGCAAGCCTAAACCAGGGAAACGACAACGTATGTGTATGAAGTTGGAGTCGGACAAG 686

Qy       2804 ACATTTCCGATCATGCTGAACGGCCAAGTGAATGGATATGCCTGCGTTGTCGGAGGAAGG 2863
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Qy       2864 CTGATGAAACCACTCCACGTTGAAGGAAAAATTGATAATGAGCAATTAGCGGCCGTGAAA 2923
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Db        747 CTGATGAAACCACTCCACGTTGAAGGAAAAATTGATAATGAGCAATTAGCGGCCGTGAAA 806

Qy       2924 TTGAAGAAGGCTAGCATGTACGACTTGGAGTACGGCGACGTTCCCCAGAACATGAAATCA 2983
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Qy       2984 GACACGCTGCAGTACACCAGCGACAAACCACCGGGCTTCTACAACTGGCACCACGGCGCA 3043
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 GACACGCTGCAGTACACCAGCGACAAACCACCGGGCTTCTACAACTGGCACCACGGCGCA 926

Qy       3044 GTCCAGTATGAGAATGGGAGATTTACCGTACCGAGAGGAGTGGGCGGGAAAGGCGACAGC 3103
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Qy       3104 GGAAGACCGATCCTGGACAACAGAGGCAGAGTTGTGGCTATTGTTCTAGGAGGTGCAAAT 3163
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Qy       3164 GAGGGCACGCGTACGGCGCTTTCAGTGGTCACTTGGAACCAGAAAGGGGTGACCATTAGG 3223
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Db       1047 GAGGGCACGCGTACGGCGCTTTCAGTGGTCACTTGGAACCAGAAAGGGGTGACCATTAGG 1106

Qy       3224 GATACCCCCGAAGGTTCTGAACCGTGGTCACTAGTTACAGCGCTATGCGTGCTTTCGAAT 3283
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Db       1107 GATACCCCCGAAGGTTCTGAACCGTGGTCACTAGTTACAGCGCTATGCGTGCTTTCGAAT 1166

Qy       3284 GTCACGTTCCCATGCGACAAACCACCCGTGTGCTATTCACTGACGCCAGAACGAACACTC 3343
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1167 GTCACGTTCCCATGCGACAAACCACCCGTGTGCTATTCACTGACGCCAGAACGAACACTC 1226

Qy       3344 GACGTGCTCGAAGAGAACGTCGACAATCCAAATTACGACACGCTGCTGGAGAACGTCTTG 3403
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3404 AAATGTCCATCACGCCGGCCCAAACGAAGCATTACCGATGACTTCACACTGACCAGTCCC 3463
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1287 AAATGTCCATCACGCCGGCCCAAACGAAGCATTACCGATGACTTCACACTGACCAGTCCC 1346

Qy       3464 TACCTGGGGTTCTGCCCGTATTGCAGACACTCAACGCCGTGTTTCAGCCCAATAAAAATT 3523
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1347 TACCTGGGGTTCTGCCCGTATTGCAGACACTCAACGCCGTGTTTCAGCCCAATAAAAATT 1406

Qy       3524 GAGAACGTGTGGGACGAATCTGATGATGGATCGATTAGAATCCAGGTCTCGGCACAATTC 3583
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Db       1407 GAGAACGTGTGGGACGAATCTGATGATGGATCGATTAGAATCCAGGTCTCGGCACAATTC 1466

Qy       3584 GGCTACAATCAGGCAGGCACTGCGGATGTCACCAAATTCCGTTACATGTCTTTCGACCAC 3643
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1467 GGCTACAATCAGGCAGGCACTGCGGATGTCACCAAATTCCGTTACATGTCTTTCGACCAC 1526

Qy       3644 GACCATGACATCAAGGAAGACAGTATGGAGAAAATAGCTATCAGCACATCTGGACCCTGC 3703
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Qy       3704 CGTCGTCTTGGCCACAAAGGGTACTTCCTGTTAGCTCAATGTCCTCCAGGTGACAGTGTA 3763
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Db       1587 CGTCGTCTTGGCCACAAAGGGTACTTCCTGTTAGCTCAATGTCCTCCAGGTGACAGTGTA 1646

Qy       3764 ACCGTCAGTATCACGAGCGGAGCATCTGAGAATTCATGCACCGTGGAGAAAAAGATCAGG 3823
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Db       1647 ACCGTCAGTATCACGAGCGGAGCATCTGAGAATTCATGCACCGTGGAGAAAAAGATCAGG 1706

Qy       3824 AGGAAGTTTGTCGGTAGAGAGGAGTACTTGTTCCCACCCGTCCATGGAAAGCTGGTAAAG 3883
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Qy       3884 TGCCACGTTTACGATCACTTGAAGGAGACGTCTGCCGGGTACATAACCATGCACAGGCCA 3943
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Db       1767 TGCCACGTTTACGATCACTTGAAGGAGACGTCTGCCGGGTACATAACCATGCACAGGCCA 1826

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Db       1827 GGCCCACACGCGTATAAGTCCTATCTGGAGGAAGCGTCAGGCGAAGTGTACATTAAACCA 1886

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Db       1887 CCTTCTGGCAAGAACGTCACCTACGAATGTAAGTGTGGCGACTACAGCACAGGTATCGTG 1946

Qy       4064 AGCACGCGAACGAAGATGAACGGCTGCACTAAAGCAAAACAGTGCATTGCCTACAAGAGC 4123
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Db      1947 AGCACGCGAACGAAGATGAACGGCTGCACTAAAGCAAAACAGTGCATTGCCTACAAGAGC 2006
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Db      2007 GACCAAACGAAATGGGTCTTCAACTCGCCGGATCTTATTAGGCACACAGACCACTCAGTG 2066
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Db      2067 CAAGGTAAATTGCACATTCCATTCCGCTTGACACCGACAGTCTGCCCGGTTCCGTTAGCT 2126
Qy      4244 CACACGCCTACAGTCACGAAGTGGTTCAAAGGCATCACCCTCCACCTGACTGCAATGCGA 4303
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Db      2247 ACAGGGTCTACATCCAGGAATTTTTCTGTGGGGCGAGAAGGGCTGGAGTACGTATGGGGT 2306
Qy      4424 AACCATGAACCAGTCAGAGTCTGGGCCCAGGAGTCGGCACCAGGCGACCCACATGGATGG 4483
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Qy      4544 TGTGGTGTCGCTCTTGCTATCCTGGTAGGCACTGCATCATCAGCAGCTTGCATCGCCAAA 4603
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Qy      4604 GCAAGAAGAGACTGCCTGACGCCATACGCGCTTGCACCGAACGCAACGGTACCCACAGCA 4663
Db      2487 GCAAGAAGAGACTGCCTGACGCCATACGCGCTTGCACCGAACGCAACGGTACCCACAGCA 2546
Qy      4664 TTAGCGGTTTTGTGCTGCATTCGGCCAACCAACGCTGAAACATTTGGAGAAACTTTGAAC 4723
Db      2547 TTAGCGGTTTTGTGCTGCATTCGGCCAACCAACGCTGAAACATTTGGAGAAACTTTGAAC 2606
Qy      4724 CATCTGTGGTTTAACAACCAACCGTTTCTCTGGGCACAGTTGTGCATTCCTCTGGCAGCG 4783
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Qy      4844 TGCCTGGGGAAGGTAGACGCCTTCGAACATGCGACCACTGTGCCAAATGTTCCGGGGATC 4903
Db      2727 TGCCTGGGGAAGGTAGACGCCTTCGAACATGCGACCACTGTGCCAAATGTTCCGGGGATC 2786
Qy      4904 CCGTATAAGGCGTTGGTCGAACGCGCAGGTTACGCGCCACTTAACCTGGAGATCACGGTC 4963
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Qy      5084 GCGGATTACACATGCCGCGTTTTTGGCGGTGTGTACCCTTTCATGTGGGGAGGCGCACAA 5143
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Db      3147 CGTATAGTATACGGCAACACCACCGCGCACCTGGATACGTTTGTCAATGGCGTCACGCCA 3206
Qy      5324 GGTTCCTCACGGGACCTGAAGGTCATAGCAGGGCCGATATCAGCCGCTTTTTCACCCTTT 5383
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Qy      5384 GACCATAAGGTCGTCATCAGAAAGGGGCTTGTTTACAACTACGACTTCCCTGAGTATGGA 5443
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Qy      5504 GTAGCCCGCACTGACATACGGCTGCTGAAGCCTTCTGTCAAGAACATCCACGTCCCCTAC 5563
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Qy      5804 GGTTCTCTAACATTACAGTACAAAGCTGACAGGGAGGGACATTGTCCAGTTCACTCCCAC 5863
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Qy      5924 CTACATTTTAGCACATCGAGCCCACAAGCAAATTTTATAGTTTCGCTATGCGGCAAGAAG 5983
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Qy      5984 TCCACCTGCAATGCTGAATGTAAACCACCGGCCGACCACATAATTGGAGAACCACATAAA 6043
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Db      3927 GTCGACCAAGAATTCCAGGCGGCAGTTTCCAAAACATCTTGGAACTGGCTGCTTGCACTG 3986
Qy      6104 TTTGGGGGAGCATCATCCCTCATTGTTGTAGGACTTATAGTGTTGGTCTGCAGCTCTATG 6163
Db      3987 TTTGGGGGAGCATCATCCCTCATTGTTGTAGGACTTATAGTGTTGGTCTGCAGCTCTATG 4046
Qy      6164 CTTATAAACACACGTAGATGACTGAGCGCGGACACTGACATAGCGGTAAAACTCGATGTA 6223
Db      4047 CTTATAAACACACGTAGATGACTGAGCGCGGACACTGACATAGCGGTAAAACTCGATGTA 4106
Qy      6224 CTTCCGAGGAAGCGTGGTGCATAATGCCACGCGCCGCTTGACACTAAAACTCGATGTATT 6283
Db      4107 CTTCCGAGGAAGCGTGGTGCATAATGCCACGCGCCGCTTGACACTAAAACTCGATGTATT 4166
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Qy       6284 TCCGAGGAAGCACAGTGCATAATGCTGTGCAGTGTCACATTAATCGTATATCACACTACA 6343
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Db       4167 TCCGAGGAAGCACAGTGCATAATGCTGTGCAGTGTCACATTAATCGTATATCACACTACA 4226

Qy       6344 TATTAACAACACTATATCACTTTTATGAGACTCACTATGGGTCTCTAATATACACTACAC 6403
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4227 TATTAACAACACTATATCACTTTTATGAGACTCACTATGGGTCTCTAATATACACTACAC 4286

Qy       6404 ATATTTTACTTAAAAACACTATACACACTTTATAAATTCTTTTATAATTTTTCTTTTGTT 6463
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db       4287 ATATTTTACTTAAAAACACTATACACACTTTATAAATTCTTTTATAATTTTTCTTTTGCT 4346

Qy       6464 TT 6465
              ||
Db       4347 TT 4348


RESULT 3
US-10-023-649-5
; Sequence 5, Application US/10023649
; Publication No. US20030143201A1
; GENERAL INFORMATION:
;  APPLICANT: The Minister of National Defence, Government of Canada
;  APPLICANT:  Nagata, Leslie P
;  APPLICANT:  Wong, Jonathon P
;  TITLE OF INVENTION: No. US20030143201A1el DNA-Based Vaccine Against the Encephalitis
;  FILE REFERENCE: NEL-001
;  CURRENT APPLICATION NUMBER: US/10/023,649
;  CURRENT FILING DATE:  2002-12-27
;  PRIOR APPLICATION NUMBER: 60/256,948
;  PRIOR FILING DATE: 2000-12-21
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 4150
;   TYPE: DNA
;   ORGANISM: Western equine encephalomyelitis virus - strain 71V-1658
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (159)..(3869)
;   OTHER INFORMATION: vector sequence 1-9; 5' SacI primer 9-20; 3' end of NS4 gene 16-1
;   OTHER INFORMATION: 14; intragenic region 115-158; polyprotein (C-E3-E2-6K-E1) 159-38
;   OTHER INFORMATION: 56; pcDW-XH7 nontranslated region 3857-4150
US-10-023-649-5

  Query Match             63.7%;  Score 4129.8;  DB 12;  Length 4150;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 4134;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2325 GAGATCATACTGGCAGGCCTGATCATCACGTCTCTGTCCACGTTAGCCGAAAGCGTTAAG 2384
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 GAGCTCATACTGGCAGGCCTGATCATCACGTCTCTGTCCACGTTAGCCGAAAGCGTTAAG 69

Qy       2385 AACTTCAAGAGCATAAGAGGGAGCCCAATCACCCTCTACGGCTGACCTAAATAGGTGACG 2444
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 AACTTCAAGAGCATAAGAGGGAGCCCAATCACCCTCTACGGCTGACCTAAATAGGTGACG 129

Qy       2445 TAGTAGACACGCACCTACCCACCGGCAGAATGTTTCCATACCCTCAGCTGAACTTTCCAC 2504
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 TAGTAGACACGCACCTACCCACCGGCAGAATGTTTCCATACCCTCAGCTGAACTTTCCAC 189

Qy       2505 CAGTTTACCCTACAAATCCGATGGCTTACCGAGATCCAAACCCTCCTAGGCGCCGCTGGA 2564
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CAGTTTACCCTACAAATCCGATGGCTTACCGAGATCCAAACCCTCCTAGGCGCCGCTGGA 249

Qy       2565 GGCCGTTTCGGCCCCCGCTGGCTGCTCAAATCGAAGATCTTAGGAGGTCGATAGTCAACT 2624
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GGCCGTTTCGGCCCCCGCTGGCTGCTCAAATCGAAGATCTTAGGAGGTCGATAGTCAACT 309

Qy       2625 TGACTTTCAAACAACGATCACCTAATCCGCCGCCAGGTCCACCGCCAAAGAAGAAGAAGA 2684
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 TGACTTTCAAACAACGATCACCTAATCCGCCGCCAGGTCCACCGCCAAAGAAGAAGAAGA 369

Qy       2685 GTGCTCCTAAGCCAAAACCTACTCAGCCTAAAAAGAAGAAGCAGCAAGCCAAGAGGACGA 2744
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         370 GTGCTCCTAAGCCAAAACCTACTCAGCCTAAAAAGAAGAAGCAGCAAGCCAAGAGGACGA 429

Qy       2745 AACGCAAGCCTAAACCAGGGAAACGACAACGTATGTGTATGAAGTTGGAGTCGGACAAGA 2804
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         430 AACGCAAGCCTAAACCAGGGAAACGACAACGTATGTGTATGAAGTTGGAGTCGGACAAGA 489

Qy       2805 CATTTCCGATCATGCTGAACGGCCAAGTGAATGGATATGCCTGCGTTGTCGGAGGAAGGC 2864
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         490 CATTTCCGATCATGCTGAACGGCCAAGTGAATGGATATGCCTGCGTTGTCGGAGGAAGGC 549

Qy       2865 TGATGAAACCACTCCACGTTGAAGGAAAAATTGATAATGAGCAATTAGCGGCCGTGAAAT 2924
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         550 TGATGAAACCACTCCACGTTGAAGGAAAAATTGATAATGAGCAATTAGCGGCCGTGAAAT 609

Qy       2925 TGAAGAAGGCTAGCATGTACGACTTGGAGTACGGCGACGTTCCCCAGAACATGAAATCAG 2984
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         610 TGAAGAAGGCTAGCATGTACGACTTGGAGTACGGCGACGTTCCCCAGAACATGAAATCAG 669

Qy       2985 ACACGCTGCAGTACACCAGCGACAAACCACCGGGCTTCTACAACTGGCACCACGGCGCAG 3044
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         670 ACACGCTGCAGTACACCAGCGACAAACCACCGGGCTTCTACAACTGGCACCACGGCGCAG 729

Qy       3045 TCCAGTATGAGAATGGGAGATTTACCGTACCGAGAGGAGTGGGCGGGAAAGGCGACAGCG 3104
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         730 TCCAGTATGAGAATGGGAGATTTACCGTACCGAGAGGAGTGGGCGGGAAAGGCGACAGCG 789

Qy       3105 GAAGACCGATCCTGGACAACAGAGGCAGAGTTGTGGCTATTGTTCTAGGAGGTGCAAATG 3164
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         790 GAAGACCGATCCTGGACAACAGAGGCAGAGTTGTGGCTATTGTTCTAGGAGGTGCAAATG 849

Qy       3165 AGGGCACGCGTACGGCGCTTTCAGTGGTCACTTGGAACCAGAAAGGGGTGACCATTAGGG 3224
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         850 AGGGCACGCGTACGGCGCTTTCAGTGGTCACTTGGAACCAGAAAGGGGTGACCATTAGGG 909

Qy       3225 ATACCCCCGAAGGTTCTGAACCGTGGTCACTAGTTACAGCGCTATGCGTGCTTTCGAATG 3284
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         910 ATACCCCCGAAGGTTCTGAACCGTGGTCACTAGTTACAGCGCTATGCGTGCTTTCGAATG 969

Qy       3285 TCACGTTCCCATGCGACAAACCACCCGTGTGCTATTCACTGACGCCAGAACGAACACTCG 3344
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         970 TCACGTTCCCATGCGACAAACCACCCGTGTGCTATTCACTGACGCCAGAACGAACACTCG 1029

Qy       3345 ACGTGCTCGAAGAGAACGTCGACAATCCAAATTACGACACGCTGCTGGAGAACGTCTTGA 3404
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1030 ACGTGCTCGAAGAGAACGTCGACAATCCAAATTACGACACGCTGCTGGAGAACGTCTTGA 1089

Qy       3405 AATGTCCATCACGCCGGCCCAAACGAAGCATTACCGATGACTTCACACTGACCAGTCCCT 3464
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1090 AATGTCCATCACGCCGGCCCAAACGAAGCATTACCGATGACTTCACACTGACCAGTCCCT 1149

Qy       3465 ACCTGGGGTTCTGCCCGTATTGCAGACACTCAACGCCGTGTTTCAGCCCAATAAAAATTG 3524
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1150 ACCTGGGGTTCTGCCCGTATTGCAGACACTCAACGCCGTGTTTCAGCCCAATAAAAATTG 1209

Qy       3525 AGAACGTGTGGGACGAATCTGATGATGGATCGATTAGAATCCAGGTCTCGGCACAATTCG 3584
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1210 AGAACGTGTGGGACGAATCTGATGATGGATCGATTAGAATCCAGGTCTCGGCACAATTCG 1269

Qy       3585 GCTACAATCAGGCAGGCACTGCGGATGTCACCAAATTCCGTTACATGTCTTTCGACCACG 3644
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1270 GCTACAATCAGGCAGGCACTGCGGATGTCACCAAATTCCGTTACATGTCTTTCGACCACG 1329

Qy       3645 ACCATGACATCAAGGAAGACAGTATGGAGAAAATAGCTATCAGCACATCTGGACCCTGCC 3704
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1330 ACCATGACATCAAGGAAGACAGTATGGAGAAAATAGCTATCAGCACATCTGGACCCTGCC 1389

Qy       3705 GTCGTCTTGGCCACAAAGGGTACTTCCTGTTAGCTCAATGTCCTCCAGGTGACAGTGTAA 3764
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1390 GTCGTCTTGGCCACAAAGGGTACTTCCTGTTAGCTCAATGTCCTCCAGGTGACAGTGTAA 1449

Qy       3765 CCGTCAGTATCACGAGCGGAGCATCTGAGAATTCATGCACCGTGGAGAAAAAGATCAGGA 3824
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Db      1450 CCGTCAGTATCACGAGCGGAGCATCTGAGAATTCATGCACCGTGGAGAAAAAGATCAGGA 1509
Qy      3825 GGAAGTTTGTCGGTAGAGAGGAGTACTTGTTCCCACCCGTCCATGGAAAGCTGGTAAAGT 3884
Db      1510 GGAAGTTTGTCGGTAGAGAGGAGTACTTGTTCCCACCCGTCCATGGAAAGCTGGTAAAGT 1569
Qy      3885 GCCACGTTTACGATCACTTGAAGGAGACGTCTGCCGGGTACATAACCATGCACAGGCCAG 3944
Db      1570 GCCACGTTTACGATCACTTGAAGGAGACGTCTGCCGGGTACATAACCATGCACAGGCCAG 1629
Qy      3945 GCCCACACGCGTATAAGTCCTATCTGGAGGAAGCGTCAGGCGAAGTGTACATTAAACCAC 4004
Db      1630 GCCCACACGCGTATAAGTCCTATCTGGAGGAAGCGTCAGGCGAAGTGTACATTAAACCAC 1689
Qy      4005 CTTCTGGCAAGAACGTCACCTACGAATGTAAGTGTGGCGACTACAGCACAGGTATCGTGA 4064
Db      1690 CTTCTGGCAAGAACGTCACCTACGAATGTAAGTGTGGCGACTACAGCACAGGTATCGTGA 1749
Qy      4065 GCACGCGAACGAAGATGAACGGCTGCACTAAAGCAAAACAGTGCATTGCCTACAAGAGCG 4124
Db      1750 GCACGCGAACGAAGATGAACGGCTGCACTAAAGCAAAACAGTGCATTGCCTACAAGAGCG 1809
Qy      4125 ACCAAACGAAATGGGTCTTCAACTCGCCGGATCTTATTAGGCACACAGACCACTCAGTGC 4184
Db      1810 ACCAAACGAAATGGGTCTTCAACTCGCCGGATCTTATTAGGCACACAGACCACTCAGTGC 1869
Qy      4185 AAGGTAAATTGCACATTCCATTCCGCTTGACACCGACAGTCTGCCCGGTTCCGTTAGCTC 4244
Db      1870 AAGGTAAATTGCACATTCCATTCCGCTTGACACCGACAGTCTGCCCGGTTCCGTTAGCTC 1929
Qy      4245 ACACGCCTACAGTCACGAAGTGGTTCAAAGGCATCACCCTCCACCTGACTGCAATGCGAC 4304
Db      1930 ACACGCCTACAGTCACGAAGTGGTTCAAAGGCATCACCCTCCACCTGACTGCAATGCGAC 1989
Qy      4305 CAACATTGCTGACAACGAGAAAATTGGGGCTGCGAGCAGACGCAACAGCAGAATGGATTA 4364
Db      1990 CAACATTGCTGACAACGAGAAAATTGGGGCTGCGAGCAGACGCAACAGCAGAATGGATTA 2049
Qy      4365 CAGGGTCTACATCCAGGAATTTTTCTGTGGGGCGAGAAGGGCTGGAGTACGTATGGGGTA 4424
Db      2050 CAGGGTCTACATCCAGGAATTTTTCTGTGGGGCGAGAAGGGCTGGAGTACGTATGGGGTA 2109
Qy      4425 ACCATGAACCAGTCAGAGTCTGGGCCCAGGAGTCGGCACCAGGCGACCCACATGGATGGC 4484
Db      2110 ACCATGAACCAGTCAGAGTCTGGGCCCAGGAGTCGGCACCAGGCGACCCACATGGATGGC 2169
Qy      4485 CGCATGAGATCATCATCCACTATTATCATCGGCATCCAGTCTACACTGTCATTGTGCTGT 4544
Db      2170 CGCATGAGATCATCATCCACTATTATCATCGGCATCCAGTCTACACTGTCATTGTGCTGT 2229
Qy      4545 GTGGTGTCGCTCTTGCTATCCTGGTAGGCACTGCATCATCAGCAGCTTGCATCGCCAAAG 4604
Db      2230 GTGGTGTCGCTCTTGCTATCCTGGTAGGCACTGCATCATCAGCAGCTTGCATCGCCAAAG 2289
Qy      4605 CAAGAAGAGACTGCCTGACGCCATACGCGCTTGCACCGAACGCAACGGTACCCACAGCAT 4664
Db      2290 CAAGAAGAGACTGCCTGACGCCATACGCGCTTGCACCGAACGCAACGGTACCCACAGCAT 2349
Qy      4665 TAGCGGTTTTGTGCTGCATTCGGCCAACCAACGCTGAAACATTTGGAGAAACTTTGAACC 4724
Db      2350 TAGCGGTTTTGTGCTGCATTCGGCCAACCAACGCTGAAACATTTGGAGAAACTTTGAACC 2409
Qy      4725 ATCTGTGGTTTAACAACCAACCGTTTCTCTGGGCACAGTTGTGCATTCCTCTGGCAGCGC 4784
Db      2410 ATCTGTGGTTTAACAACCAACCGTTTCTCTGGGCACAGTTGTGCATTCCTCTGGCAGCGC 2469
Qy      4785 TTGTTATTCTGTTCCGCTGCTTTTCATGCTGCATGCCTTTTTTATTGGTTGCAGGCGTCT 4844
Db      2470 TTGTTATTCTGTTCCGCTGCTTTTCATGCTGCATGCCTTTTTTATTGGTTGCAGGCGTCT 2529
Qy      4845 GCCTGGGGAAGGTAGACGCCTTCGAACATGCGACCACTGTGCCAAATGTTCCGGGGATCC 4904
Db      2530 GCCTGGGGAAGGTAGACGCCTTCGAACATGCGACCACTGTGCCAAATGTTCCGGGGATCC 2589
Qy      4905 CGTATAAGGCGTTGGTCGAACGCGCAGGTTACGCGCCACTTAACCTGGAGATCACGGTCG 4964
Db      2590 CGTATAAGGCGTTGGTCGAACGCGCAGGTTACGCGCCACTTAACCTGGAGATCACGGTCG 2649
Qy      4965 TCTCATCGGAATTAACACCTTCAACTAACAAGGAGTACGTGACCTGCAAATTCCACACAG 5024
Db      2650 TCTCATCGGAATTAACACCTTCAACTAACAAGGAGTACGTGACCTGCAAATTCCACACAG 2709
Qy      5025 TCATTCCTTCACCACAAGTTAAATGCTGCGGGTCCCTCGAGTGCAAGGCATCCTCAAAGG 5084
Db      2710 TCATTCCTTCACCACAAGTTAAATGCTGCGGGTCCCTCGAGTGCAAGGCATCCTCAAAGG 2769
Qy      5085 CGGATTACACATGCCGCGTTTTTGGCGGTGTGTACCCTTTCATGTGGGGAGGCGCACAAT 5144
Db      2770 CGGATTACACATGCCGCGTTTTTGGCGGTGTGTACCCTTTCATGTGGGGAGGCGCACAAT 2829
Qy      5145 GCTTCTGTGACAGTGAGAACACACAACTGAGTGAGGCGTACGTCGAGTTCGCTCCAGACT 5204
Db      2830 GCTTCTGTGACAGTGAGAACACACAACTGAGTGAGGCGTACGTCGAGTTCGCTCCAGACT 2889
Qy      5205 GCACTATAGATCACGCAGTCGCACTAAAAGTTCACACAGCTGCTCTGAAAGTCGGCCTGC 5264
Db      2890 GCACTATAGATCACGCAGTCGCACTAAAAGTTCACACAGCTGCTCTGAAAGTCGGCCTGC 2949
Qy      5265 GTATAGTATACGGCAACACCACCGCGCACCTGGATACGTTTGTCAATGGCGTCACGCCAG 5324
Db      2950 GTATAGTATACGGCAACACCACCGCGCACCTGGATACGTTTGTCAATGGCGTCACGCCAG 3009
Qy      5325 GTTCCTCACGGGACCTGAAGGTCATAGCAGGGCCGATATCAGCCGCTTTTTCACCCTTTG 5384
Db      3010 GTTCCTCACGGGACCTGAAGGTCATAGCAGGGCCGATATCAGCCGCTTTTTCACCCTTTG 3069
Qy      5385 ACCATAAGGTCGTCATCAGAAAGGGGCTTGTTTACAACTACGACTTCCCTGAGTATGGAG 5444
Db      3070 ACCATAAGGTCGTCATCAGAAAGGGGCTTGTTTACAACTACGACTTCCCTGAGTATGGAG 3129
Qy      5445 CTATGAAACCAGGAGCGTTCGGCGATATTCAAGCATCCTCGCTTGATGCTACAGACATAG 5504
Db      3130 CTATGAAACCAGGAGCGTTCGGCGATATTCAAGCATCCTCGCTTGATGCTACAGACATAG 3189
Qy      5505 TAGCCCGCACTGACATACGGCTGCTGAAGCCTTCTGTCAAGAACATCCACGTCCCCTACA 5564
Db      3190 TAGCCCGCACTGACATACGGCTGCTGAAGCCTTCTGTCAAGAACATCCACGTCCCCTACA 3249
Qy      5565 CCCAAGCAGTATCAGGGTATGAAATGTGGAAGAACAACTCAGGACGACCCCTGCAAGAAA 5624
Db      3250 CCCAAGCAGTATCAGGGTATGAAATGTGGAAGAACAACTCAGGACGACCCCTGCAAGAAA 3309
Qy      5625 CAGCACCATTTGGATGTAAAATTGAAGTGGAGCCTCTGCGAGCGTCTAACTGTGCTTACG 5684
Db      3310 CAGCACCATTTGGATGTAAAATTGAAGTGGAGCCTCTGCGAGCGTCTAACTGTGCTTACG 3369
Qy      5685 GGCACATCCCTATCTCGATTGACATCCCTGATGCAGCTTTTGTGAGATCATCAGAATCAC 5744
Db      3370 GGCACATCCCTATCTCGATTGACATCCCTGATGCAGCTTTTGTGAGATCATCAGAATCAC 3429
Qy      5745 CAACAATTTTAGAAGTTAGCTGCACAGTAGCAGACTGCATTTATTCTGCAGACTTTGGTG 5804
Db      3430 CAACAATTTTAGAAGTTAGCTGCACAGTAGCAGACTGCATTTATTCTGCAGACTTTGGTG 3489
Qy      5805 GTTCTCTAACATTACAGTACAAAGCTGACAGGGAGGGACATTGTCCAGTTCACTCCCACT 5864
Db      3490 GTTCTCTAACATTACAGTACAAAGCTGACAGGGAGGGACATTGTCCAGTTCACTCCCACT 3549
Qy      5865 CCACGACAGCTGTTTTGAAGGAAGCGACCACACATGTGACTGCCGTAGGCAGCATAACAC 5924
Db      3550 CCACGACAGCTGTTTTGAAGGAAGCGACCACACATGTGACTGCCGTAGGCAGCATAACAC 3609
Qy      5925 TACATTTTAGCACATCGAGCCCACAAGCAAATTTTATAGTTTCGCTATGCGGCAAGAAGT 5984
Db      3610 TACATTTTAGCACATCGAGCCCACAAGCAAATTTTATAGTTTCGCTATGCGGCAAGAAGT 3669
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Qy       5985 CCACCTGCAATGCTGAATGTAAACCACCGGCCGACCACATAATTGGAGAACCACATAAAG 6044
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3670 CCACCTGCAATGCTGAATGTAAACCACCGGCCGACCACATAATTGGAGAACCACATAAAG 3729

Qy       6045 TCGACCAAGAATTCCAGGCGGCAGTTTCCAAAACATCTTGGAACTGGCTGCTTGCACTGT 6104
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3730 TCGACCAAGAATTCCAGGCGGCAGTTTCCAAAACATCTTGGAACTGGCTGCTTGCACTGT 3789

Qy       6105 TTGGGGGAGCATCATCCCTCATTGTTGTAGGACTTATAGTGTTGGTCTGCAGCTCTATGC 6164
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3790 TTGGGGGAGCATCATCCCTCATTGTTGTAGGACTTATAGTGTTGGTCTGCAGCTCTATGC 3849

Qy       6165 TTATAAACACACGTAGATGACTGAGCGCGGACACTGACATAGCGGTAAAACTCGATGTAC 6224
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3850 TTATAAACACACGTAGATGACTGAGCGCGGACACTGACATAGCGGTAAAACTCGATGTAC 3909

Qy       6225 TTCCGAGGAAGCGTGGTGCATAATGCCACGCGCCGCTTGACACTAAAACTCGATGTATTT 6284
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3910 TTCCGAGGAAGCGTGGTGCATAATGCCACGCGCCGCTTGACACTAAAACTCGATGTATTT 3969

Qy       6285 CCGAGGAAGCACAGTGCATAATGCTGTGCAGTGTCACATTAATCGTATATCACACTACAT 6344
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3970 CCGAGGAAGCACAGTGCATAATGCTGTGCAGTGTCACATTAATCGTATATCACACTACAT 4029

Qy       6345 ATTAACAACACTATATCACTTTTATGAGACTCACTATGGGTCTCTAATATACACTACACA 6404
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4030 ATTAACAACACTATATCACTTTTATGAGACTCACTATGGGTCTCTAATATACACTACACA 4089

Qy       6405 TATTTTACTTAAAAACACTATACACACTTTATAAATTCTTTTATAATTTTTCTTTTGTTT 6464
             |||||||||||||||||||||||||||||||||| | |||||||  |||| | ||
Db       4090 TATTTTACTTAAAAACACTATACACACTTTATAAATTCTCTCATAATTTCACTTTAGGTT 4149

Qy       6465 T 6465
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Db       4150 T 4150
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RESULT 4
US-09-507-362-103
; Sequence 103, Application US/09507362
; Publication No. US20030096397A1
;   GENERAL INFORMATION:
;        APPLICANT: Dubensky Jr., Thomas W.
;                   Polo, John M.
;                   Belli, Barbara A.
;                   Schlesinger, Sondra
;                   Dryga, Sergey A.
;                   Frolov, Ilya
;        TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
;                            WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
;                            SYNTHESIS
;        NUMBER OF SEQUENCES: 125
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Seed Intellectual Property Law Group PLLC
;             STREET: 701 Fifth Avenue, Suite 6300
;             CITY: Seattle
;             STATE: Washington
;             COUNTRY: USA
;             ZIP: 98104-7092
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/507,362
;             FILING DATE: 18-Feb-2000
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McMasters, David D.
;             REGISTRATION NUMBER: 33,963
;             REFERENCE/DOCKET NUMBER: 930049.457D6 /1196.011
;             TELECOMMUNICATION INFORMATION:
;                  TELEPHONE: (206) 622-4900
;                  TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 103:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 11740 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-09-507-362-103

  Query Match             36.7%;  Score 2380.4;  DB 11;  Length 11740;
  Best Local Similarity   64.6%;  Pred. No. 0;
  Matches 3693;  Conservative    0;  Mismatches 1986;  Indels   41;  Gaps    8;

Qy        580 ACTGACGGTATGAAGCGGGAGCGTATATTTTCTCATCGGAAACAGGCCAAGGTCACCTTC 639
              ||||||     |  |  || | ||| || || ||  |||| |||||||  || ||| | |
Db       5746 ACTGACTAACCGGGGTAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGC 5805

Qy        640 AACAGAAATCAGTACGTCAATGTAAACTACAAGAACCTATATTGGATCGGGCCGTCCATG 699
              || |||| || || |  ||     | ||   |||||| |  ||||| ||    ||||  |
Db       5806 AAAAGAAGTCCGTTCTGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGG 5865

Qy        700 AGAAGTATTACGCCCCGCGCCTCGATCTCGAAAGAGAGAAAATGTTACAGAAGAAACTGC 759
              | |     | | ||||||  |||||         | |||| ||     |  |      |
Db       5866 AAAGAATTCATGCCCCGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACC 5925

Qy        760 AATTATGCGCCTCTGAAGGAAATAGAAGCAGGTATCAATCACGAAAAGTAGAAAATATGA 819
              | |     || | ||||  || | ||| |||||| || || || ||||||||||||  ||
Db       5926 AGATGATGCCCACCGAAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGA 5985

Qy        820 AAGCAATTACAGCGGAGCGACTCATTTCTGGATTGGGCACATATCTATCATCAGAAGTGA 879
              |||| || ||  | ||||||||  | || ||| |  |  ||| || |  ||
Db       5986 AAGCCATAACCACTGAGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAG--- 6042

Qy        880 ATCCTGTCGAGTGTTACAGAGTCAATTATCCTGTACCAATCTACTCGTCAACGGTAATTA 939
              |||      || || || |   |||  |||||  |||| | |||||    |  |||
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Qy        940 ACAGGTTTACATCTGCAGAGGTCGCGGTTAAAACGTGCAACTTAGTTATCCAAGAGAATT 999
                |  |   |  | || || |||| ||        || |||     | | || ||||| |
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Qy       1000 ACCCTACAGTAGCCAGTTATTGTATAACAGATGAATACGATGCGTATCTTGACATGGTGG 1059
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Qy       1060 ACGGCGCATCGTGCTGTCTAGATACAGCCACTTTTTGTCCGGCTAAACTGAGAAGCTACC 1119
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Qy       1240 GAGAATTACCTGTCTTAGATTCGGCGGCATTTAATGTTGATTGTTTCAAGAAATACGCAT 1299
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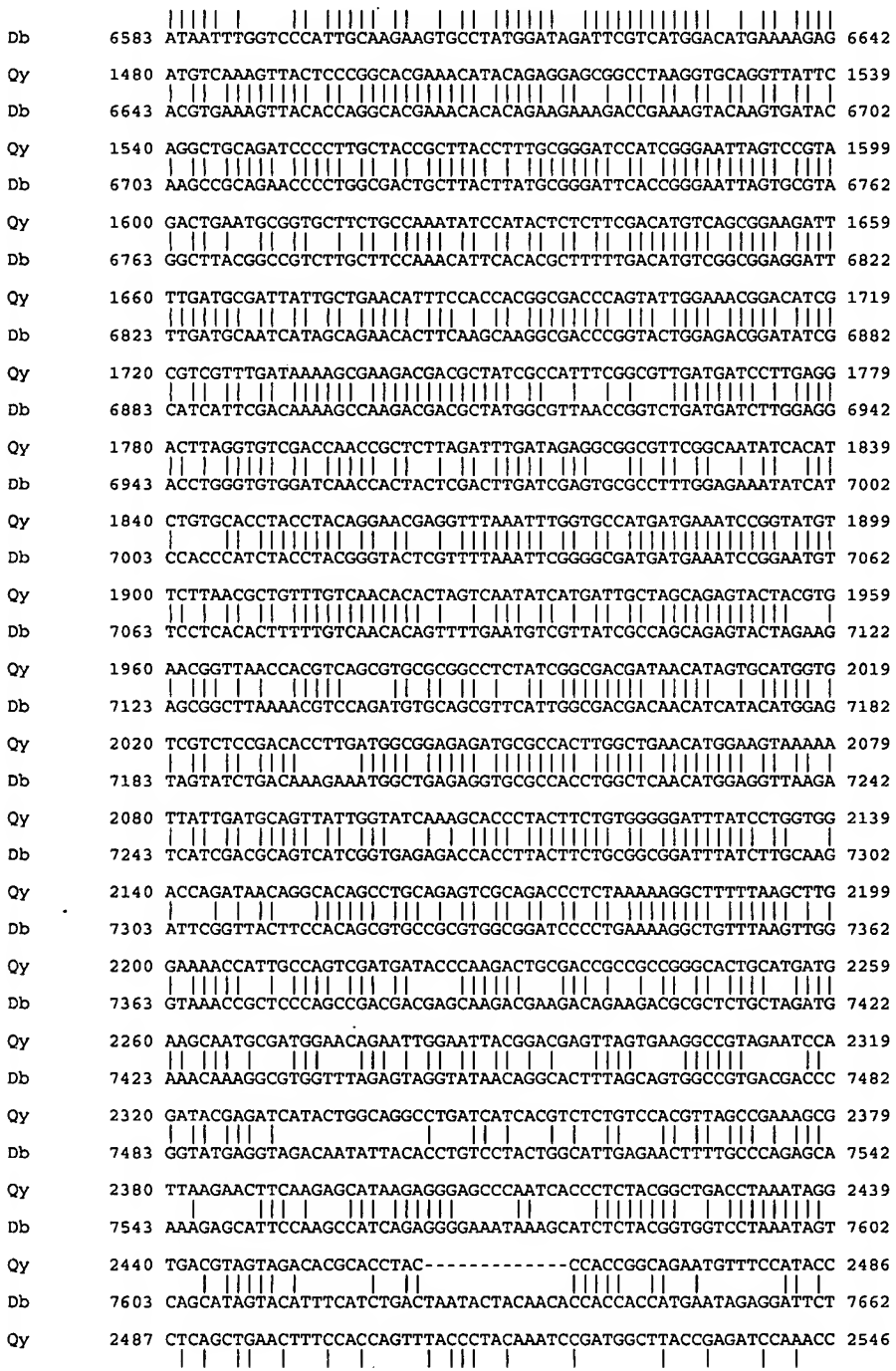

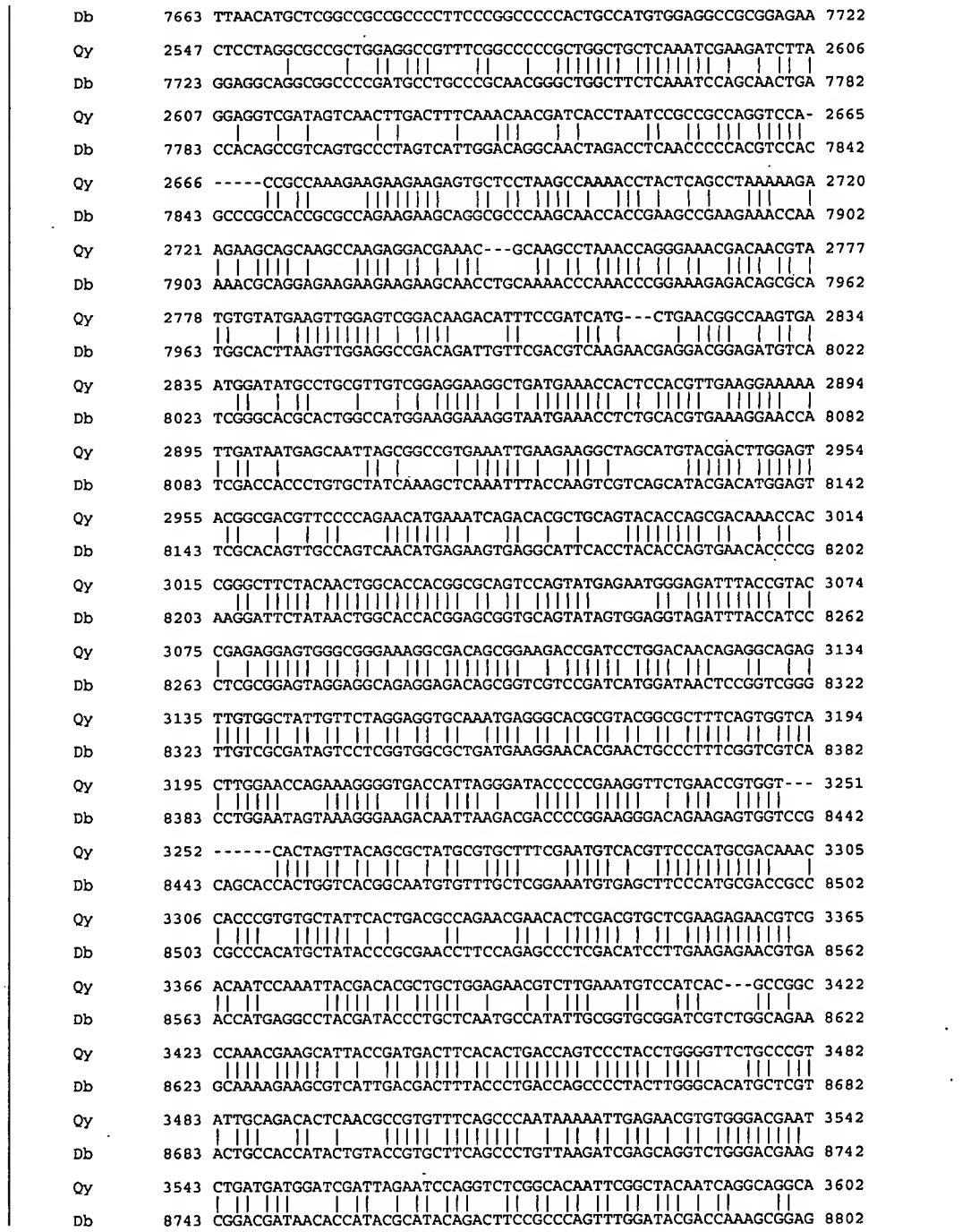

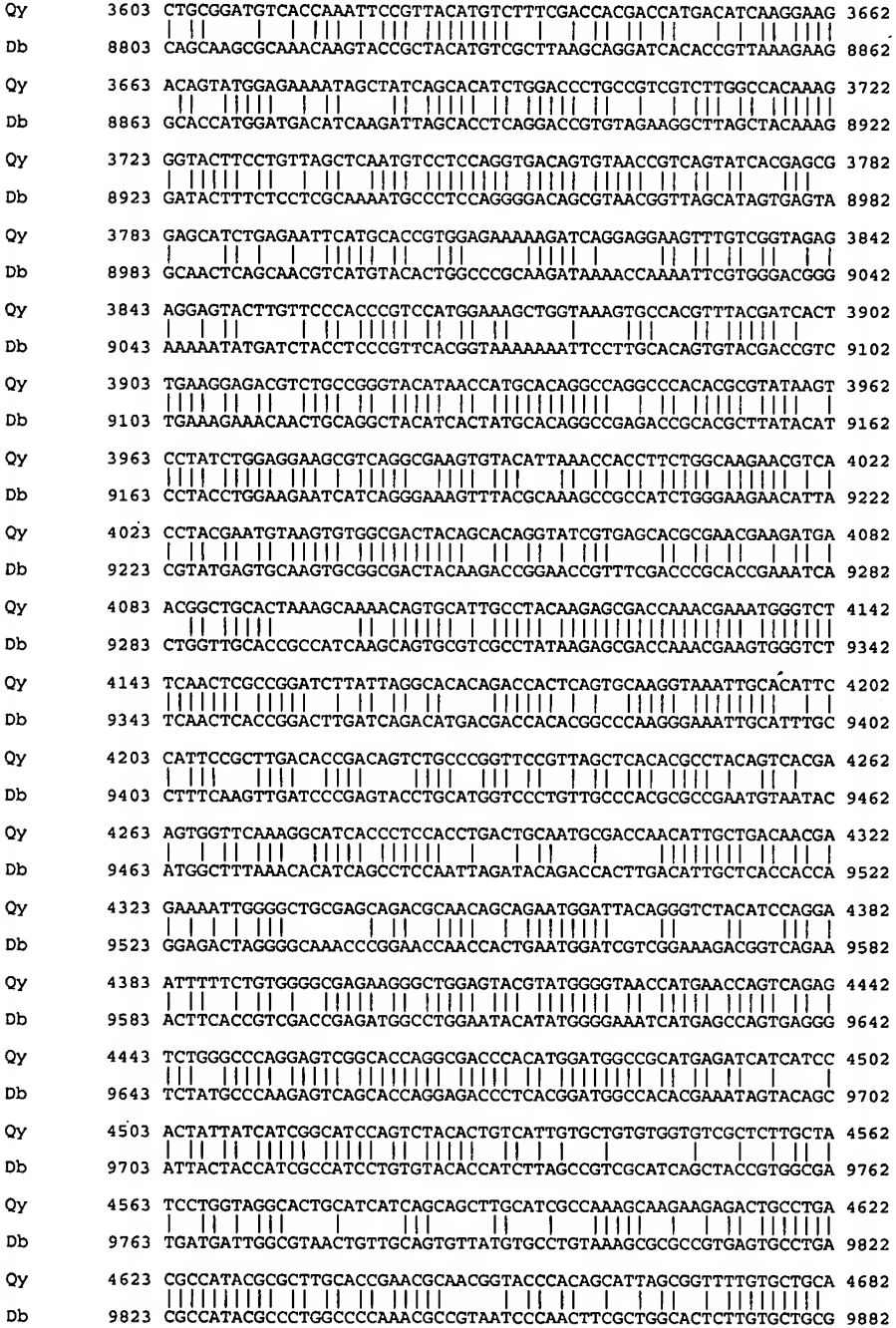

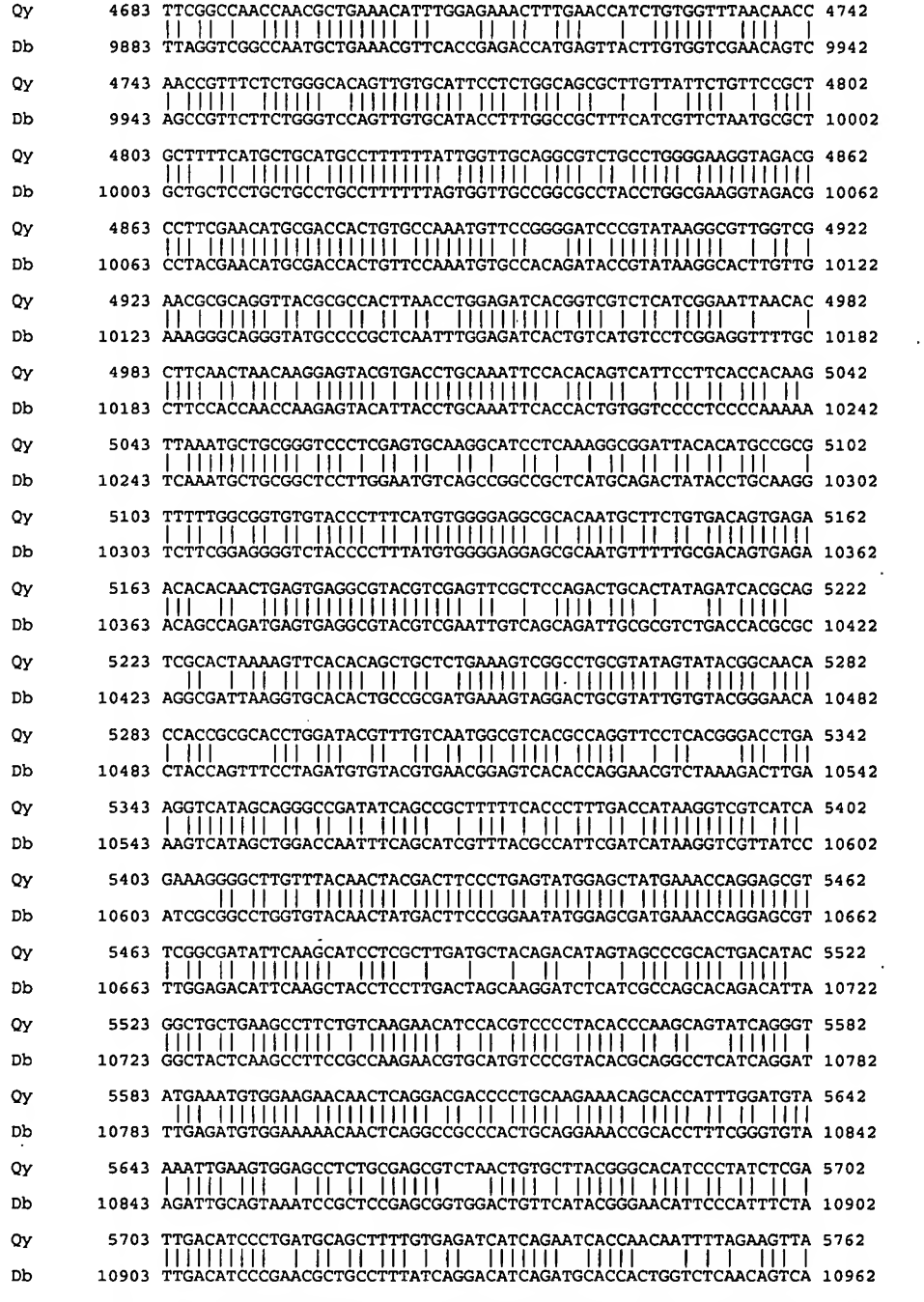

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Db      11083 AAGAGTCGACAGTACATGTCCTGGAGAAAGGAGCGGTGACAGTACACTTTAGCACCGCGA 11142

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Qy       6242 GCATAATGCCACGCGCCGCT 6261

Db      11443 GCATAATGCATCAGGCTGGT 11462


RESULT 5
US-09-901-106-1
; Sequence 1, Application US/09901106
; Patent No. US20020151067A1
;   GENERAL INFORMATION:
;        APPLICANT: Garoff, Henrik
;                   Liljestrom, Peter
;        TITLE OF INVENTION: DNA Expression Systems Based on
;                            Alphaviruses
;        NUMBER OF SEQUENCES: 27
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Birch, Stewart, Kolasch & Birch
;             STREET: P.O. Box 747
;             CITY: Falls Church
;             STATE: Virginia
;             COUNTRY: USA
;             ZIP: 22040-0747
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/901,106
;             FILING DATE: 10-Jul-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/07/920,281C
;             FILING DATE: 13-AUG-1992
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Murphy Jr., Gerald M.
;             REGISTRATION NUMBER: 28,977
;             REFERENCE/DOCKET NUMBER: 828-103P
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 703-241-1300
;             TELEFAX: 703-241-2848
;             TELEX: 248345
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 11517 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: RNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        ORIGINAL SOURCE:
;             ORGANISM: Semliki Forest Virus
;        FEATURE:
;             NAME/KEY:  -
;             LOCATION:  1..11517
;             OTHER INFORMATION:  /label= genome
;             /note= "Semliki Forest Virus complete nucleotide
;             sequence, presented as a cloned DNA sequence; see
;             Figure 5."
;        FEATURE:
;             NAME/KEY:  CDS
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;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-901-106-1

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  Matches 3130;  Conservative    0;  Mismatches 2409;  Indels  102;  Gaps   14;

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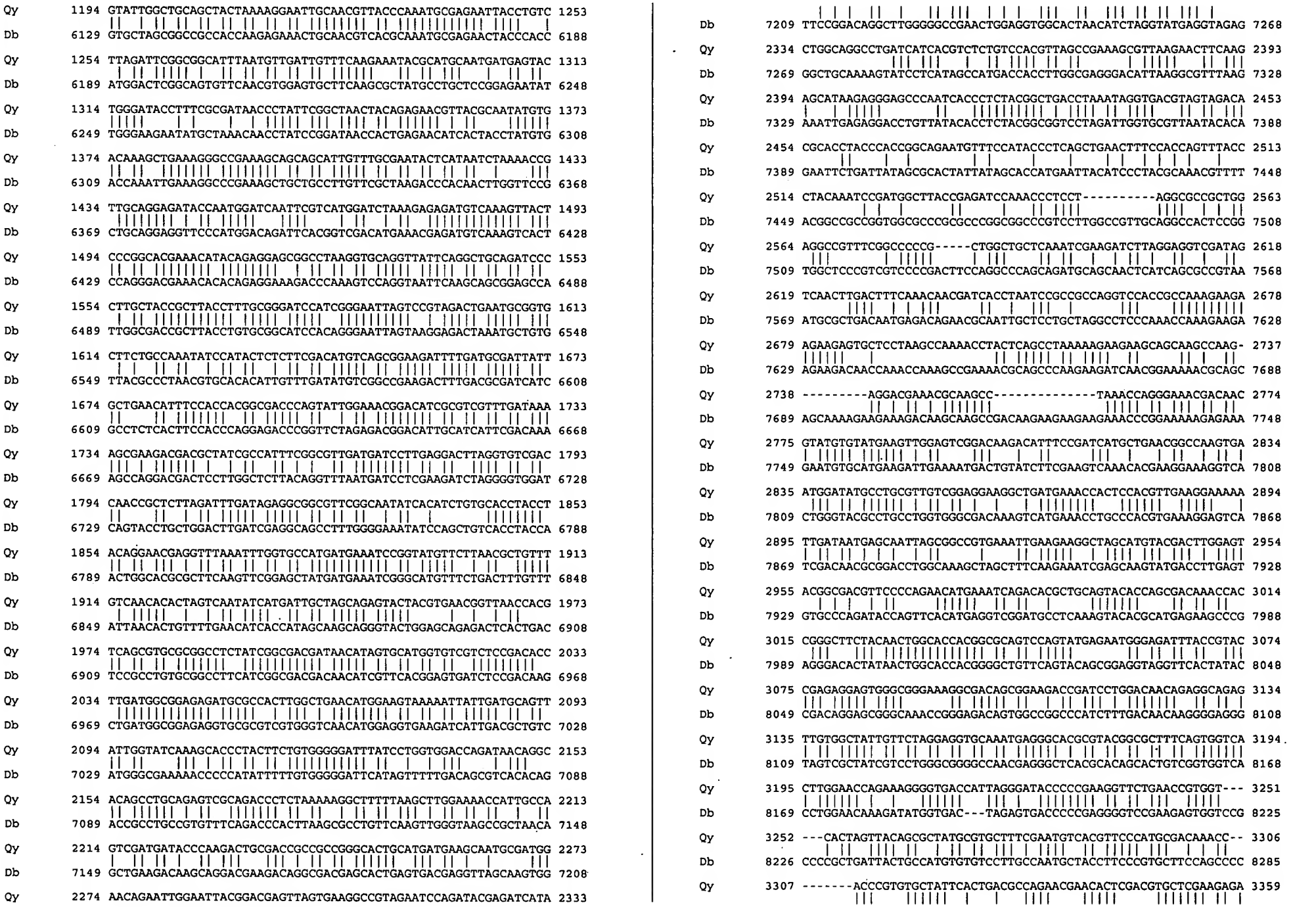

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Qy       6150 T 6150
Db      11151 T 11151
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US-09-991-258-1
; Sequence 1, Application US/09991258
; Patent No. US20020141975A1
; GENERAL INFORMATION:
;  APPLICANT: Olmsted, Robert
;  APPLICANT:  Keith, Paula
;  APPLICANT:  Dryga, Sergey
;  APPLICANT:  Caley, Ian
;  APPLICANT:  Maughan, Maureen
;  APPLICANT:  Johnston, Robert
;  APPLICANT:  Davis, Nancy
;  APPLICANT:  Swanstrom, Ronald
;  TITLE OF INVENTION: ALPHAVIRUS VECTORS AND VIROSOMES WITH MODIFIED HIV GENES FOR USE
;  TITLE OF INVENTION:  VACCINES
;  FILE REFERENCE: 01113.0001U3
;  CURRENT APPLICATION NUMBER: US/09/991,258
;  CURRENT FILING DATE:  2001-11-16
;  PRIOR APPLICATION NUMBER: 09/902,537
;  PRIOR FILING DATE: 2001-07-09
;  PRIOR APPLICATION NUMBER: 60/216,995
;  PRIOR FILING DATE: 2000-07-07
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 1
;   LENGTH: 12523
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence; No. US20020141975A1e =
;   OTHER INFORMATION: synthetic construct
US-09-991-258-1

  Query Match           14.3%;  Score 926.2;  DB 10;  Length 12523;
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  Matches 1320;  Conservative    0;  Mismatches  613;  Indels    6;  Gaps    2;

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Db       5677 A---ACAATGACGGTTTGATGCGGGTGCATACATCTTTTCCTCCGACACCGGTCAAGGGC 5733

Qy        634 ACCTTCAACAGAAATCAGTACGTCAATGTAAACTACAAGAACCTATATTGGATCGGGCCG 693
Db       5734 ATTTACAACAAAAATCAGTAAGGCAAACGGTGCTATCCGAAGTGGTGTTGGAGAGGACCG 5793

Qy        694 TCCATGAGAAGTATTACGCCCCGCGCCTCGATCTCGAAAGAGAGAAAATGTTACAGAAGA 753
Db       5794 AATTGGAGATTTCGTATGCCCCGCGCCTCGACCAAGAAAAAGAAGAATTACTACGCAAGA 5853

Qy        754 AACTGCAATTATGCGCCTCTGAAGGAAATAGAAGCAGGTATCAATCACGAAAAGTAGAAA 813
Db       5854 AATTACAGTTAAATCCCACACCTGCTAACAGAAGCAGATACCAGTCCAGGAAGGTGGAGA 5913

Qy        814 ATATGAAAGCAATTACAGCGGAGCGACTCATTTCTGGATTGGGCACATATCTATCATCAG 873
Db       5914 ACATGAAAGCCATAACAGCTAGACGTATTCTGCAAGGCCTAGGGCATTATTTGAAGGCAG 5973

Qy        874 AAGTGAATCCTGTCGAGTGTTACAGAGTCAATTATCCTGTACCAATCTACTCGTCAACGG 933
Db       5974 AAGGAAA---AGTGGAGTGCTACCGAACCCTGCATCCTGTTCCTTTGTATTCATCTAGTG 6030

Qy        934 TAATTAACAGGTTTACATCTGCAGAGGTCGCGGTTAAAACGTGCAACTTAGTTATCCAAG 993
Db       6031 TGAACCGTGCCTTTTCAAGCCCCAAGGTCGCAGTGGAAGCCTGTAACGCCATGTTGAAAG 6090

Qy        994 AGAATTACCCTACAGTAGCCAGTTATTGTATAACAGATGAATACGATGCGTATCTTGACA 1053
Db       6091 AGAACTTTCCGACTGTGGCTTCTTACTGTATTATTCCAGAGTACGATGCCTATTTGGACA 6150

Qy       1054 TGGTGGACGGCGCATCGTGCTGTCTAGATACAGCCACTTTTTGTCCGGCTAAACTGAGAA 1113
Db       6151 TGGTTGACGGAGCTTCATGCTGCTTAGACACTGCCAGTTTTTGCCCTGCAAAGCTGCGCA 6210

Qy       1114 GCTACCCAAAGAAGCATAGCTATTTGCAGCCAGAGATAAGATCAGCCGTCCCATCGCCTA 1173
Db       6211 GCTTTCCAAAGAAACACTCCTATTTGGAACCCACAATACGATCGGCAGTGCCTTCAGCGA 6270

Qy       1174 TACAGAATACATTACAAAATGTATTGGCTGCAGCTACTAAAAGGAATTGCAACGTTACCC 1233
Db       6271 TCCAGAACACGCTCCAGAACGTCCTGGCAGCTGCCACAAAAAGAAATTGCAATGTCACGC 6330

Qy       1234 AAATGCGAGAATTACCTGTCTTAGATTCGGCGGCATTTAATGTTGATTGTTTCAAGAAAT 1293
Db       6331 AAATGAGAGAATTGCCCGTATTGGATTCGGCGGCCTTTAATGTGGAATGCTTCAAGAAAT 6390

Qy       1294 ACGCATGCAATGATGAGTACTGGGATACCTTTCGCGATAACCCTATTCGGCTAACTACAG 1353
Db       6391 ATGCGTGTAATAATGAATATTGGGAAACGTTTAAAGAAAACCCCATCAGGCTTACTGAAG 6450

Qy       1354 AGAACGTTACGCAATATGTGACAAAGCTGAAAGGGCCGAAAGCAGCAGCATTGTTTGCGA 1413
Db       6451 AAAACGTGGTAAATTACATTACCAAATTAAAAGGACCAAAAGCTGCTGCTCTTTTTGCGA 6510
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Qy       1414 ATACTCATAATCTAAAACCGTTGCAGGAGATACCAATGGATCAATTCGTCATGGATCTAA 1473
Db       6511 AGACACATAATTTGAATATGTTGCAGGACATACCAATGGACAGGTTTGTAATGGACTTAA 6570

Qy       1474 AGAGAGATGTCAAAGTTACTCCCGGCACGAAACATACAGAGGAGCGGCCTAAGGTGCAGG 1533
Db       6571 AGAGAGACGTGAAAGTGACTCCAGGAACAAAACATACTGAAGAACGGCCCAAGGTACAGG 6630

Qy       1534 TTATTCAGGCTGCAGATCCCCTTGCTACCGCTTACCTTTGCGGGATCCATCGGGAATTAG 1593
Db       6631 TGATCCAGGCTGCCGATCCGCTAGCAACAGCGTATCTGTGCGGAATCCACCGAGAGCTGG 6690

Qy       1594 TCCGTAGACTGAATGCGGTGCTTCTGCCAAATATCCATACTCTCTTCGACATGTCAGCGG 1653
Db       6691 TTAGGAGATTAAATGCGGTCCTGCTTCCGAACATTCATACACTGTTTGATATGTCGGCTG 6750

Qy       1654 AAGATTTTGATGCGATTATTGCTGAACATTTCCACCACGGCGACCCAGTATTGGAAACGG 1713
Db       6751 AAGACTTTGACGCTATTATAGCCGAGCACTTCCAGCCTGGGGATTGTGTTCTGGAAACTG 6810

Qy       1714 ACATCGCGTCGTTTGATAAAAGCGAAGACGACGCTATCGCCATTTCGGCGTTGATGATCC 1773
Db       6811 ACATCGCGTCGTTTGATAAAAGTGAGGACGACGCCATGGCTCTGACCGCGTTAATGATTC 6870

Qy       1774 TTGAGGACTTAGGTGTCGACCAACCGCTCTTAGATTTGATAGAGGCGGCGTTCGGCAATA 1833
Db       6871 TGGAAGACTTAGGTGTGGACGCAGAGCTGTTGACGCTGATTGAGGCGGCTTTCGGCGAAA 6930

Qy       1834 TCACATCTGTGCACCTACCTACAGGAACGAGGTTTAAATTTGGTGCCATGATGAAATCCG 1893
Db       6931 TTTCATCAATACATTTGCCCACTAAAACTAAATTTAAATTCGGAGCCATGATGAAATCTG 6990

Qy       1894 GTATGTTCTTAACGCTGTTTGTCAACACACTAGTCAATATCATGATTGCTAGCAGAGTAC 1953
Db       6991 GAATGTTCCTCACACTGTTTGTGAACACAGTCATTAACATTGTAATCGCAAGCAGAGTGT 7050

Qy       1954 TACGTGAACGGTTAACCACGTCAGCGTGCGCGGCCTCTATCGGCGACGATAACATAGTGC 2013
Db       7051 TGAGAGAACGGCTAACCGGATCACCATGTGCAGCATTCATTGGAGATGACAATATCGTGA 7110

Qy       2014 ATGGTGTCGTCTCCGACACCTTGATGGCGGAGAGATGCGCCACTTGGCTGAACATGGAAG 2073
Db       7111 AAGGAGTCAAATCGGACAAATTAATGGCAGACAGGTGCGCCACCTGGTTGAATATGGAAG 7170

Qy       2074 TAAAAATTATTGATGCAGTTATTGGTATCAAAGCACCCTACTTCTGTGGGGGATTTATCC 2133
Db       7171 TCAAGATTATAGATGCTGTGGTGGGCGAGAAAGCGCCCTATTTCTGTGGAGGGTTTATTT 7230

Qy       2134 TGGTGGACCAGATAACAGGCACAGCCTGCAGAGTCGCAGACCCTCTAAAAAGGCTTTTTA 2193
Db       7231 TGTGTGACTCCGTGACCGGCACAGCGTGCCGTGTGGCAGACCCCCTAAAAAGGCTGTTTA 7290

Qy       2194 AGCTTGGAAAACCATTGCCAGTCGATGATACCCAAGACTGCGACCGCCGCCGGGCACTGC 2253
Db       7291 AGCTTGGCAAACCTCTGGCAGCAGACGATGAACATGATGATGACAGGAGAAGGGCATTGC 7350

Qy       2254 ATGATGAAGCAATGCGATGGAACAGAATTGGAATTACGGACGAGTTAGTGAAGGCCGTAG 2313
Db       7351 ATGAAGAGTCAACACGCTGGAACCGAGTGGGTATTCTTTCAGAGCTGTGCAAGGCAGTAG 7410

Qy       2314 AATCCAGATACGAGATCATACTGGCAGGCCTGATCATCACGTCTCTGTCCACGTTAGCCG 2373
Db       7411 AATCAAGGTATGAAACCGTAGGAACTTCCATCATAGTTATGGCCATGACTACTCTAGCTA 7470

Qy       2374 AAAGCGTTAAGAACTTCAAGAGCATAAGAGGGAGCCCAATCACCCTCTACGGCTGACCTA 2433
Db       7471 GCAGTGTTAAATCATTCAGCTACCTGAGAGGGGCCCCTATAACTCTCTACGGCTAACCTG 7530

Qy       2434 AATAGGTGACGTAGTAGAC 2452
Db       7531 AATGGACTACGACATAGTC 7549
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RESULT 7
US-09-991-258-14
; Sequence 14, Application US/09991258
; Patent No. US20020141975A1
; GENERAL INFORMATION:
;  APPLICANT: Olmsted, Robert
;  APPLICANT:  Keith, Paula
;  APPLICANT:  Dryga, Sergey
;  APPLICANT:  Caley, Ian
;  APPLICANT:  Maughan, Maureen
;  APPLICANT:  Johnston, Robert
;  APPLICANT:  Davis, Nancy
;  APPLICANT:  Swanstrom, Ronald
;  TITLE OF INVENTION: ALPHAVIRUS VECTORS AND VIROSOMES WITH MODIFIED HIV GENES FOR USE I
;  TITLE OF INVENTION:  VACCINES
;  FILE REFERENCE: 01113.0001U3
;  CURRENT APPLICATION NUMBER: US/09/991,258
;  CURRENT FILING DATE:  2001-11-16
;  PRIOR APPLICATION NUMBER: 09/902,537
;  PRIOR FILING DATE: 2001-07-09
;  PRIOR APPLICATION NUMBER: 60/216,995
;  PRIOR FILING DATE: 2000-07-07
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 12379
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence; No. US20020141975A1e =
;   OTHER INFORMATION: synthetic construct
US-09-991-258-14

  Query Match             14.3%;  Score 924.6;  DB 10;  Length 12379;
  Best Local Similarity   68.0%;  Pred. No. 6.5e-265;
  Matches 1319;  Conservative    0;  Mismatches  614;  Indels    6;  Gaps    2;

Qy        514 AACCACCAGGAGTCGCTAGAGCGATCTCAGAAGCGGAGTTGGACGAGTACATCCGTCAAC 573
Db       5617 ACCCGCCAGGCGTAAATAGGGTGATTACAAGAGAGGAGTTTGAGGCGTTCGTAGCACAAC 5676

Qy        574 ACTCCAACTGACGGTATGAAGCGGGAGCGTATATTTTCTCATCGGAAACAGGCCAAGGTC 633
Db       5677 A---ACAATGACGGTTTGATGCGGGTGCATACATCTTTTCCTCCGACACCGGTCAAGGGC 5733

Qy        634 ACCTTCAACAGAAATCAGTACGTCAATGTAAACTACAAGAACCTATATTGGATCGGGCCG 693
Db       5734 ATTTACAACAAAAATCAGTAAGGCAAACGGTGCTATCCGAAGTGGTGTTGGAGAGGACCG 5793

Qy        694 TCCATGAGAAGTATTACGCCCCGCGCCTCGATCTCGAAAGAGAGAAAATGTTACAGAAGA 753
Db       5794 AATTGGAGATTTCGTATGCCCCGCGCCTCGACCAAGAAAAAGAAGAATTACTACGCAAGA 5853

Qy        754 AACTGCAATTATGCGCCTCTGAAGGAAATAGAAGCAGGTATCAATCACGAAAAGTAGAAA 813
Db       5854 AATTACAGTTAAATCCCACACCTGCTAACAGAAGCAGATACCAGTCCAGGAAGGTGGAGA 5913

Qy        814 ATATGAAAGCAATTACAGCGGAGCGACTCATTTCTGGATTGGGCACATATCTATCATCAG 873
Db       5914 ACATGAAAGCCATAACAGCTAGACGTATTCTGCAAGGCCTAGGGCATTATTTGAAGGCAG 5973

Qy        874 AAGTGAATCCTGTCGAGTGTTACAGAGTCAATTATCCTGTACCAATCTACTCGTCAACGG 933
Db       5974 AAGGAAA---AGTGGAGTGCTACCGAACCCTGCATCCTGTTCCTTTGTATTCATCTAGTG 6030

Qy        934 TAATTAACAGGTTTACATCTGCAGAGGTCGCGGTTAAAACGTGCAACTTAGTTATCCAAG 993
Db       6031 TGAACCGTGCCTTTTCAAGCCCCAAGGTCGCAGTGGAAGCCTGTAACGCCATGTTGAAAG 6090

Qy        994 AGAATTACCCTACAGTAGCCAGTTATTGTATAACAGATGAATACGATGCGTATCTTGACA 1053
Db       6091 AGAACTTTCCGACTGTGGCTTCTTACTGTATTATTCCAGAGTACGATGCCTATTTGGACA 6150
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Qy       1054 TGGTGGACGGCGCATCGTGCTGTCTAGATACAGCCACTTTTTGTCCGGCTAAACTGAGAA 1113
             |||| ||||| || || |||||  |||| || |||| ||||||  || || || ||| | |
Db       6151 TGGTTGACGGAGCTTCATGCTGCTTAGACACTGCCAGTTTTTGCCCTGCAAAGCTGCGCA 6210

Qy       1114 GCTACCCAAAGAAGCATAGCTATTTGCAGCCAGAGATAAGATCAGCCGTCCCATCGCCTA 1173
             |||  |||||||| ||   ||||||| | ||     ||| |||| || || || ||  | |
Db       6211 GCTTTCCAAAGAAACACTCCTATTTGGAACCCACAATACGATCGGCAGTGCCTTCAGCGA 6270

Qy       1174 TACAGAATACATTACAAAATGTATTGGCTGCAGCTACTAAAAGGAATTGCAACGTTACCC 1233
             | ||||| ||  | || || ||  |||| || || || ||||| |||||||| || || |
Db       6271 TCCAGAACACGCTCCAGAACGTCCTGGCAGCTGCCACAAAAAGAAATTGCAATGTCACGC 6330

Qy       1234 AAATGCGAGAATTACCTGTCTTAGATTCGGCGGCATTTAATGTTGATTGTTTCAAGAAAT 1293
             ||||| ||||||| || || || |||||||||||| |||||||| || || ||||||||||
Db       6331 AAATGAGAGAATTGCCCGTATTGGATTCGGCGGCCTTTAATGTGGAATGCTTCAAGAAAT 6390

Qy       1294 ACGCATGCAATGATGAGTACTGGGATACCTTTCGCGATAACCCTATTCGGCTAACTACAG 1353
             | || || ||| |||| || ||||| || |||   || ||||| ||  |||| |||  ||
Db       6391 ATGCGTGTAATAATGAATATTGGGAAACGTTTAAAGAAAACCCCATCAGGCTTACTGAAG 6450

Qy       1354 AGAACGTTACGCAATATGTGACAAAGCTGAAAGGGCCGAAAGCAGCAGCATTGTTTGCGA 1413
             | |||||     | ||  | || ||  | ||||| || ||||| || ||  | |||||||
Db       6451 AAAACGTGGTAAATTACATTACCAAATTAAAAGGACCAAAAGCTGCTGCTCTTTTTGCGA 6510

Qy       1414 ATACTCATAATCTAAAACCGTTGCAGGAGATACCAATGGATCAATTCGTCATGGATCTAA 1473
             | || |||||| | ||   |||||||||| ||||||||||    || || |||||  |||
Db       6511 AGACACATAATTTGAATATGTTGCAGGACATACCAATGGACAGGTTTGTAATGGACTTAA 6570

Qy       1474 AGAGAGATGTCAAAGTTACTCCCGGCACGAAACATACAGAGGAGCGGCCTAAGGTGCAGG 1533
             ||||||| || ||||| ||||| || || |||||||| || || ||||| ||||| ||||
Db       6571 AGAGAGACGTGAAAGTGACTCCAGGAACAAAACATACTGAAGAACGGCCCAAGGTACAGG 6630

Qy       1534 TTATTCAGGCTGCAGATCCCCTTGCTACCGCTTACCTTTGCGGGATCCATCGGGAATTAG 1593
             | || |||||||| ||||| || || || || || || ||||| ||||| || ||  | |
Db       6631 TGATCCAGGCTGCCGATCCGCTAGCAACAGCGTATCTGTGCGGAATCCACCGAGAGCTGG 6690

Qy       1594 TCCGTAGACTGAATGCGGTGCTTCTGCCAAATATCCATACTCTCTTCGACATGTCAGCGG 1653
             |  | ||| | |||||||| || || || || || |||| || || ||  ||||||| |
Db       6691 TTAGGAGATTAAATGCGGTCCTGCTTCCGAACATTCATACACTGTTTGATATGTCGGCTG 6750

Qy       1654 AAGATTTTGATGCGATTATTGCTGAACATTTCCACCACGGCGACCCAGTATTGGAAACGG 1713
             |||| ||||| || ||||| || || || ||||| |  || ||    ||  ||||||| |
Db       6751 AAGACTTTGACGCTATTATAGCCGAGCACTTCCAGCCTGGGGATTGTGTTCTGGAAACTG 6810

Qy       1714 ACATCGCGTCGTTTGATAAAAGCGAAGACGACGCTATCGCCATTTCGGCGTTGATGATCC 1773
             |||||||||||||||||||||| || |||||||| || ||  |  | ||||| ||||| |
Db       6811 ACATCGCGTCGTTTGATAAAAGTGAGGACGACGCCATGGCTCTGACCGCGTTAATGATTC 6870

Qy       1774 TTGAGGACTTAGGTGTCGACCAACCGCTCTTAGATTTGATAGAGGCGGCGTTCGGCAATA 1833
             | || |||||||||||| |||  |  ||| ||     |||| |||||||| |||||| | |
Db       6871 TGGAAGACTTAGGTGTGGACGCAGAGCTGTTGACGCTGATTGAGGCGGCTTTCGGCGAAA 6930

Qy       1834 TCACATCTGTGCACCTACCTACAGGAACGAGGTTTAAATTTGGTGCCATGATGAAATCCG 1893
             |  ||||  | ||  | || ||   ||| |  |||||||| || ||||||||||||| |
Db       6931 TTTCATCAATACATTTGCCCACTAAAACTAAATTTAAATTCGGAGCCATGATGAAATCTG 6990

Qy       1894 GTATGTTCTTAACGCTGTTTGTCAACACACTAGTCAATATCATGATTGCTAGCAGAGTAC 1953
             | |||||| | || |||||||| ||||||  |  | || ||  | || || |||||||
Db       6991 GAATGTTCCTCACACTGTTTGTGAACACAGTCATTAACATTGTAATCGCAAGCAGAGTGT 7050

Qy       1954 TACGTGAACGGTTAACCACGTCAGCGTGCGCGGCCTCTATCGGCGACGATAACATAGTGC 2013
             |  | |||||| ||||  | || || || ||  || || || || || || || ||| |||
Db       7051 TGAGAGAACGGCTAACCGGATCACCATGTGCAGCATTCATTGGAGATGACAATATCGTGA 7110

Qy       2014 ATGGTGTCGTCTCCGACACCTTGATGGCGGAGAGATGCGCCACTTGGCTGAACATGGAAG 2073
             | || |||   || ||||  || ||||| || || |||||||| ||| |||| |||||||
Db       7111 AAGGAGTCAAATCGGACAAATTAATGGCAGACAGGTGCGCCACCTGGTTGAATATGGAAG 7170

Qy       2074 TAAAAATTATTGATGCAGTTATTGGTATCAAAGCACCCTACTTCTGTGGGGGATTTATCC 2133
             | || ||||| ||||| ||  | ||    ||||| || || |||||||| || |||||
Db       7171 TCAAGATTATAGATGCTGTGGTGGGCGAGAAAGCGCCTTATTTCTGTGGAGGGTTTATTT 7230

Qy       2134 TGGTGGACCAGATAACAGGCACAGCCTGCAGAGTCGCAGACCCTCTAAAAAGGCTTTTTA 2193
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             ||  |||    | || |||||||| ||| | || |||||||| |||||||||| ||||
Db       7231 TGTGTGACTCCGTGACCGGCACAGCGTGCCGTGTGGCAGACCCCCTAAAAAGGCTGTTTA 7290

Qy       2194 AGCTTGGAAAACCATTGCCAGTCGATGATACCCAAGACTGCGACCGCCGCCGGGCACTGC 2253
             ||||||| ||||| || ||| || |||   || ||     ||| |  | ||||| |||
Db       7291 AGCTTGGCAAACCTCTGGCAGCAGACGATGAACATGATGATGACAGGAGAAGGGCATTGC 7350

Qy       2254 ATGATGAAGCAATGCGATGGAACAGAATTGGAATTACGGACGAGTTAGTGAAGGCCGTAG 2313
             |||| ||  |||  || |||||| || | || |||       ||| |   ||||| ||||
Db       7351 ATGAAGAGTCAACACGCTGGAACCGAGTGGGTATTCTTTCAGAGCTGTGCAAGGCAGTAG 7410

Qy       2314 AATCCAGATACGAGATCATACTGGCAGGCCTGATCATCACGTCTCTGTCCACGTTAGCCG 2373
             |||| || || || | | ||    |   | | ||  | | | |  || | ||  ||||
Db       7411 AATCAAGGTATGAAACCGTAGGAACTTCCATCATAGTTATGGCCATGACTACTCTAGCTA 7470

Qy       2374 AAAGCGTTAAGAACTTCAAGAGCATAAGAGGGAGCCCAATCACCCTCTACGGCTGACCTA 2433
               || |||||    ||||    | | |||||| ||| || || |||||||||| ||||
Db       7471 GCAGTGTTAAATCATTCAGCTACCTGAGAGGGGCCCCTATAACTCTCTACGGCTAACCTG 7530

Qy       2434 AATAGGTGACGTAGTAGAC 2452
             ||| |   |||  ||| |
Db       7531 AATGGACTACGACATAGTC 7549


RESULT 8
US-09-991-258-17
; Sequence 17, Application US/09991258
; Patent No. US20020141975A1
; GENERAL INFORMATION:
;  APPLICANT: Olmsted, Robert
;  APPLICANT:  Keith, Paula
;  APPLICANT:  Dryga, Sergey
;  APPLICANT:  Caley, Ian
;  APPLICANT:  Maughan, Maureen
;  APPLICANT:  Johnston, Robert
;  APPLICANT:  Davis, Nancy
;  APPLICANT:  Swanstrom, Ronald
;  TITLE OF INVENTION: ALPHAVIRUS VECTORS AND VIROSOMES WITH MODIFIED HIV GENES FOR USE
;  TITLE OF INVENTION:  VACCINES
;  FILE REFERENCE: 01113.0001U3
;  CURRENT APPLICATION NUMBER: US/09/991,258
;  CURRENT FILING DATE:  2001-11-16
;  PRIOR APPLICATION NUMBER: 09/902,537
;  PRIOR FILING DATE: 2001-07-09
;  PRIOR APPLICATION NUMBER: 60/216,995
;  PRIOR FILING DATE: 2000-07-07
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 13584
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence; No. US20020141975A1e =
;   OTHER INFORMATION: synthetic construct
US-09-991-258-17

  Query Match           14.3%;  Score 924.6;  DB 10;  Length 13584;
  Best Local Similarity   68.0%;  Pred. No. 7e-265;
  Matches 1319;  Conservative    0;  Mismatches  614;  Indels    6;  Gaps    2;

Qy        514 AACCACCAGGAGTCGCTAGAGCGATCTCAGAAGCGGAGTTGGACGAGTACATCCGTCAAC 573
              | || ||||| ||   ||| | |||  ||  || |||||| || | || | |    ||||
Db       5617 ACCCGCCAGGCGTAAATAGGGTGATTACAAGAGAGGAGTTTGAGGCGTTCGTAGCACAAC 5676

Qy        574 ACTCCAACTGACGGTATGAAGCGGGAGCGTATATTTTCTCATCGGAAACAGGCCAAGGTC 633
              |      | ||||||| ||| ||||| || || || || || || || || || ||||| |
Db       5677 A---ACAATGACGGTTTGATGCGGGTGCATACATCTTTTCCTCCGACACCGGTCAAGGGC 5733

Qy        634 ACCTTCAACAGAAATCAGTACGTCAATGTAAACTACAAGAACCTATATTGGATCGGGCCG 693
              |  | ||||| |||||||||| | |||       |||   |||    | |||||  || |||
Db       5734 ATTTACAACAAAAATCAGTAAGGCAAACGGTGCTATCCGAAGTGGTGTTGGAGAGGACCG 5793
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Qy       694 TCCATGAGAAGTATTACGCCCCGCGCCTCGATCTCGAAAGAGAGAAAATGTTACAGAAGA 753
Db      5794 AATTGGAGATTTCGTATGCCCCGCGCCTCGACCAAGAAAAAGAAGAATTACTACGCAAGA 5853

Qy       754 AACTGCAATTATGCGCCTCTGAAGGAAATAGAAGCAGGTATCAATCACGAAAAGTAGAAA 813
Db      5854 AATTACAGTTAAATCCCACACCTGCTAACAGAAGCAGATACCAGTCCAGGAAGGTGGAGA 5913

Qy       814 ATATGAAAGCAATTACAGCGGAGCGACTCATTTCTGGATTGGGCACATATCTATCATCAG 873
Db      5914 ACATGAAAGCCATAACAGCTAGACGTATTCTGCAAGGCCTAGGGCATTATTTGAAGGCAG 5973

Qy       874 AAGTGAATCCTGTCGAGTGTTACAGAGTCAATTATCCTGTACCAATCTACTCGTCAACGG 933
Db      5974 AAGGAAA---AGTGGAGTGCTACCGAACCCTGCATCCTGTTCCTTTGTATTCATCTAGTG 6030

Qy       934 TAATTAACAGGTTTACATCTGCAGAGGTCGCGGTTAAAACGTGCAACTTAGTTATCCAAG 993
Db      6031 TGAACCGTGCCTTTTCAAGCCCCAAGGTCGCAGTGGAAGCCTGTAACGCCATGTTGAAAG 6090

Qy       994 AGAATTACCCTACAGTAGCCAGTTATTGTATAACAGATGAATACGATGCGTATCTTGACA 1053
Db      6091 AGAACTTTCCGACTGTGGCTTCTTACTGTATTATTCCAGAGTACGATGCCTATTTGGACA 6150

Qy      1054 TGGTGGACGGCGCATCGTGCTGTCTAGATACAGCCACTTTTTGTCCGGCTAAACTGAGAA 1113
Db      6151 TGGTTGACGGAGCTTCATGCTGCTTAGACACTGCCAGTTTTTGCCCTGCAAAGCTGCGCA 6210

Qy      1114 GCTACCCAAAGAAGCATAGCTATTTGCAGCCAGAGATAAGATCAGCCGTCCCATCGCCTA 1173
Db      6211 GCTTTCCAAAGAAACACTCCTATTTGGAACCCACAATACGATCGGCAGTGCCTTCAGCGA 6270

Qy      1174 TACAGAATACATTACAAAATGTATTGGCTGCAGCTACTAAAAGGAATTGCAACGTTACCC 1233
Db      6271 TCCAGAACACGCTCCAGAACGTCCTGGCAGCTGCCACAAAAAGAAATTGCAATGTCACGC 6330

Qy      1234 AAATGCGAGAATTACCTGTCTTAGATTCGGCGGCATTTAATGTTGATTGTTTCAAGAAAT 1293
Db      6331 AAATGAGAGAATTGCCCGTATTGGATTCGGCGGCCTTTAATGTGGAATGCTTCAAGAAAT 6390

Qy      1294 ACGCATGCAATGATGAGTACTGGGATACCTTTCGCGATAACCCTATTCGGCTAACTACAG 1353
Db      6391 ATGCGTGTAATAATGAATATTGGGAAACGTTTAAAGAAAACCCCATCAGGCTTACTGAAG 6450

Qy      1354 AGAACGTTACGCAATATGTGACAAAGCTGAAAGGGCCGAAAGCAGCAGCATTGTTTGCGA 1413
Db      6451 AAAACGTGGTAAATTACATTACCAAATTAAAAGGACCAAAAGCTGCTGCTCTTTTTGCGA 6510

Qy      1414 ATACTCATAATCTAAAACCGTTGCAGGAGATACCAATGGATCAATTCGTCATGGATCTAA 1473
Db      6511 AGACACATAATTTGAATATGTTGCAGGACATACCAATGGACAGGTTTGTAATGGACTTAA 6570

Qy      1474 AGAGAGATGTCAAAGTTACTCCCGGCACGAAACATACAGAGGAGCGGCCTAAGGTGCAGG 1533
Db      6571 AGAGAGACGTGAAAGTGACTCCAGGAACAAAACATACTGAAGAACGGCCCAAGGTACAGG 6630

Qy      1534 TTATTCAGGCTGCAGATCCCCTTGCTACCGCTTACCTTTGCGGGATCCATCGGGAATTAG 1593
Db      6631 TGATCCAGGCTGCCGATCCGCTAGCAACAGCGTATCTGTGCGGAATCCACCGAGAGCTGG 6690

Qy      1594 TCCGTAGACTGAATGCGGTGCTTCTGCCAAATATCCATACTCTCTTCGACATGTCAGCGG 1653
Db      6691 TTAGGAGATTAAATGCGGTCCTGCTTCCGAACATTCATACACTGTTTGATATGTCGGCTG 6750

Qy      1654 AAGATTTTGATGCGATTATTGCTGAACATTTCCACCACGGCGACCCAGTATTGGAAACGG 1713
Db      6751 AAGACTTTGACGCTATTATAGCCGAGCACTTCCAGCCTGGGGATTGTGTTCTGGAAACTG 6810

Qy      1714 ACATCGCGTCGTTTGATAAAAGCGAAGACGACGCTATCGCCATTTCGGCGTTGATGATCC 1773
Db      6811 ACATCGCGTCGTTTGATAAAAGTGAGGACGACGCCATGGCTCTGACCGCGTTAATGATTC 6870

Qy      1774 TTGAGGACTTAGGTGTCGACCAACCGCTCTTAGATTTGATAGAGGCGGCGTTCGGCAATA 1833
Db      6871 TGGAAGACTTAGGTGTGGACGCAGAGCTGTTGACGCTGATTGAGGCGGCTTTCGGCGAAA 6930

Qy      1834 TCACATCTGTGCACCTACCTACAGGAACGAGGTTTAAATTTGGTGCCATGATGAAATCCG 1893
Db      6931 TTTCATCAATACATTTGCCCACTAAAACTAAATTTAAATTCGGAGCCATGATGAAATCTG 6990

Qy      1894 GTATGTTCTTAACGCTGTTTGTCAACACACTAGTCAATATCATGATTGCTAGCAGAGTAC 1953
Db      6991 GAATGTTCCTCACACTGTTTGTGAACACAGTCATTAACATTGTAATCGCAAGCAGAGTGT 7050

Qy      1954 TACGTGAACGGTTAACCACGTCAGCGTGCGCGGCCTCTATCGGCGACGATAACATAGTGC 2013
Db      7051 TGAGAGAACGGCTAACCGGATCACCATGTGCAGCATTCATTGGAGATGACAATATCGTGA 7110

Qy      2014 ATGGTGTCGTCTCCGACACCTTGATGGCGGAGAGATGCGCCACTTGGCTGAACATGGAAG 2073
Db      7111 AAGGAGTCAAATCGGACAAATTAATGGCAGACAGGTGCGCCACCTGGTTGAATATGGAAG 7170

Qy      2074 TAAAAATTATTGATGCAGTTATTGGTATCAAAGCACCCTACTTCTGTGGGGGATTTATCC 2133
Db      7171 TCAAGATTATAGATGCTGTGGTGGGCGAGAAAGCGCCTTATTTCTGTGGAGGGTTTATTT 7230

Qy      2134 TGGTGGACCAGATAACAGGCACAGCCTGCAGAGTCGCAGACCCTCTAAAAAGGCTTTTTA 2193
Db      7231 TGTGTGACTCCGTGACCGGCACAGCGTGCCGTGTGGCAGACCCCCTAAAAAGGCTGTTTA 7290

Qy      2194 AGCTTGGAAAACCATTGCCAGTCGATGATACCCAAGACTGCGACCGCCGCCGGGCACTGC 2253
Db      7291 AGCTTGGCAAACCTCTGGCAGCAGACGATGAACATGATGATGACAGGAGAAGGGCATTGC 7350

Qy      2254 ATGATGAAGCAATGCGATGGAACAGAATTGGAATTACGGACGAGTTAGTGAAGGCCGTAG 2313
Db      7351 ATGAAGAGTCAACACGCTGGAACCGAGTGGGTATTCTTTCAGAGCTGTGCAAGGCAGTAG 7410

Qy      2314 AATCCAGATACGAGATCATACTGGCAGGCCTGATCATCACGTCTCTGTCCACGTTAGCCG 2373
Db      7411 AATCAAGGTATGAAACCGTAGGAACTTCCATCATAGTTATGGCCATGACTACTCTAGCTA 7470

Qy      2374 AAAGCGTTAAGAACTTCAAGAGCATAAGAGGGAGCCCAATCACCCTCTACGGCTGACCTA 2433
Db      7471 GCAGTGTTAAATCATTCAGCTACCTGAGAGGGGCCCCTATAACTCTCTACGGCTAACCTG 7530

Qy      2434 AATAGGTGACGTAGTAGAC 2452
Db      7531 AATGGACTACGACATAGTC 7549
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RESULT 9
US-09-991-258-2
; Sequence 2, Application US/09991258
; Patent No. US20020141975A1
; GENERAL INFORMATION:
; APPLICANT: Olmsted, Robert
; APPLICANT: Keith, Paula
; APPLICANT: Dryga, Sergey
; APPLICANT: Caley, Ian
; APPLICANT: Maughan, Maureen
; APPLICANT: Johnston, Robert
; APPLICANT: Davis, Nancy
; APPLICANT: Swanstrom, Ronald
; TITLE OF INVENTION: ALPHAVIRUS VECTORS AND VIROSOMES WITH MODIFIED HIV GENES FOR USE I
; TITLE OF INVENTION: VACCINES
; FILE REFERENCE: 01113.0001U3
; CURRENT APPLICATION NUMBER: US/09/991,258
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 09/902,537
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/216,995
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2

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;   LENGTH: 7479
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence; No. US20020141975A1e =
;   OTHER INFORMATION: synthetic construct
;   NAME/KEY: CDS
;   LOCATION: (1)...(7479)
US-09-991-258-2

  Query Match           14.1%;  Score 916.2;  DB 10;  Length 7479;
  Best Local Similarity  68.2%;  Pred. No. 1.5e-262;
  Matches 1304;  Conservative    0;  Mismatches  603;  Indels    6;  Gaps    2;

Qy       514 AACCACCAGGAGTCGCTAGAGCGATCTCAGAAGCGGAGTTGGACGAGTACATCCGTCAAC 573
Db      5573 ACCCGCCAGGCGTAAATAGGGTGATTACAAGAGAGGAGTTTGAGGCGTTCGTAGCACAAC 5632

Qy       574 ACTCCAACTGACGGTATGAAGCGGGAGCGTATATTTTCTCATCGGAAACAGGCCAAGGTC 633
Db      5633 A---ACAATGACGGTTTGATGCGGGTGCATACATCTTTTCCTCCGACACCGGTCAAGGGC 5689

Qy       634 ACCTTCAACAGAAATCAGTACGTCAATGTAAACTACAAGAACCTATATTGGATCGGGCCG 693
Db      5690 ATTTACAACAAAAATCAGTAAGGCAAACGGTGCTATCCGAAGTGGTGTTGGAGAGGACCG 5749

Qy       694 TCCATGAGAAGTATTACGCCCCGCGCCTCGATCTCGAAAGAGAGAAAATGTTACAGAAGA 753
Db      5750 AATTGGAGATTTCGTATGCCCCGCGCCTCGACCAAGAAAAAGAAGAATTACTACGCAAGA 5809

Qy       754 AACTGCAATTATGCGCCTCTGAAGGAAATAGAAGCAGGTATCAATCACGAAAAGTAGAAA 813
Db      5810 AATTACAGTTAAATCCCACACCTGCTAACAGAAGCAGATACCAGTCCAGGAAGGTGGAGA 5869

Qy       814 ATATGAAAGCAATTACAGCGGAGCGACTCATTTCTGGATTGGGCACATATCTATCATCAG 873
Db      5870 ACATGAAAGCCATAACAGCTAGACGTATTCTGCAAGGCCTAGGGCATTATTTGAAGGCAG 5929

Qy       874 AAGTGAATCCTGTCGAGTGTTACAGAGTCAATTATCCTGTACCAATCTACTCGTCAACGG 933
Db      5930 AAGGAAA---AGTGGAGTGCTACCGAACCCTGCATCCTGTTCCTTTGTATTCATCTAGTG 5986

Qy       934 TAATTAACAGGTTTACATCTGCAGAGGTCGCGGTTAAAACGTGCAACTTAGTTATCCAAG 993
Db      5987 TGAACCGTGCCTTTTCAAGCCCCAAGGTCGCAGTGGAAGCCTGTAACGCCATGTTGAAAG 6046

Qy       994 AGAATTACCCTACAGTAGCCAGTTATTGTATAACAGATGAATACGATGCGTATCTTGACA 1053
Db      6047 AGAACTTTCCGACTGTGGCTTCTTACTGTATTATTCCAGAGTACGATGCCTATTTGGACA 6106

Qy      1054 TGGTGGACGGCGCATCGTGCTGTCTAGATACAGCCACTTTTTGTCCGGCTAAACTGAGAA 1113
Db      6107 TGGTTGACGGAGCTTCATGCTGCTTAGACACTGCCAGTTTTTGCCCTGCAAAGCTGCGCA 6166

Qy      1114 GCTACCCAAAGAAGCATAGCTATTTGCAGCCAGAGATAAGATCAGCCGTCCCATCGCCTA 1173
Db      6167 GCTTTCCAAAGAAACACTCCTATTTGGAACCCACAATACGATCGGCAGTGCCTTCAGCGA 6226

Qy      1174 TACAGAATACATTACAAAATGTATTGGCTGCAGCTACTAAAAGGAATTGCAACGTTACCC 1233
Db      6227 TCCAGAACACGCTCCAGAACGTCCTGGCAGCTGCCACAAAAAGAAATTGCAATGTCACGC 6286

Qy      1234 AAATGCGAGAATTACCTGTCTTAGATTCGGCGGCATTTAATGTTGATTGTTTCAAGAAAT 1293
Db      6287 AAATGAGAGAATTGCCCGTATTGGATTCGGCGGCCTTTAATGTGGAATGCTTCAAGAAAT 6346

Qy      1294 ACGCATGCAATGATGAGTACTGGGATACCTTTCGCGATAACCCTATTCGGCTAACTACAG 1353
Db      6347 ATGCGTGTAATAATGAATATTGGGAAACGTTTAAAGAAAACCCCATCAGGCTTACTGAAG 6406

Qy      1354 AGAACGTTACGCAATATGTGACAAAGCTGAAAGGGCCGAAAGCAGCAGCATTGTTTGCGA 1413
Db      6407 AAAACGTGGTAAATTACATTACCAAATTAAAAGGACCAAAAGCTGCTGCTCTTTTTGCGA 6466

Qy      1414 ATACTCATAATCTAAAACCGTTGCAGGAGATACCAATGGATCAATTCGTCATGGATCTAA 1473
Db      6467 AGACACATAATTTGAATATGTTGCAGGACATACCAATGGACAGGTTTGTAATGGACTTAA 6526

Qy      1474 AGAGAGATGTCAAAGTTACTCCCGGCACGAAACATACAGAGGAGCGGCCTAAGGTGCAGG 1533
Db      6527 AGAGAGACGTGAAAGTGACTCCAGGAACAAAACATACTGAAGAACGGCCCAAGGTACAGG 6586

Qy      1534 TTATTCAGGCTGCAGATCCCCTTGCTACCGCTTACCTTTGCGGGATCCATCGGGAATTAG 1593
Db      6587 TGATCCAGGCTGCCGATCCGCTAGCAACAGCGTATCTGTGCGGAATCCACCGAGAGCTGG 6646

Qy      1594 TCCGTAGACTGAATGCGGTGCTTCTGCCAAATATCCATACTCTCTTCGACATGTCAGCGG 1653
Db      6647 TTAGGAGATTAAATGCGGTCCTGCTTCCGAACATTCATACACTGTTTGATATGTCGGCTG 6706

Qy      1654 AAGATTTTGATGCGATTATTGCTGAACATTTCCACCACGGCGACCCAGTATTGGAAACGG 1713
Db      6707 AAGACTTTGACGCTATTATAGCCGAGCACTTCCAGCCTGGGGATTGTGTTCTGGAAACTG 6766

Qy      1714 ACATCGCGTCGTTTGATAAAAGCGAAGACGACGCTATCGCCATTTCGGCGTTGATGATCC 1773
Db      6767 ACATCGCGTCGTTTGATAAAAGTGAGGACGACGCCATGGCTCTGACCGCGTTAATGATTC 6826

Qy      1774 TTGAGGACTTAGGTGTCGACCAACCGCTCTTAGATTTGATAGAGGCGGCGTTCGGCAATA 1833
Db      6827 TGGAAGACTTAGGTGTGGACGCAGAGCTGTTGACGCTGATTGAGGCGGCTTTCGGCGAAA 6886

Qy      1834 TCACATCTGTGCACCTACCTACAGGAACGAGGTTTAAATTTGGTGCCATGATGAAATCCG 1893
Db      6887 TTTCATCAATACATTTGCCCACTAAAACTAAATTTAAATTCGGAGCCATGATGAAATCTG 6946

Qy      1894 GTATGTTCTTAACGCTGTTTGTCAACACACTAGTCAATATCATGATTGCTAGCAGAGTAC 1953
Db      6947 GAATGTTCCTCACACTGTTTGTGAACACAGTCATTAACATTGTAATCGCAAGCAGAGTGT 7006

Qy      1954 TACGTGAACGGTTAACCACGTCAGCGTGCGCGGCCTCTATCGGCGACGATAACATAGTGC 2013
Db      7007 TGAGAGAACGGCTAACCGGATCACCATGTGCAGCATTCATTGGAGATGACAATATCGTGA 7066

Qy      2014 ATGGTGTCGTCTCCGACACCTTGATGGCGGAGAGATGCGCCACTTGGCTGAACATGGAAG 2073
Db      7067 AAGGAGTCAAATCGGACAAATTAATGGCAGACAGGTGCGCCACCTGGTTGAATATGGAAG 7126

Qy      2074 TAAAAATTATTGATGCAGTTATTGGTATCAAAGCACCCTACTTCTGTGGGGGATTTATCC 2133
Db      7127 TCAAGATTATAGATGCTGTGGTGGGCGAGAAAGCGCCCTATTTCTGTGGAGGGTTTATTT 7186

Qy      2134 TGGTGGACCAGATAACAGGCACAGCCTGCAGAGTCGCAGACCCTCTAAAAAGGCTTTTTA 2193
Db      7187 TGTGTGACTCCGTGACCGGCACAGCGTGCCGTGTGGCAGACCCCCTAAAAAGGCTGTTTA 7246

Qy      2194 AGCTTGGAAAACCATTGCCAGTCGATGATACCCAAGACTGCGACCGCCGCCGGGCACTGC 2253
Db      7247 AGCTTGGCAAACCTCTGGCAGCAGACGATGAACATGATGATGACAGGAGAAGGGCATTGC 7306

Qy      2254 ATGATGAAGCAATGCGATGGAACAGAATTGGAATTACGGACGAGTTAGTGAAGGCCGTAG 2313
Db      7307 ATGAAGAGTCAACACGCTGGAACCGAGTGGGTATTCTTTCAGAGCTGTGCAAGGCAGTAG 7366

Qy      2314 AATCCAGATACGAGATCATACTGGCAGGCCTGATCATCACGTCTCTGTCCACGTTAGCCG 2373
Db      7367 AATCAAGGTATGAAACCGTAGGAACTTCCATCATAGTTATGGCCATGACTACTCTAGCTA 7426

Qy      2374 AAAGCGTTAAGAACTTCAAGAGCATAAGAGGGAGCCCAATCACCCTCTACGGC 2426
Db      7427 GCAGTGTTAAATCATTCAGCTACCTGAGAGGGGCCCCTATAACTCTCTACGGC 7479


RESULT 10
US-09-507-362-102
; Sequence 102, Application US/09507362
```

```
; Publication No. US20030096397A1
;   GENERAL INFORMATION:
;        APPLICANT: Dubensky Jr., Thomas W.
;                   Polo, John M.
;                   Belli, Barbara A.
;                   Schlesinger, Sondra
;                   Dryga, Sergey A.
;                   Frolov, Ilya
;        TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
;                            WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
;                            SYNTHESIS
;        NUMBER OF SEQUENCES: 125
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Seed Intellectual Property Law Group PLLC
;             STREET: 701 Fifth Avenue, Suite 6300
;             CITY: Seattle
;             STATE: Washington
;             COUNTRY: USA
;             ZIP: 98104-7092
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/507,362
;             FILING DATE: 18-Feb-2000
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McMasters, David D.
;             REGISTRATION NUMBER: 33,963
;             REFERENCE/DOCKET NUMBER: 930049.457D6 /1196.011
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (206) 622-4900
;             TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 102:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 8000 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 102:
US-09-507-362-102

  Query Match             12.8%;  Score 827.6;  DB 11;  Length 8000;
  Best Local Similarity   61.9%;  Pred. No. 5.9e-236;
  Matches 1390;  Conservative    0;  Mismatches  829;  Indels   25;  Gaps    4;

Qy        580 ACTGACGGTATGAAGCGGGAGCGTATATTTTCTCATCGGAAACAGGCCAAGGTCACCTTC 639
              ||||||     |  |  || | ||| || || ||  |||| |||||||  || ||| | |
Db       5746 ACTGACTAACCGGGGTAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGC 5805

Qy        640 AACAGAAATCAGTACGTCAATGTAAACTACAAGAACCTATATTGGATCGGGCCGTCCATG 699
              || |||| || || |  ||     | ||   |||||| |  ||||| ||    ||||  |
Db       5806 AAAAGAAGTCCGTTCTGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGG 5865

Qy        700 AGAAGTATTACGCCCCGCGCCTCGATCTCGAAAGAGAGAAAATGTTACAGAAGAAACTGC 759
              | |    | | ||||||   |||||       | |||| ||    |  |    |    |
Db       5866 AAAGAATTCATGCCCCGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACC 5925

Qy        760 AATTATGCGCCTCTGAAGGAAATAGAAGCAGGTATCAATCACGAAAAGTAGAAAATATGA 819
              |  |      || | ||||  || | ||| ||||| || || || ||||||||||||  ||
Db       5926 AGATGATGCCCACCGAAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGA 5985

Qy        820 AAGCAATTACAGCGGAGCGACTCATTTCTGGATTGGGCACATATCTATCATCAGAAGTGA 879
              |||| || ||  | |||||||| | || ||| |  |    |||  ||  |   ||
Db       5986 AAGCCATAACCACTGAGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATC 6045

Qy        880 ATCCTGTCGAGTGTTACAGAGTCAATTATCCTGTACCAATCTACTCGTCAACGGTAATTA 939
              | ||    || || || |   |||  |||||   |||| | |||||    |  |||
Db       6046 AGCCA---GAATGCTATAAGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGG 6102

Qy        940 ACAGGTTTACATCTGCAGAGGTCGCGGTTAAAACGTGCAACTTAGTTATCCAAGAGAATT 999
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                |  |   |  | || || |||| ||       || |||     | | || |||||  |
Db       6103 CGAACTACTCCGATCCACAGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACT 6162

Qy       1000 ACCCTACAGTAGCCAGTTATTGTATAACAGATGAATACGATGCGTATCTTGACATGGTGG 1059
              | || ||||||||    ||||   || || || || |||||||| ||  | ||| |||| |
Db       6163 ATCCGACAGTAGCATCTTATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAG 6222

Qy       1060 ACGGCGCATCGTGCTGTCTAGATACAGCCACTTTTTGTCCGGCTAAACTGAGAAGCTACC 1119
              ||||  ||     ||| || ||||| || || || || || ||||| || ||||| ||||
Db       6223 ACGGGACAGTCGCCTGCCTGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACC 6282

Qy       1120 CAAAGAAGCATAGCTATTTGCAGCCAGAGATAAGATCAGCCGTCCCATCGCCTATACAGA 1179
              | || || |||   |||      ||  | ||  |    || || |||||  | || ||||
Db       6283 CGAAAAAACATGAGTATAGAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGA 6342

Qy       1180 ATACATTACAAAATGTATTGGCTGCAGCTACTAAAAGGAATTGCAACGTTACCCAAATGC 1239
              | ||  ||||||||||    |   ||| || |||||||| ||||||||||| || ||||
Db       6343 ACACGCTACAAAATGTGCTCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGC 6402

Qy       1240 GAGAATTACCTGTCTTAGATTCGGCGGCATTTAATGTTGATTGTTTCAAGAAATACGCAT 1299
              | ||| | ||     | || || ||| |||| ||||| || || ||     ||||| ||||
Db       6403 GTGAACTGCCAACACTGGACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCAT 6462

Qy       1300 GCAATGATGAGTACTGGGATACCTTTCGCGATAACCCTATTCGGCTAACTACAGAGAACG 1359
              | ||||| ||||| |||||     ||        || || ||| || | || || |||   |
Db       6463 GTAATGACGAGTATTGGGAGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTG 6522

Qy       1360 TTACGCAATATGTGACAAAGCTGAAAGGGCCGAAAGCAGCAGCATTGTTTGCGAATACTC 1419
              | ||   ||||||  | |  |||||||| || || || || ||| | ||||| || ||
Db       6523 TCACCGCATATGTAGCTAGACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGT 6582

Qy       1420 ATAATCTAAAACCGTTGCAGGAGATACCAATGGATCAATTCGTCATGGATCTAAAGAGAG 1479
              |||||  |    || ||||| ||  | || ||||||  |||||||||||  | || ||||
Db       6583 ATAATTTGGTCCCATTGCAAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAG 6642

Qy       1480 ATGTCAAAGTTACTCCCGGCACGAAACATACAGAGGAGCGGCCTAAGGTGCAGGTTATTC 1539
              | || |||||||| || |||||||||| ||||| ||  | || || || || || || | |
Db       6643 ACGTGAAAGTTACACCAGGCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATAC 6702

Qy       1540 AGGCTGCAGATCCCCTTGCTACCGCTTACCTTTGCGGGATCCATCGGGAATTAGTCCGTA 1599
              | ||  |||||  ||||| || ||||||  | |||||||| || ||||||||||| ||||
Db       6703 AAGCCGCAGAACCCCTGGCGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTA 6762

Qy       1600 GACTGAATGCGGTGCTTCTGCCAAATATCCATACTCTCTTCGACATGTCAGCGGAAGATT 1659
              | || |  || ||  | || ||||| || || || || || |||||||| |||| ||||
Db       6763 GGCTTACGGCCGTCTTGCTTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATT 6822

Qy       1660 TTGATGCGATTATTGCTGAACATTTCCACCACGGCGACCCAGTATTGGAAACGGACATCG 1719
              ||||||| || || || ||||| ||| | || |||||||| ||| |||| ||||| ||||
Db       6823 TTGATGCAATCATAGCAGAACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCG 6882

Qy       1720 CGTCGTTTGATAAAAGCGAAGACGACGCTATCGCCATTTCGGCGTTGATGATCCTTGAGG 1779
              | || || || |||||| |||||||||||| ||  |  | |  |||||||| | ||||
Db       6883 CATCATTCGACAAAAGCCAAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGG 6942

Qy       1780 ACTTAGGTGTCGACCAACCGCTCTTAGATTTGATAGAGGCGGCGTTCGGCAATATCACAT 1839
              || | ||||| || ||||| ||  | || ||||| |||   || || ||  | ||  |||
Db       6943 ACCTGGGTGTGGATCAACCACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCAT 7002

Qy       1840 CTGTGCACCTACCTACAGGAACGAGGTTTAAATTTGGTGCCATGATGAAATCCGGTATGT 1899
              |    || |||||||| || ||  | |||||||| || || ||||||||||||| ||||
Db       7003 CCACCCATCTACCTACGGGTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGT 7062

Qy       1900 TCTTAACGCTGTTTGTCAACACACTAGTCAATATCATGATTGCTAGCAGAGTACTACGTG 1959
              || | || || |||||||||||| |  | ||| || | || || ||||||||||||  |
Db       7063 TCCTCACACTTTTTGTCAACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAG 7122

Qy       1960 AACGGTTAACCACGTCAGCGTGCGCGGCCTCTATCGGCGACGATAACATAGTGCATGGTG 2019
              | ||| | |  |||||     || || || |  || |||||||| |||||  | ||||| |
Db       7123 AGCGGCTTAAAACGTCCAGATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAG 7182

Qy       2020 TCGTCTCCGACACCTTGATGGCGGAGAGATGCGCCACTTGGCTGAACATGGAAGTAAAAA 2079
              | || || ||||     ||||| ||||| |||||||| ||||| |||||||| || || |
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Db       7183 TAGTATCTGACAAAGAAATGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGA 7242

Qy       2080 TTATTGATGCAGTTATTGGTATCAAAGCACCCTACTTCTGTGGGGGATTTATCCTGGTGG 2139

Db       7243 TCATCGACGCAGTCATCGGTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAG 7302

Qy       2140 ACCAGATAACAGGCACAGCCTGCAGAGTCGCAGACCCTCTAAAAAGGCTTTTTAAGCTTG 2199

Db       7303 ATTCGGTTACTTCCACAGCGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGG 7362

Qy       2200 GAAAACCATTGCCAGTCGATGATACCCAAGACTGCGACCGCCGCCGGGCACTGCATGATG 2259

Db       7363 GTAAACCGCTCCCAGCCGACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATG 7422

Qy       2260 AAGCAATGCGATGGAACAGAATTGGAATTACGGACGAGTTAGTGAAGGCCGTAGAATCCA 2319

Db       7423 AAACAAAGGCGTGGTTTAGAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCC 7482

Qy       2320 GATACGAGATCATACTGGCAGGCCTGATCATCACGTCTCTGTCCACGTTAGCCGAAAGCG 2379

Db       7483 GGTATGAGGTAGACAATATTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCA 7542

Qy       2380 TTAAGAACTTCAAGAGCATAAGAGGGAGCCCAATCACCCTCTACGGCTGACCTAAATAGG 2439

Db       7543 AAAGAGCATTCCAAGCCATCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGT 7602

Qy       2440 TGACGTAGTAGACACGCACCTAC----------CCACCGGCAGAATGTTTCCATACC 2486

Db       7603 CAGCATAGTACATTTCATCTGACTAATACTACAACACCACCACCATGAATAGAGGATTCT 7662

Qy       2487 CTCAGCTGAACTTTCCACCAGTTTACCCTACAAATCCGATGGCTTACCGAGATCCAAACC 2546

Db       7663 TTAACATGCTCGGCCGCCGCCCCTTCCCGGCCCCCACTGCCATGTGGAGGCCGCGGAGAA 7722

Qy       2547 CTCCTAGGCGCCGCTGGAGGCCGTTTCGGCCCCCGCTGGCTGCTCAAATCGAAGATCTTA 2606

Db       7723 GGAGGCAGGCGGCCCCGATGCCTGCCCGCAACGGGCTGGCTTCTCAAATCCAGCAACTGA 7782

Qy       2607 GGAGGTCGATAGTCAACTTGACTTTCAAACAACGATCACCTAATCCGCCGCCAGGTCCA- 2665

Db       7783 CCACAGCCGTCAGTGCCCTAGTCATTGGACAGGCAACTAGACCTCAACCCCCACGTCCAC 7842

Qy       2666 -----CCGCCAAAGAAGAAGAAGAGTGCTCCTAAGCCAAAACCTACTCAGCCTAAAAAGA 2720

Db       7843 GCCCGCCACCGCGCCAGAAGAAGCAGGCGCCCAAGCAACCACCGAAGCCGAAGAAACCAA 7902

Qy       2721 AGAAGCAGCAAGCCAAGAGGACGAAACGC---AAGCCTAAACCAGGGAAACGACAACGTA 2777

Db       7903 AAACGCAGGAGAAGAAGAAGAAGCAACCTGCAAAACCCAAACCCGGAAAGAGACAGCGCA 7962

Qy       2778 TGTGTATGAAGTTGGAGTCGGACA 2801

Db       7963 TGGCACTTAAGTTGGAGGCCGACA 7986


RESULT 11
US-09-507-362-101
; Sequence 101, Application US/09507362
; Publication No. US20030096397A1
;  GENERAL INFORMATION:
;       APPLICANT: Dubensky Jr., Thomas W.
;                  Polo, John M.
;                  Belli, Barbara A.
;                  Schlesinger, Sondra
;                  Dryga, Sergey A.
;                  Frolov, Ilya
;       TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
;                           WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
;                           SYNTHESIS
;       NUMBER OF SEQUENCES: 125
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Seed Intellectual Property Law Group PLLC
;            STREET: 701 Fifth Avenue, Suite 6300
;            CITY: Seattle
;            STATE: Washington
;            COUNTRY: USA
;            ZIP: 98104-7092
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/507,362
;            FILING DATE: 18-Feb-2000
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: McMasters, David D.
;            REGISTRATION NUMBER: 33,963
;            REFERENCE/DOCKET NUMBER: 930049.457D6 /1196.011
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (206) 622-4900
;            TELEFAX: (206) 682-6031
;  INFORMATION FOR SEQ ID NO: 101:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 8000 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-09-507-362-101

  Query Match             12.7%;  Score 824.4;  DB 11;  Length 8000;
  Best Local Similarity   61.9%;  Pred. No. 5.4e-235;
  Matches 1388;  Conservative    0;  Mismatches  831;  Indels   25;  Gaps    4;

Qy        580 ACTGACGGTATGAAGCGGGAGCGTATATTTTCTCATCGGAAACAGGCCAAGGTCACCTTC 639

Db       5746 ACTGACTAACCGGGGTAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGC 5805

Qy        640 AACAGAAATCAGTACGTCAATGTAAACTACAAGAACCTATATTGGATCGGGCCGTCCATG 699

Db       5806 AAAAGAAGTCCGTTCTGCAGAACCAGCTTACAGAACCGACCTTGGAGCACAATGTCCTGG 5865

Qy        700 AGAAGTATTACGCCCCGCGCCTCGATCTCGAAAGAGAGAAAATGTTACAGAAGAAACTGC 759

Db       5866 AAAGAATTCATGCCCCGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACC 5925

Qy        760 AATTATGCGCCTCTGAAGGAAATAGAAGCAGGTATCAATCACGAAAAGTAGAAAATATGA 819

Db       5926 AGATGATGCCCACCGAAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGA 5985

Qy        820 AAGCAATTACAGCGGAGCGACTCATTTCTGGATTGGGCACATATCTATCATCAGAAGTGA 879

Db       5986 AAGCCATAACCACTGAGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAGATC 6045

Qy        880 ATCCTGTCGAGTGTTACAGAGTCAATTATCCTGTACCAATCTACTCGTCAACGGTAATTA 939

Db       6046 AGCCA---GAATGCTATAAGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGG 6102

Qy        940 ACAGGTTTACATCTGCAGAGGTCGCGGTTAAAACGTGCAACTTAGTTATCCAAGAGAATT 999

Db       6103 CGAACTACTCCGATCCACAGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACT 6162

Qy       1000 ACCCTACAGTAGCCAGTTATTGTATAACAGATGAATACGATGCGTATCTTGACATGGTGG 1059

Db       6163 ATCCGACAGTAGCATCTTATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAG 6222

Qy       1060 ACGGCGCATCGTGCTGTCTAGATACAGCCACTTTTTGTCCGGCTAAACTGAGAAGCTACC 1119

Db       6223 ACGGGACAGTCGCCTGCCTGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACC 6282

Qy       1120 CAAAGAAGCATAGCTATTTGCAGCCAGAGATAAGATCAGCCGTCCCATCGCCTATACAGA 1179

Db       6283 CGAAAAAACATGAGTATAGAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGA 6342
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Qy       1180 ATACATTACAAAATGTATTGGCTGCAGCTACTAAAAGGAATTGCAACGTTACCCAAATGC 1239
Db       6343 ACACGCTACAAAATGTGCTCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGC 6402

Qy       1240 GAGAATTACCTGTCTTAGATTCGGCGGCATTTAATGTTGATTGTTTCAAGAAATACGCAT 1299
Db       6403 GTGAACTGCCAACACTGGACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCAT 6462

Qy       1300 GCAATGATGAGTACTGGGATACCTTTCGCGATAACCCTATTCGGCTAACTACAGAGAACG 1359
Db       6463 GTAATGACGAGTATTGGGAGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTG 6522

Qy       1360 TTACGCAATATGTGACAAAGCTGAAAGGGCCGAAAGCAGCAGCATTGTTTGCGAATACTC 1419
Db       6523 TCACCGCATATGTAGCTAGACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGT 6582

Qy       1420 ATAATCTAAAACCGTTGCAGGAGATACCAATGGATCAATTCGTCATGGATCTAAAGAGAG 1479
Db       6583 ATAATTTGGTCCCATTGCAAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAG 6642

Qy       1480 ATGTCAAAGTTACTCCCGGCACGAAACATACAGAGGAGCGGCCTAAGGTGCAGGTTATTC 1539
Db       6643 ACGTGAAAGTTACACCAGGCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATAC 6702

Qy       1540 AGGCTGCAGATCCCCTTGCTACCGCTTACCTTTGCGGGATCCATCGGGAATTAGTCCGTA 1599
Db       6703 AAGCCGCAGAACCCCTGGCGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTA 6762

Qy       1600 GACTGAATGCGGTGCTTCTGCCAAATATCCATACTCTCTTCGACATGTCAGCGGAAGATT 1659
Db       6763 GGCTTACGGCCGTCTTGCTTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATT 6822

Qy       1660 TTGATGCGATTATTGCTGAACATTTCCACCACGGCGACCCAGTATTGGAAACGGACATCG 1719
Db       6823 TTGATGCAATCATAGCAGAACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCG 6882

Qy       1720 CGTCGTTTGATAAAAGCGAAGACGACGCTATCGCCATTTCGGCGTTGATGATCCTTGAGG 1779
Db       6883 CATCATTCGACAAAAGCCAAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGG 6942

Qy       1780 ACTTAGGTGTCGACCAACCGCTCTTAGATTTGATAGAGGCGGCGTTCGGCAATATCACAT 1839
Db       6943 ACCTGGGTGTGGATCAACCACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCAT 7002

Qy       1840 CTGTGCACCTACCTACAGGAACGAGGTTTAAATTTGGTGCCATGATGAAATCCGGTATGT 1899
Db       7003 CCACCCATCTACCTACGGGTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGT 7062

Qy       1900 TCTTAACGCTGTTTGTCAACACACTAGTCAATATCATGATTGCTAGCAGAGTACTACGTG 1959
Db       7063 TCCTCACACTTTTTGTCAACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAG 7122

Qy       1960 AACGGTTAACCACGTCAGCGTGCGCGGCCTCTATCGGCGACGATAACATAGTGCATGGTG 2019
Db       7123 AGCGGCTTAAAACGTCCAGATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAG 7182

Qy       2020 TCGTCTCCGACACCTTGATGGCGGAGAGATGCGCCACTTGGCTGAACATGGAAGTAAAAA 2079
Db       7183 TAGTATCTGACAAAGAAATGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGA 7242

Qy       2080 TTATTGATGCAGTTATTGGTATCAAAGCACCCTACTTCTGTGGGGGATTTATCCTGGTGG 2139
Db       7243 TCATCGACGCAGTCATCGGTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAG 7302

Qy       2140 ACCAGATAACAGGCACAGCCTGCAGAGTCGCAGACCCTCTAAAAAGGCTTTTTAAGCTTG 2199
Db       7303 ATTCGGTTACTTCCACAGCGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGG 7362

Qy       2200 GAAAACCATTGCCAGTCGATGATACCCAAGACTGCGACCGCCGCCGGGCACTGCATGATG 2259
Db       7363 GTAAACCGCTCCCAGCCGACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATG 7422

Qy       2260 AAGCAATGCGATGGAACAGAATTGGAATTACGGACGAGTTAGTGAAGGCCGTAGAATCCA 2319

Db       7423 AAACAAAGGCGTGGTTTAGAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCC 7482

Qy       2320 GATACGAGATCATACTGGCAGGCCTGATCATCACGTCTCTGTCCACGTTAGCCGAAAGCG 2379
Db       7483 GGTATGAGGTAGACAATATTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCA 7542

Qy       2380 TTAAGAACTTCAAGAGCATAAGAGGGAGCCCAATCACCCTCTACGGCTGACCTAAATAGG 2439
Db       7543 AAAGAGCATTCCAAGCCATCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGT 7602

Qy       2440 TGACGTAGTAGACACGCACCTAC----------CCACCGGCAGAATGTTTCCATACC 2486
Db       7603 CAGCATAGTTCATTTCATCTGACTAATACTACAACACCACCACCATGAATAGAGGATTCT 7662

Qy       2487 CTCAGCTGAACTTTCCACCAGTTTACCCTACAAATCCGATGGCTTACCGAGATCCAAACC 2546
Db       7663 TTAACATGCTCGGCCGCCGCCCCTTCCCGGCCCCCACTGCCATGTGGAGGCCGCGGAGAA 7722

Qy       2547 CTCCTAGGCGCCGCTGGAGGCCGTTTCGGCCCCCGCTGGCTGCTCAAATCGAAGATCTTA 2606
Db       7723 GGAGGCAGGCGGCCCCGATGCCTGCCCGCAACGGGCTGGCTTCTCAAATCCAGCAACTGA 7782

Qy       2607 GGAGGTCGATAGTCAACTTGACTTTCAAACAACGATCACCTAATCCGCCGCCAGGTCCA- 2665
Db       7783 CCACAGCCGTCAGTGCCCTAGTCATTGGACAGGCAACTAGACCTCAACCCCCATGTCCAC 7842

Qy       2666 -----CCGCCAAAGAAGAAGAAGAGTGCTCCTAAGCCAAAACCTACTCAGCCTAAAAAGA 2720
Db       7843 GCCCGCCACCGCGCCAGAAGAAGCAGGCGCCCAAGCAACCACCGAAGCCGAAGAAACCAA 7902

Qy       2721 AGAAGCAGCAAGCCAAGAGGACGAAACGC---AAGCCTAAACCAGGGAAACGACAACGTA 2777
Db       7903 AAACGCAGGAGAAGAAGAAGAAGCAACCTGCAAAACCCAAACCCGGAAAGAGACAGCGCA 7962

Qy       2778 TGTGTATGAAGTTGGAGTCGGACA 2801
Db       7963 TGGCACTTAAGTTGGAGGCCGACA 7986
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RESULT 12
US-09-733-042-1
; Sequence 1, Application US/09733042
; Patent No. US20020168709A1
; GENERAL INFORMATION:
; APPLICANT: Hennecke, Frank
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Replicon Based Activation of Endogenous Genes
; FILE REFERENCE: 1700.0100001
; CURRENT APPLICATION NUMBER: US/09/733,042
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,988
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 11282
; TYPE: DNA
; ORGANISM: pCYTts
US-09-733-042-1

Query Match 12.6%; Score 816; DB 10; Length 11282;
Best Local Similarity 65.1%; Pred. No. 2.3e-232;
Matches 1219; Conservative 0; Mismatches 650; Indels 3; Gaps 1;

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Qy        580 ACTGACGGTATGAAGCGGGAGCGTATATTTTCTCATCGGAAACAGGCCAAGGTCACCTTC 639
Db       6638 ACTGACTAACCGGGGTAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGC 6697

Qy        640 AACAGAAATCAGTACGTCAATGTAAACTACAAGAACCTATATTGGATCGGGCCGTCCATG 699
Db       6698 AAAAGAAGTCCGTTCTGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGG 6757
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Qy       700 AGAAGTATTACGCCCCGCGCCTCGATCTCGAAAGAGAGAAAATGTTACAGAAGAAACTGC 759
Db      6758 AAAGAATTCATGCCCCGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACC 6817

Qy       760 AATTATGCGCCTCTGAAGGAAATAGAAGCAGGTATCAATCACGAAAAGTAGAAAATATGA 819
Db      6818 AGATGATGCCCACCGAAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGA 6877

Qy       820 AAGCAATTACAGCGGAGCGACTCATTTCTGGATTGGGCACATATCTATCATCAGAAGTGA 879
Db      6878 AAGCCATAACCACTGAGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAG--- 6934

Qy       880 ATCCTGTCGAGTGTTACAGAGTCAATTATCCTGTACCAATCTACTCGTCAACGGTAATTA 939
Db      6935 ATCAGCCAGAATGCTATAAGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGG 6994

Qy       940 ACAGGTTTACATCTGCAGAGGTCGCGGTTAAAACGTGCAACTTAGTTATCCAAGAGAATT 999
Db      6995 CGAACTACTCCGATCCACAGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACT 7054

Qy      1000 ACCCTACAGTAGCCAGTTATTGTATAACAGATGAATACGATGCGTATCTTGACATGGTGG 1059
Db      7055 ATCCGACAGTAGCATCTTATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAG 7114

Qy      1060 ACGGCGCATCGTGCTGTCTAGATACAGCCACTTTTTGTCCGGCTAAACTGAGAAGCTACC 1119
Db      7115 ACGAGACAGTCGCATGCCTGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACC 7174

Qy      1120 CAAAGAAGCATAGCTATTTGCAGCCAGAGATAAGATCAGCCGTCCCATCGCCTATACAGA 1179
Db      7175 CGAAAAAACATGAGTATAGAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGA 7234

Qy      1180 ATACATTACAAAATGTATTGGCTGCAGCTACTAAAAGGAATTGCAACGTTACCCAAATGC 1239
Db      7235 ACACGCTACAAAATGTGCTCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGC 7294

Qy      1240 GAGAATTACCTGTCTTAGATTCGGCGGCATTTAATGTTGATTGTTTCAAGAAATACGCAT 1299
Db      7295 GTGAACTGCCAACACTGGACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCAT 7354

Qy      1300 GCAATGATGAGTACTGGGATACCTTTCGCGATAACCCTATTCGGCTAACTACAGAGAACG 1359
Db      7355 GTAATGACGAGTATTGGGAGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTG 7414

Qy      1360 TTACGCAATATGTGACAAAGCTGAAAGGGCCGAAAGCAGCAGCATTGTTTGCGAATACTC 1419
Db      7415 TCACCGCATATGTAGCTAGACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGT 7474

Qy      1420 ATAATCTAAAACCGTTGCAGGAGATACCAATGGATCAATTCGTCATGGATCTAAAGAGAG 1479
Db      7475 ATAATTTGGTCCCATTGCAAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAG 7534

Qy      1480 ATGTCAAAGTTACTCCCGGCACGAAACATACAGAGGAGCGGCCTAAGGTGCAGGTTATTC 1539
Db      7535 ACGTGAAAGTTACACCAGGCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATAC 7594

Qy      1540 AGGCTGCAGATCCCCTTGCTACCGCTTACCTTTGCGGGATCCATCGGGAATTAGTCCGTA 1599
Db      7595 AAGCCGCAGAACCCCTGGCGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTA 7654

Qy      1600 GACTGAATGCGGTGCTTCTGCCAAATATCCATACTCTCTTCGACATGTCAGCGGAAGATT 1659
Db      7655 GGCTTACGGCCGTCTTGCTTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATT 7714

Qy      1660 TTGATGCGATTATTGCTGAACATTTCCACCACGGCGACCCAGTATTGGAAACGGACATCG 1719
Db      7715 TTGATGCAATCATAGCAGAACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCG 7774

Qy      1720 CGTCGTTTGATAAAAGCGAAGACGACGCTATCGCCATTTCGGCGTTGATGATCCTTGAGG 1779
Db      7775 CATCATTCGACAAAAGCCAAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGG 7834

Qy      1780 ACTTAGGTGTCGACCAACCGCTCTTAGATTTGATAGAGGCGGCGTTCGGCAATATCACAT 1839
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Db      7835 ACCTGGGTGTGGATCAACCACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCAT 7894

Qy      1840 CTGTGCACCTACCTACAGGAACGAGGTTTAAATTTGGTGCCATGATGAAATCCGGTATGT 1899
Db      7895 CCACCCATCTACCTACGGGTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGT 7954

Qy      1900 TCTTAACGCTGTTTGTCAACACACTAGTCAATATCATGATTGCTAGCAGAGTACTACGTG 1959
Db      7955 TCCTCACACTTTTTGTCAACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAG 8014

Qy      1960 AACGGTTAACCACGTCAGCGTGCGCGGCCTCTATCGGCGACGATAACATAGTGCATGGTG 2019
Db      8015 AGCGGCTTAAAACGTCCAGATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAG 8074

Qy      2020 TCGTCTCCGACACCTTGATGGCGGAGAGATGCGCCACTTGGCTGAACATGGAAGTAAAAA 2079
Db      8075 TAGTATCTGACAAAGAAATGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGA 8134

Qy      2080 TTATTGATGCAGTTATTGGTATCAAAGCACCCTACTTCTGTGGGGGATTTATCCTGGTGG 2139
Db      8135 TCATCGACGCAGTCATCGGTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAG 8194

Qy      2140 ACCAGATAACAGGCACAGCCTGCAGAGTCGCAGACCCTCTAAAAAGGCTTTTTAAGCTTG 2199
Db      8195 ATTCGGTTACTTCCACAGCGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGG 8254

Qy      2200 GAAAACCATTGCCAGTCGATGATACCCAAGACTGCGACCGCCGCCGGGCACTGCATGATG 2259
Db      8255 GTAAACCGCTCCCAGCCGACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATG 8314

Qy      2260 AAGCAATGCGATGGAACAGAATTGGAATTACGGACGAGTTAGTGAAGGCCGTAGAATCCA 2319
Db      8315 AAACAAAGGCGTGGTTTAGAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCC 8374

Qy      2320 GATACGAGATCATACTGGCAGGCCTGATCATCACGTCTCTGTCCACGTTAGCCGAAAGCG 2379
Db      8375 GGTATGAGGTAGACAATATTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCA 8434

Qy      2380 TTAAGAACTTCAAGAGCATAAGAGGGAGCCCAATCACCCTCTACGGCTGACCTAAATAGG 2439
Db      8435 AAAGAGCATTCCAAGCCATCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGT 8494

Qy      2440 TGACGTAGTAGA 2451
Db      8495 CAGCATAGTACA 8506
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RESULT 13
US-09-275-883-1
; Sequence 1, Application US/09275883
; Publication No. US20030053988A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Nieba, Lars
; APPLICANT: Boorsma, Marco
; TITLE OF INVENTION: Inducible Alphaviral Gene Expression System
; FILE REFERENCE: 1700.0020001
; CURRENT APPLICATION NUMBER: US/09/275,883
; CURRENT FILING DATE: 1999-03-25
; EARLIER APPLICATION NUMBER: US 60/079,562
; EARLIER FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 11282
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:cDNA
US-09-275-883-1

Query Match 12.6%; Score 816; DB 11; Length 11282;

Best Local Similarity 65.1%; Pred. No. 2.3e-232;
Matches 1219; Conservative 0; Mismatches 650; Indels 3; Gaps 1;

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Qy        580 ACTGACGGTATGAAGCGGGAGCGTATATTTTCTCATCGGAAACAGGCCAAGGTCACCTTC 639
Db       6638 ACTGACTAACCGGGGTAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGC 6697

Qy        640 AACAGAAATCAGTACGTCAATGTAAACTACAAGAACCTATATTGGATCGGGCCGTCCATG 699
Db       6698 AAAAGAAGTCCGTTCTGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGG 6757

Qy        700 AGAAGTATTACGCCCCGCGCCTCGATCTCGAAAGAGAGAAAATGTTACAGAAGAAACTGC 759
Db       6758 AAAGAATTCATGCCCCGGTGCTCGACACGTCGAAAGAGGAACAACTCAAACTCAGGTACC 6817

Qy        760 AATTATGCGCCTCTGAAGGAAATAGAAGCAGGTATCAATCACGAAAAGTAGAAAATATGA 819
Db       6818 AGATGATGCCCACCGAAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGA 6877

Qy        820 AAGCAATTACAGCGGAGCGACTCATTTCTGGATTGGGCACATATCTATCATCAGAAGTGA 879
Db       6878 AAGCCATAACCACTGAGCGACTACTGTCAGGACTACGACTGTATAACTCTGCCACAG--- 6934

Qy        880 ATCCTGTCGAGTGTTACAGAGTCAATTATCCTGTACCAATCTACTCGTCAACGGTAATTA 939
Db       6935 ATCAGCCAGAATGCTATAAGATCACCTATCCGAAACCATTGTACTCCAGTAGCGTACCGG 6994

Qy        940 ACAGGTTTACATCTGCAGAGGTCGCGGTTAAAACGTGCAACTTAGTTATCCAAGAGAATT 999
Db       6995 CGAACTACTCCGATCCACAGTTCGCTGTAGCTGTCTGTAACAACTATCTGCATGAGAACT 7054

Qy       1000 ACCCTACAGTAGCCAGTTATTGTATAACAGATGAATACGATGCGTATCTTGACATGGTGG 1059
Db       7055 ATCCGACAGTAGCATCTTATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAG 7114

Qy       1060 ACGGCGCATCGTGCTGTCTAGATACAGCCACTTTTTGTCCGGCTAAACTGAGAAGCTACC 1119
Db       7115 ACGAGACAGTCGCATGCCTGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACC 7174

Qy       1120 CAAAGAAGCATAGCTATTTGCAGCCAGAGATAAGATCAGCCGTCCCATCGCCTATACAGA 1179
Db       7175 CGAAAAAACATGAGTATAGAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGA 7234

Qy       1180 ATACATTACAAAATGTATTGGCTGCAGCTACTAAAAGGAATTGCAACGTTACCCAAATGC 1239
Db       7235 ACACGCTACAAAATGTGCTCATTGCCGCAACTAAAAGAAATTGCAACGTCACGCAGATGC 7294

Qy       1240 GAGAATTACCTGTCTTAGATTCGGCGGCATTTAATGTTGATTGTTTCAAGAAATACGCAT 1299
Db       7295 GTGAACTGCCAACACTGGACTCAGCGACATTCAATGTCGAATGCTTTCGAAAATATGCAT 7354

Qy       1300 GCAATGATGAGTACTGGGATACCTTTCGCGATAACCCTATTCGGCTAACTACAGAGAACG 1359
Db       7355 GTAATGACGAGTATTGGGAGGAGTTCGCTCGGAAGCCAATTAGGATTACCACTGAGTTTG 7414

Qy       1360 TTACGCAATATGTGACAAAGCTGAAAGGGCCGAAAGCAGCAGCATTGTTTGCGAATACTC 1419
Db       7415 TCACCGCATATGTAGCTAGACTGAAAGGCCCTAAGGCCGCCGCACTATTTGCAAAGACGT 7474

Qy       1420 ATAATCTAAAACCGTTGCAGGAGATACCAATGGATCAATTCGTCATGGATCTAAAGAGAG 1479
Db       7475 ATAATTTGGTCCCATTGCAAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAG 7534

Qy       1480 ATGTCAAAGTTACTCCCGGCACGAAACATACAGAGGAGCGGCCTAAGGTGCAGGTTATTC 1539
Db       7535 ACGTGAAAGTTACACCAGGCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATAC 7594

Qy       1540 AGGCTGCAGATCCCCTTGCTACCGCTTACCTTTGCGGGATCCATCGGGAATTAGTCCGTA 1599
Db       7595 AAGCCGCAGAACCCCTGGCGACTGCTTACTTATGCGGGATTCACCGGGAATTAGTGCGTA 7654

Qy       1600 GACTGAATGCGGTGCTTCTGCCAAATATCCATACTCTCTTCGACATGTCAGCGGAAGATT 1659
Db       7655 GGCTTACGGCCGTCTTGCTTCCAAACATTCACACGCTTTTTGACATGTCGGCGGAGGATT 7714

Qy       1660 TTGATGCGATTATTGCTGAACATTTCCACCACGGCGACCCAGTATTGGAAACGGACATCG 1719
Db       7715 TTGATGCAATCATAGCAGAACACTTCAAGCAAGGCGACCCGGTACTGGAGACGGATATCG 7774

Qy       1720 CGTCGTTTGATAAAAGCGAAGACGACGCTATCGCCATTTCGGCGTTGATGATCCTTGAGG 1779
Db       7775 CATCATTCGACAAAAGCCAAGACGACGCTATGGCGTTAACCGGTCTGATGATCTTGGAGG 7834

Qy       1780 ACTTAGGTGTCGACCAACCGCTCTTAGATTTGATAGAGGCGGCGTTCGGCAATATCACAT 1839
Db       7835 ACCTGGGTGTGGATCAACCACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCAT 7894

Qy       1840 CTGTGCACCTACCTACAGGAACGAGGTTTAAATTTGGTGCCATGATGAAATCCGGTATGT 1899
Db       7895 CCACCCATCTACCTACGGGTACTCGTTTTAAATTCGGGGCGATGATGAAATCCGGAATGT 7954

Qy       1900 TCTTAACGCTGTTTGTCAACACACTAGTCAATATCATGATTGCTAGCAGAGTACTACGTG 1959
Db       7955 TCCTCACACTTTTTGTCAACACAGTTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAG 8014

Qy       1960 AACGGTTAACCACGTCAGCGTGCGCGGCCTCTATCGGCGACGATAACATAGTGCATGGTG 2019
Db       8015 AGCGGCTTAAAACGTCCAGATGTGCAGCGTTCATTGGCGACGACAACATCATACATGGAG 8074

Qy       2020 TCGTCTCCGACACCTTGATGGCGGAGAGATGCGCCACTTGGCTGAACATGGAAGTAAAAA 2079
Db       8075 TAGTATCTGACAAAGAAATGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAGGTTAAGA 8134

Qy       2080 TTATTGATGCAGTTATTGGTATCAAAGCACCCTACTTCTGTGGGGGATTTATCCTGGTGG 2139
Db       8135 TCATCGACGCAGTCATCGGTGAGAGACCACCTTACTTCTGCGGCGGATTTATCTTGCAAG 8194

Qy       2140 ACCAGATAACAGGCACAGCCTGCAGAGTCGCAGACCCTCTAAAAAGGCTTTTTAAGCTTG 2199
Db       8195 ATTCGGTTACTTCCACAGCGTGCCGCGTGGCGGATCCCCTGAAAAGGCTGTTTAAGTTGG 8254

Qy       2200 GAAAACCATTGCCAGTCGATGATACCCAAGACTGCGACCGCCGCCGGGCACTGCATGATG 2259
Db       8255 GTAAACCGCTCCCAGCCGACGACGAGCAAGACGAAGACAGAAGACGCGCTCTGCTAGATG 8314

Qy       2260 AAGCAATGCGATGGAACAGAATTGGAATTACGGACGAGTTAGTGAAGGCCGTAGAATCCA 2319
Db       8315 AAACAAAGGCGTGGTTTAGAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCC 8374

Qy       2320 GATACGAGATCATACTGGCAGGCCTGATCATCACGTCTCTGTCCACGTTAGCCGAAAGCG 2379
Db       8375 GGTATGAGGTAGACAATATTACACCTGTCCTACTGGCATTGAGAACTTTTGCCCAGAGCA 8434

Qy       2380 TTAAGAACTTCAAGAGCATAAGAGGGAGCCCAATCACCCTCTACGGCTGACCTAAATAGG 2439
Db       8435 AAAGAGCATTCCAAGCCATCAGAGGGGAAATAAAGCATCTCTACGGTGGTCCTAAATAGT 8494

Qy       2440 TGACGTAGTAGA 2451
Db       8495 CAGCATAGTACA 8506
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RESULT 14
US-09-190-246-4
; Sequence 4, Application US/09190246
; Publication No. US20030180257A1
; GENERAL INFORMATION:
; APPLICANT: Parrington, Mark
; APPLICANT: Li, Xiaomao
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: ALPHAVIRUS VECTORS FOR PARAMYXOVIRUS VACCINES
; FILE REFERENCE: Parrington et al.
; CURRENT APPLICATION NUMBER: US/09/190,246
; CURRENT FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4
; LENGTH: 8100
; TYPE: DNA
; ORGANISM: Semliki Forest virus
US-09-190-246-4

Query Match 11.8%; Score 764; DB 12; Length 8100;
Best Local Similarity 63.2%; Pred. No. 7.2e-217;
Matches 1175; Conservative 0; Mismatches 685; Indels 0; Gaps 0;

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Qy       594 GCGGGAGCGTATATTTTCTCATCGGAAACAGGCCAAGGTCACCTTCAACAGAAATCAGTA 653
Db      5251 GCGGGTGCATATATTTTCTCCTCGGACACTGGCAGCGGACATTTACAACAAAAATCCGTT 5310

Qy       654 CGTCAATGTAAACTACAAGAACCTATATTGGATCGGGCCGTCCATGAGAAGTATTACGCC 713
Db      5311 AGGCAGCACAATCTCCAGTGCGCACAACTGGATGCGGTCCAGGAGGAGAAAATGTACCCG 5370

Qy       714 CCGCGCCTCGATCTCGAAAGAGAGAAAATGTTACAGAAGAAACTGCAATTATGCGCCTCT 773
Db      5371 CCAAAATTGGATACTGAGAGGGAGAAGCTGTTGCTGCTGAAAATGCAGATGCACCCATCG 5430

Qy       774 GAAGGAAATAGAAGCAGGTATCAATCACGAAAAGTAGAAAATATGAAAGCAATTACAGCG 833
Db      5431 GAGGCTAATAAGAGTCGATACCAGTCTCGCAAAGTGGAGAACATGAAAGCCACGGTGGTG 5490

Qy       834 GAGCGACTCATTTCTGGATTGGGCACATATCTATCATCAGAAGTGAATCCTGTCGAGTGT 893
Db      5491 GACAGGCTCACATCGGGGGCCAGATTGTACACGGGAGCGGACGTAGGCCGCATACCAACA 5550

Qy       894 TACAGAGTCAATTATCCTGTACCAATCTACTCGTCAACGGTAATTAACAGGTTTACATCT 953
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Qy       954 GCAGAGGTCGCGGTTAAAACGTGCAACTTAGTTATCCAAGAGAATTACCCTACAGTAGCC 1013
Db      5611 CCCGATGTAGCAATCGCAGCGTGCAACGAATACCTATCCAGAAATTACCCAACAGTGGCG 5670

Qy      1014 AGTTATTGTATAACAGATGAATACGATGCGTATCTTGACATGGTGGACGGCGCATCGTGC 1073
Db      5671 TCGTACCAGATAACAGATGAATACGACGCATACTTGGACATGGTTGACGGGTCGGATAGT 5730

Qy      1074 TGTCTAGATACAGCCACTTTTTGTCCGGCTAAACTGAGAAGCTACCCAAAGAAGCATAGC 1133
Db      5731 TGCTTGGACAGAGCGACATTCTGCCCGGCGAAGCTCCGGTGCTACCCGAAACATCATGCG 5790

Qy      1134 TATTTGCAGCCAGAGATAAGATCAGCCGTCCCATCGCCTATACAGAATACATTACAAAAT 1193
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Qy      1194 GTATTGGCTGCAGCTACTAAAAGGAATTGCAACGTTACCCAAATGCGAGAATTACCTGTC 1253
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Qy      1374 ACAAAGCTGAAAGGGCCGAAAGCAGCAGCATTGTTTGCGAATACTCATAATCTAAAACCG 1433
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Qy      1434 TTGCAGGAGATACCAATGGATCAATTCGTCATGGATCTAAAGAGAGATGTCAAAGTTACT 1493
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Qy      1494 CCCGGCACGAAACATACAGAGGAGCGGCCTAAGGTGCAGGTTATTCAGGCTGCAGATCCC 1553
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Qy      1674 GCTGAACATTTCCACCACGGCGACCCAGTATTGGAAACGGACATCGCGTCGTTTGATAAA 1733
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Qy      1734 AGCGAAGACGACGCTATCGCCATTTCGGCGTTGATGATCCTTGAGGACTTAGGTGTCGAC 1793
Db      6391 AGCCAGGACGACTCCTTGGCTCTTACAGGTTTAATGATCCTCGAAGATCTAGGGGTGGAT 6450

Qy      1794 CAACCGCTCTTAGATTTGATAGAGGCGGCGTTCGGCAATATCACATCTGTGCACCTACCT 1853
Db      6451 CAGTACCTGCTGGACTTGATCGAGGCAGCCTTTGGGGAAATATCCAGCTGTCACCTACCA 6510

Qy      1854 ACAGGAACGAGGTTTAAATTTGGTGCCATGATGAAATCCGGTATGTTCTTAACGCTGTTT 1913
Db      6511 ACTGGCACGCGCTTCAAGTTCGGAGCTATGATGAAATCGGGCATGTTTCTGACTTTGTTT 6570

Qy      1914 GTCAACACACTAGTCAATATCATGATTGCTAGCAGAGTACTACGTGAACGGTTAACCACG 1973
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Qy      1974 TCAGCGTGCGCGGCCTCTATCGGCGACGATAACATAGTGCATGGTGTCGTCTCCGACACC 2033
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Qy      2034 TTGATGGCGGAGAGATGCGCCACTTGGCTGAACATGGAAGTAAAAATTATTGATGCAGTT 2093
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Qy      2094 ATTGGTATCAAAGCACCCTACTTCTGTGGGGGATTTATCCTGGTGGACCAGATAACAGGC 2153
Db      6751 ATGGGCGAAAAACCCCCATATTTTTGTGGGGGATTCATAGTTTTTGACAGCGTCACACAG 6810

Qy      2154 ACAGCCTGCAGAGTCGCAGACCCTCTAAAAAGGCTTTTTAAGCTTGGAAAACCATTGCCA 2213
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Qy      2214 GTCGATGATACCCAAGACTGCGACCGCCGCCGGGCACTGCATGATGAAGCAATGCGATGG 2273
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Qy      2274 AACAGAATTGGAATTACGGACGAGTTAGTGAAGGCCGTAGAATCCAGATACGAGATCATA 2333
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Qy      2334 CTGGCAGGCCTGATCATCACGTCTCTGTCCACGTTAGCCGAAAGCGTTAAGAACTTCAAG 2393
Db      6991 GGCTGCAAAAGTATCCTCATAGCCATGGCCACCTTGGCGAGGGACATTAAGGCGTTTAAG 7050

Qy      2394 AGCATAAGAGGGAGCCCAATCACCCTCTACGGCTGACCTAAATAGGTGACGTAGTAGACA 2453
Db      7051 AAATTGAGAGGACCTGTTATACACCTCTACGGCGGTCCTAGATTGGTGCGTTAATACACA 7110
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RESULT 15
US-09-994-412-3
; Sequence 3, Application US/09994412
; Publication No. US20030059943A1
; GENERAL INFORMATION:
; APPLICANT: Certa, Ulrich
; APPLICANT: Lundstrom, Kenneth
; TITLE OF INVENTION: Inhibition of Expression of a Target Gene
; FILE REFERENCE: 20787
; CURRENT APPLICATION NUMBER: US/09/994,412
; CURRENT FILING DATE: 2002-03-12

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;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 10610
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: pSFV2gen(PD) vector
US-09-994-412-3

  Query Match            11.8%;  Score 764;  DB 11;  Length 10610;
  Best Local Similarity   63.2%;  Pred. No. 8.8e-217;
  Matches 1175;  Conservative    0;  Mismatches  685;  Indels    0;  Gaps    0;

Qy       594 GCGGGAGCGTATATTTTCTCATCGGAAACAGGCCAAGGTCACCTTCAACAGAAATCAGTA 653
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Db      5529 GCGGGTGCATATATTTTCTCCTCGGACACTGGCAGCGGACATTTACAACAAAAATCCGTT 5588

Qy       654 CGTCAATGTAAACTACAAGAACCTATATTGGATCGGGCCGTCCATGAGAAGTATTACGCC 713
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Db      5589 AGGCAGCACAATCTCCAGTGCGCACAACTGGATGCGGTCCAGGAGGAGAAAATGTACCCG 5648

Qy       714 CCGCGCCTCGATCTCGAAAAGAGAGAAAATGTTACAGAAGAAACTGCAATTATGCGCCTCT 773
             ||     | |||   || || |||||  |||| | |  |||| ||||   |   | | ||
Db      5649 CCAAAATTGGATACTGAGAGGGAGAAGCTGTTGCTGCTGAAAATGCAGATGCACCCATCG 5708

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Qy       834 GAGCGACTCATTTCTGGATTGGGCACATATCTATCATCAGAAGTGAATCCTGTCGAGTGT 893
             ||  | ||||  || ||      |     ||       | | || ||    |   |
Db      5769 GACAGGCTCACATCGGGGGCCAGATTGTACACGGGAGCGGACGTAGGCCGCATACCAACA 5828

Qy       894 TACAGAGTCAATTATCCTGTACCAATCTACTCGTCAACGGTAATTAACAGGTTTACATCT 953
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Db      7089 ACCGCCTGCCGTGTTTCAGACCCACTTAAGCGCCTGTTCAAGTTGGGTAAGCCGCTAACA 7148

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Job time : 1807 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2003, 22:40:28 ; Search time 326 Seconds
(without alignments)
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Perfect score: 6485
Sequence: 1 caccgccagcaacgacaacc.....tattttgtttttaaaatttc 6485

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2397.6	37.0	11663	1	US-08-801-263A-7	Sequence 7, Appli
3	2397.6	37.0	11663	3	US-09-102-248-7	Sequence 7, Appli
4	2397.6	37.0	11663	4	US-09-367-764-7	Sequence 7, Appli
5	2396	36.9	11663	1	US-08-446-932-1	Sequence 1, Appli
6	2396	36.9	11663	1	US-08-801-263A-1	Sequence 1, Appli
7	2396	36.9	11663	3	US-09-102-248-1	Sequence 1, Appli
8	2396	36.9	11663	4	US-09-367-764-1	Sequence 1, Appli
9	2388.4	36.8	11703	1	US-08-801-263A-8	Sequence 8, Appli
10	2388.4	36.8	11703	3	US-09-102-248-8	Sequence 8, Appli
11	2388.4	36.8	11703	4	US-09-367-764-8	Sequence 8, Appli
12	2386.4	36.8	11717	1	US-08-801-263A-4	Sequence 4, Appli
13	2386.4	36.8	11717	3	US-09-102-248-4	Sequence 4, Appli
14	2386.4	36.8	11717	4	US-09-367-764-4	Sequence 4, Appli
15	2380.4	36.7	11740	4	US-09-415-784-103	Sequence 103, App
16	2380.4	36.7	11740	4	US-09-415-785A-103	Sequence 103, App
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18	2380.4	36.7	11740	4	US-09-415-868-103	Sequence 103, App
19	2380.4	36.7	11740	4	US-09-415-900-103	Sequence 103, App
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21	2369.2	36.5	16656	1	US-08-739-158-1	Sequence 1, Appli
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30	1717.4	26.5	11459	3	US-09-454-721A-3	Sequence 3, Appli
31	1650.8	25.5	7970	4	US-09-193-707-6	Sequence 6, Appli
32	1646.6	25.4	9521	3	US-08-972-218-2	Sequence 2, Appli
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36	863.2	13.3	4003	3	US-08-991-840A-3	Sequence 3, Appli
37	827.6	12.8	8000	4	US-09-415-784-102	Sequence 102, App
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45	824.4	12.7	8000	4	US-09-415-868-101	Sequence 101, App

ALIGNMENTS

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RESULT 1
US-08-991-840A-1
; Sequence 1, Application US/08991840A
; Patent No. 6261570
;  GENERAL INFORMATION:
;    APPLICANT:  Michael D. Parker
;    APPLICANT:  Jonathan F. Smith
;    APPLICANT:  Bruce Crise
;    APPLICANT:  Mark Steve Oberste
;    APPLICANT:  Shannon Schmura
;    TITLE OF INVENTION:  Live Attenuated Virus Vaccines for Eastern Equine Encephalitis
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Charles H. Harris
;      STREET:  USA MRMC -  MRMC-JA
;      CITY:  FORT DETRICK, FREDERICK
;      STATE:  MARYLAND
;      COUNTRY:  USA
;      ZIP:  21702-5012
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Macintosh 7.5
;      SOFTWARE:  Microsoft Word 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/991,840A
;      FILING DATE:  December 16, 1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  Provisional Application 60/047162,
;      FILING DATE:  May 20, 1997
;      APPLICATION NUMBER:  Provisional Application 60/053,652
;      FILING DATE:  July 24, 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Charles H. Harris
;      REGISTRATION NUMBER:  34,616
;      REFERENCE/DOCKET NUMBER:  003/058/SAP RIID 96-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 619-2065
;      TELEFAX:  (301) 619-5034
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11492 base pairs
;      TYPE:  Nucleic acid
;      STRANDEDNESS:  Double
;      TOPOLOGY:  Linear
;    FEATURE:  OTHER INFORMATION:  N at all occurences is = unknown.
;    FEATURE:  OTHER INFORMATION: K at all
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US-08-991-840A-1
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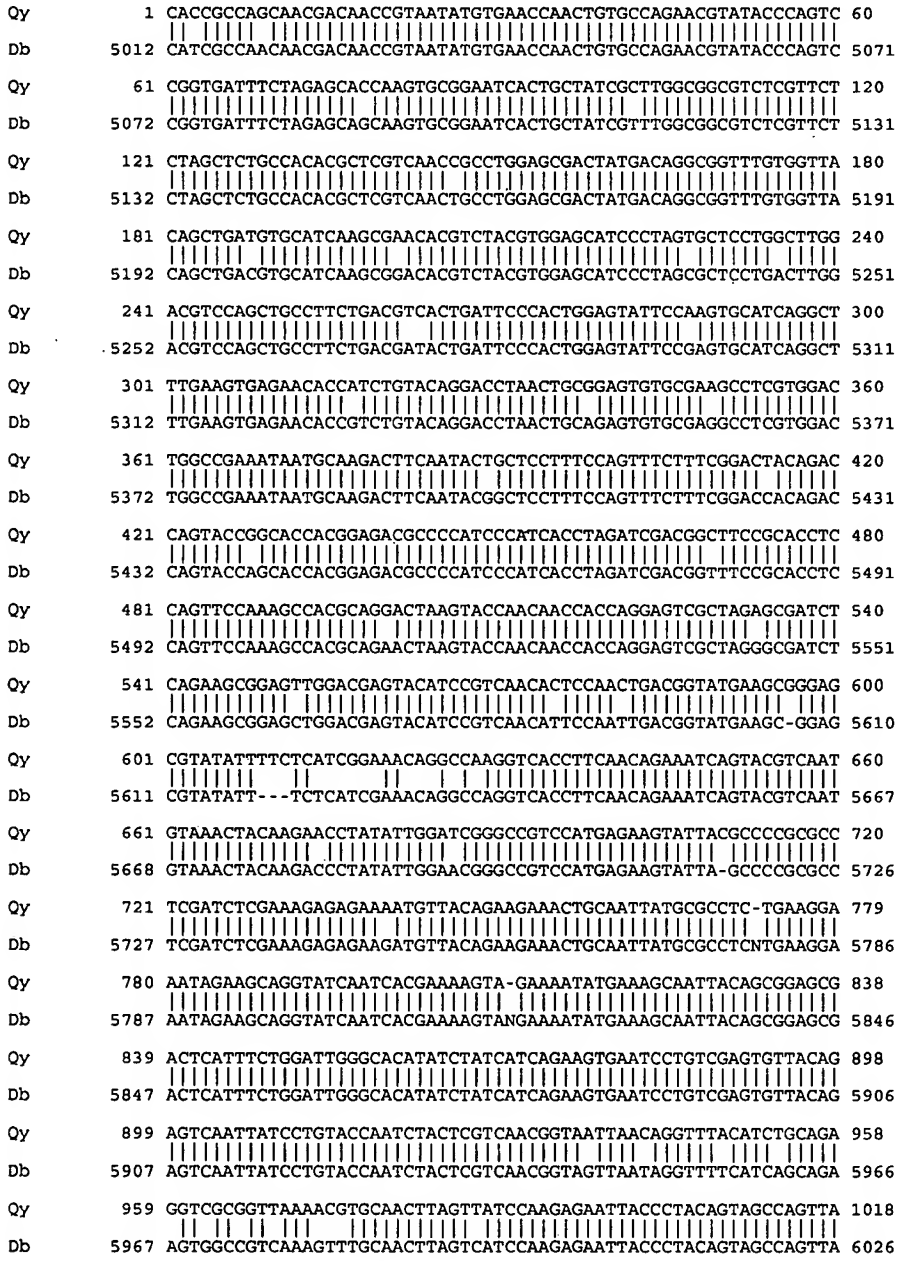

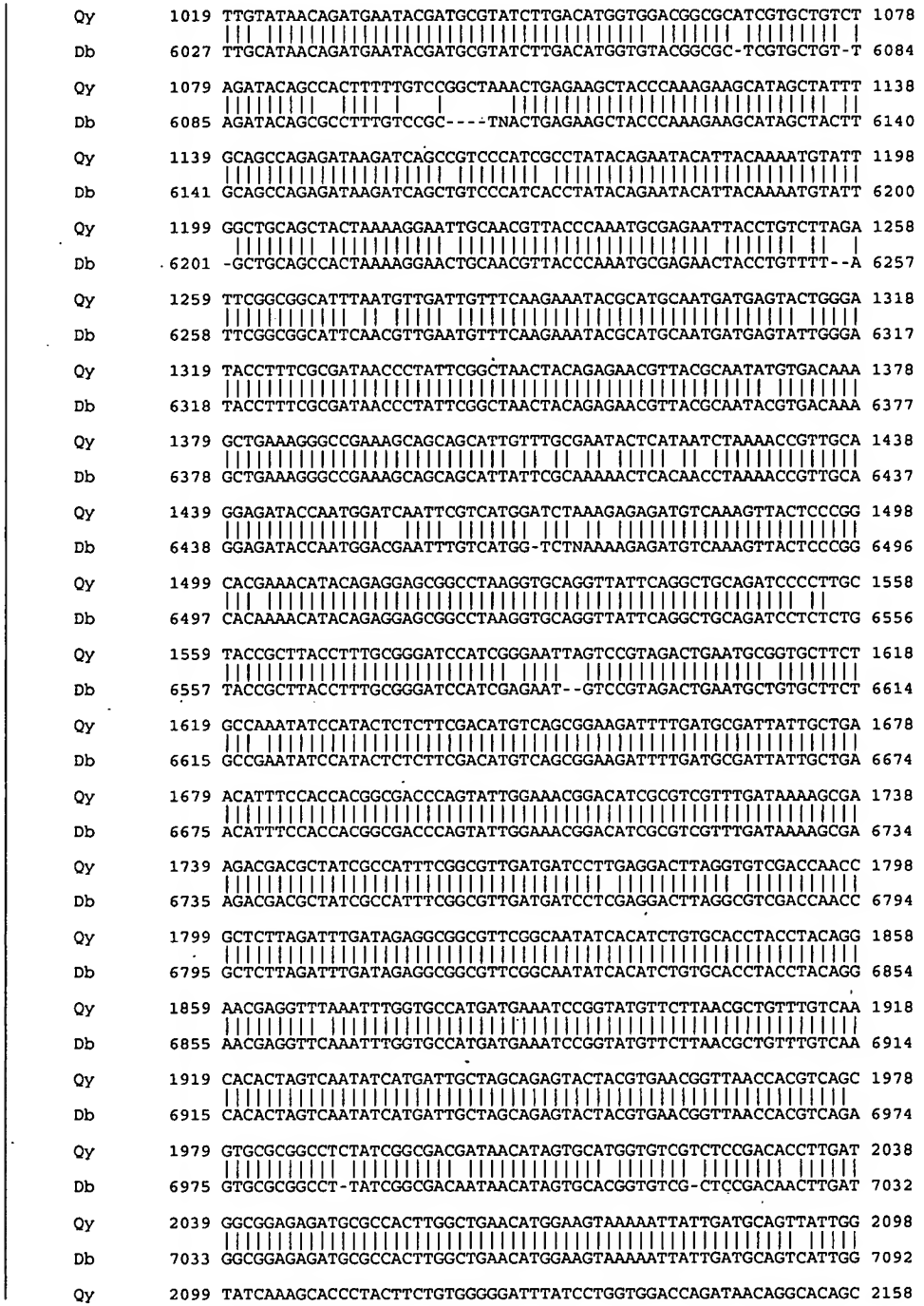

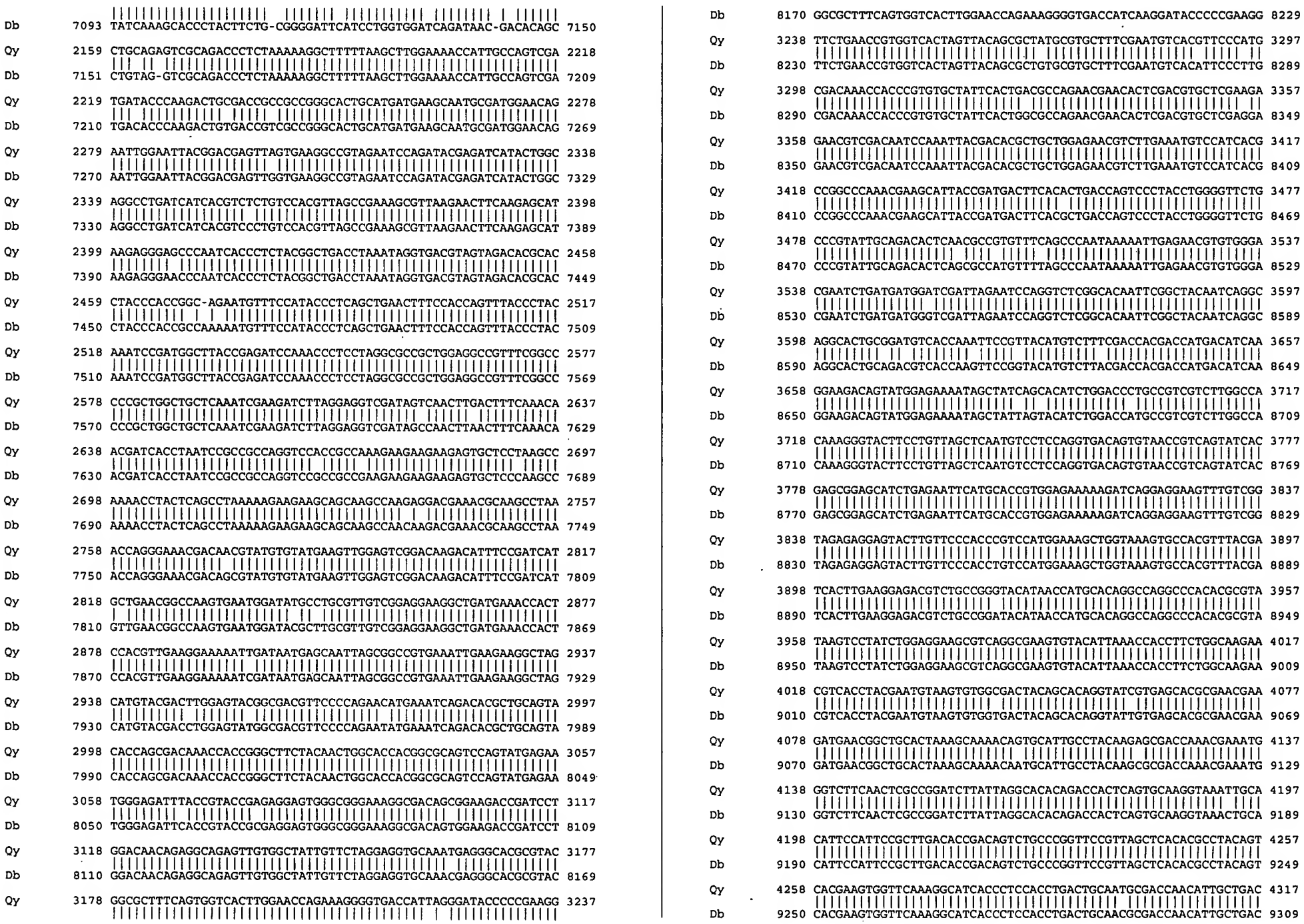

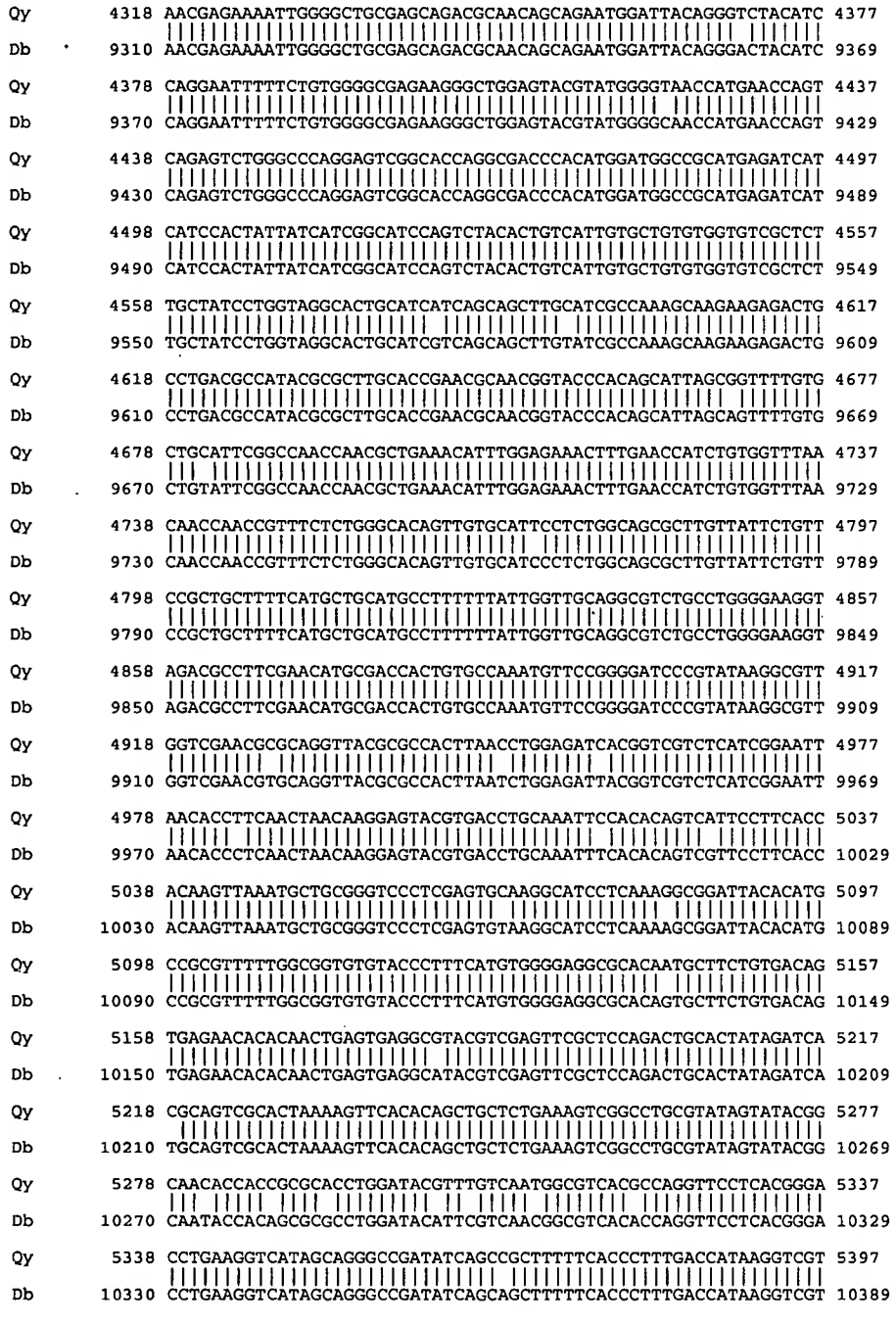
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RESULT 2
US-08-801-263A-7
; Sequence 7, Application US/08801263A
; Patent No. 5811407
;  GENERAL INFORMATION:
;    APPLICANT:  Johnston, Robert E.
;    APPLICANT:  Davis, Nancy L.
;    APPLICANT:  Simpson, Dennis A.
;    TITLE OF INVENTION:  System for the In Vivo Delivery and
;    TITLE OF INVENTION:  Expression of Heterologous Genes in the Bone Marrow
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell Seltzer Park & Gibson, P.A.
;      STREET:  1211 East Morehead Street
;      CITY:  Charlotte
;      STATE:  No. 5811407th Carolina
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/801,263A
;      FILING DATE:  19-FEB-1997
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5470-147
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-420-2200
;      TELEFAX:  919-881-3175
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11663 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-801-263A-7

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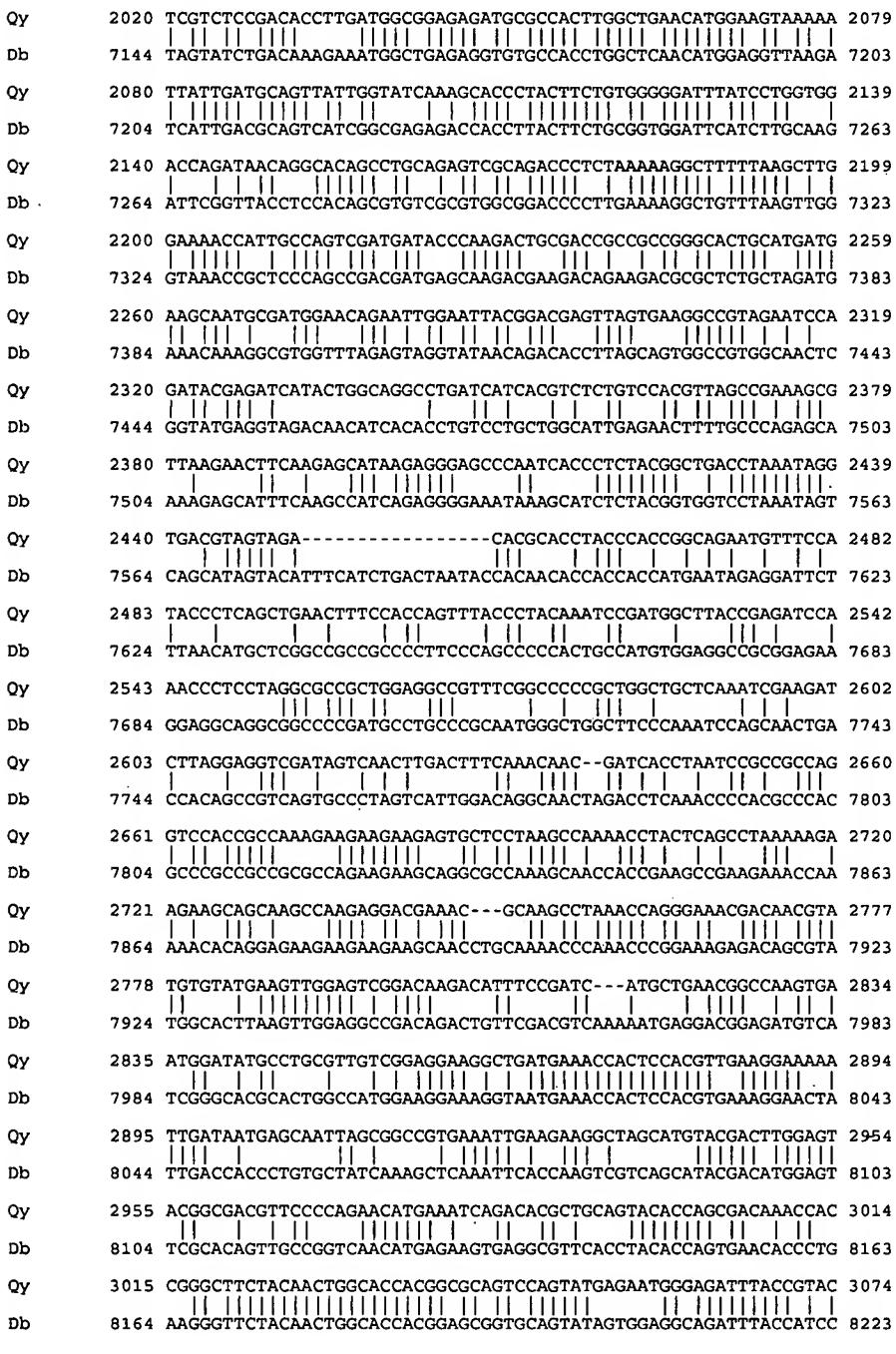

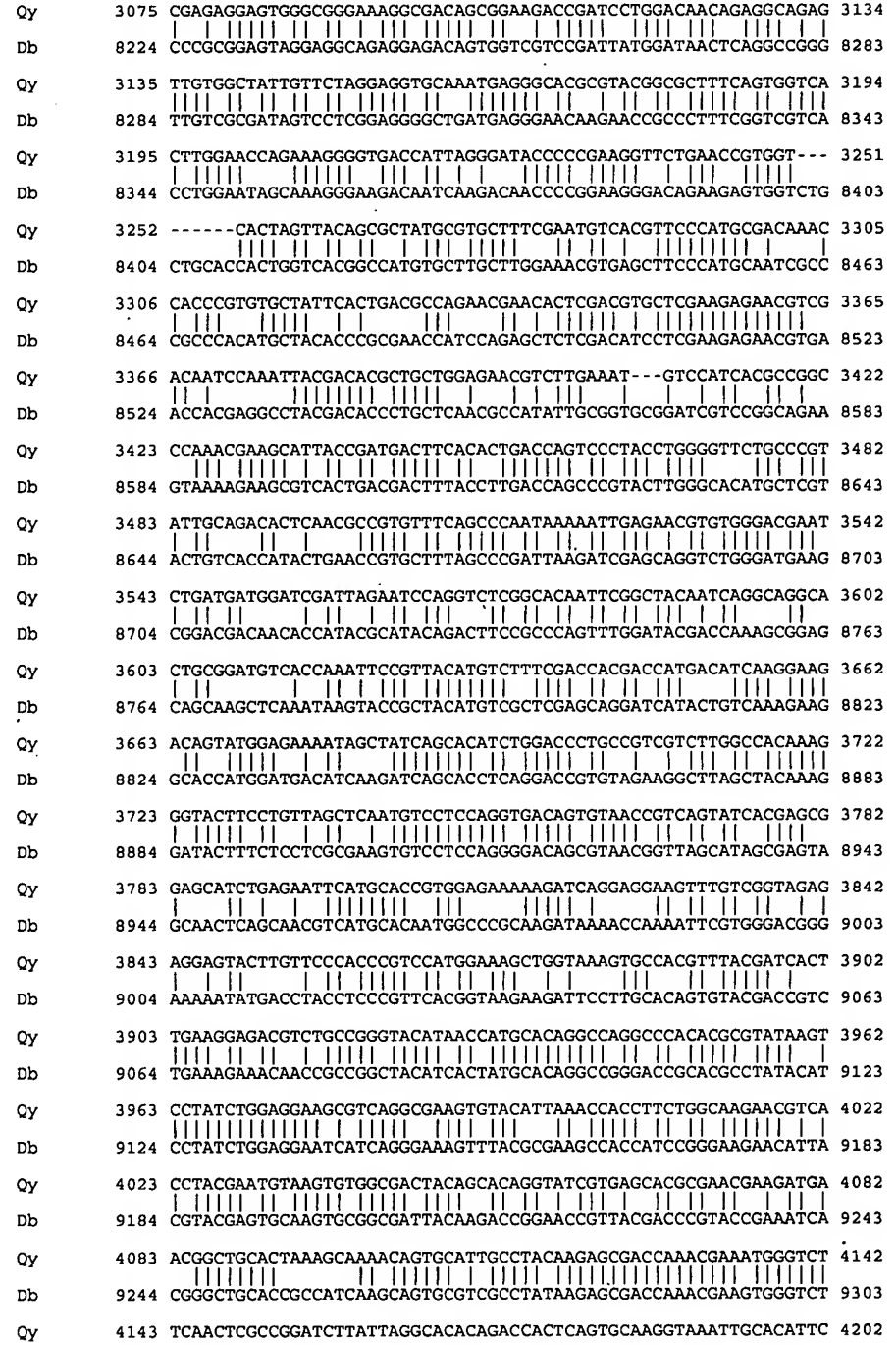

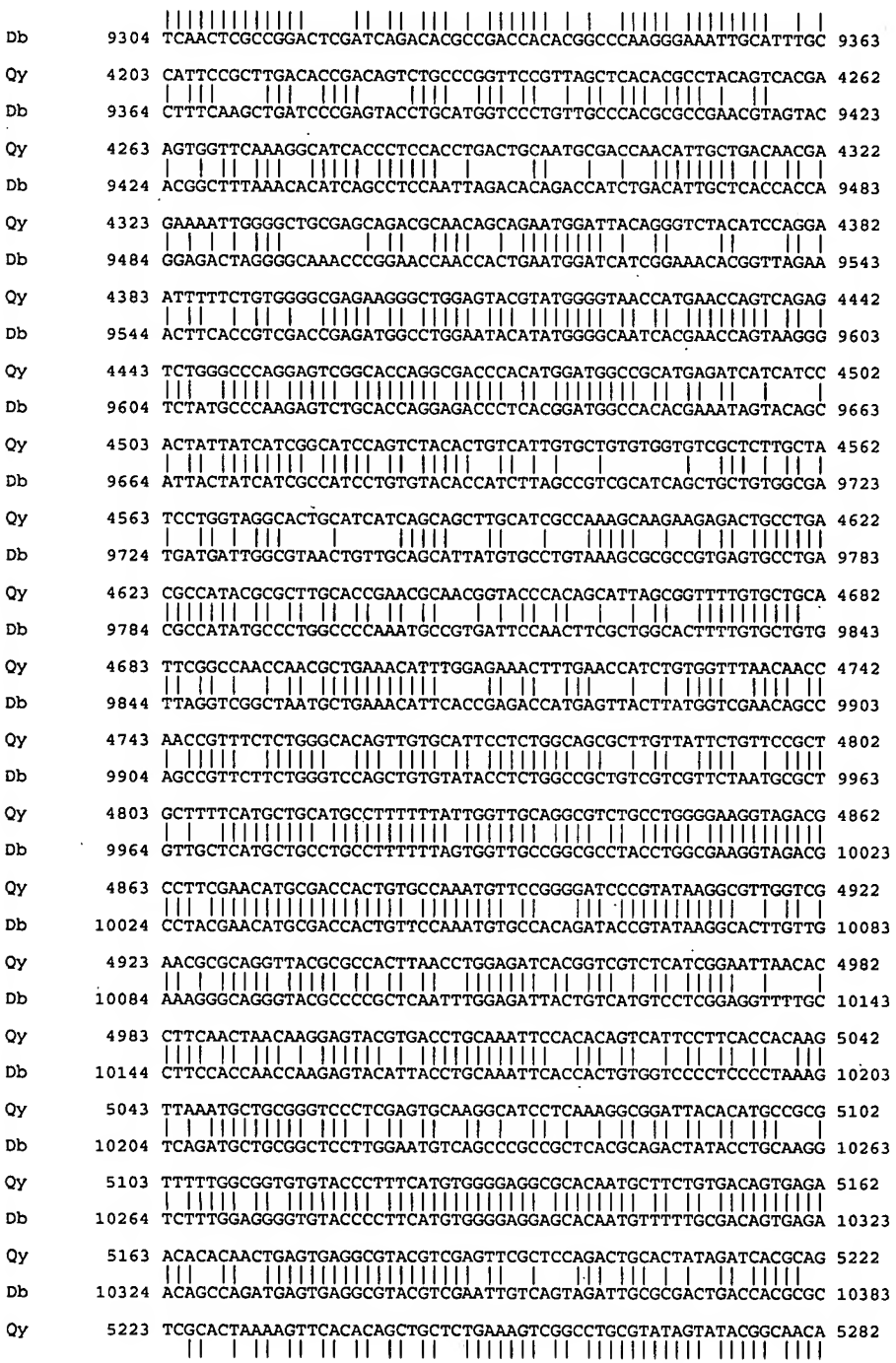
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; Sequence 7, Application US/09102248
; Patent No. 6008035
;  GENERAL INFORMATION:
;    APPLICANT:  Johnston, Robert E.
;    APPLICANT:  Davis, Nancy L.
;    APPLICANT:  Simpson, Dennis A.
;    TITLE OF INVENTION:  System for the In Vivo Delivery and
;    TITLE OF INVENTION:  Expression of Heterologous Genes in the Bone Marrow
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell Seltzer Park & Gibson, P.A.
;      STREET:  1211 East Morehead Street
;      CITY:  Charlotte
;      STATE:  No. 6008035th Carolina
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/102,248
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/801,263
;      FILING DATE:  19-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5470-147
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-420-2200
;      TELEFAX:  919-881-3175
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11663 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-102-248-7

  Query Match             37.0%;  Score 2397.6;  DB 3;  Length 11663;
  Best Local Similarity   64.6%;  Pred. No. 0;
  Matches 3752;  Conservative    0;  Mismatches 1984;  Indels   74;  Gaps    9;

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Db       6304 ACACGTTGCAAAACGTGCTCATTGCCGCGACTAAAAGAAACTGCAACGTCACACAAATGC 6363

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Db       6544 ATAATTTGGTCCCATTGCAAGAAGTGCCTATGGATAGATTCGTCATGGACATGAAAAGAG 6603

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Db       6604 ACGTGAAAGTTACACCTGGCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATAC 6663

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Db       6784 TTGATGCAATCATAGCAGAACACTTCAAGCAAGGTGACCCGGTACTGGAGACGGATATCG 6843

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Db       6844 CCTCGTTCGACAAAAGCCAAGACGACGCTATGGCGTTAACCGGCCTGATGATCTTGGAAG 6903

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              || | ||||| |||||||| ||  | || ||||| |||   || || ||  | ||  |||
Db       6904 ACCTGGGTGTGGACCAACCACTACTCGACTTGATCGAGTGCGCCTTTGGAGAAATATCAT 6963

Qy       1840 CTGTGCACCTACCTACAGGAACGAGGTTTAAATTTGGTGCCATGATGAAATCCGGTATGT 1899
              |    || || || || || ||  | || ||||| || || ||||||||||||||| ||||
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Qy       1900 TCTTAACGCTGTTTGTCAACACACTAGTCAATATCATGATTGCTAGCAGAGTACTACGTG 1959
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Db       7024 TCCTCACGCTCTTTGTCAACACAGTTCTGAATGTCGTTATCGCCAGCAGAGTATTGGAGG 7083

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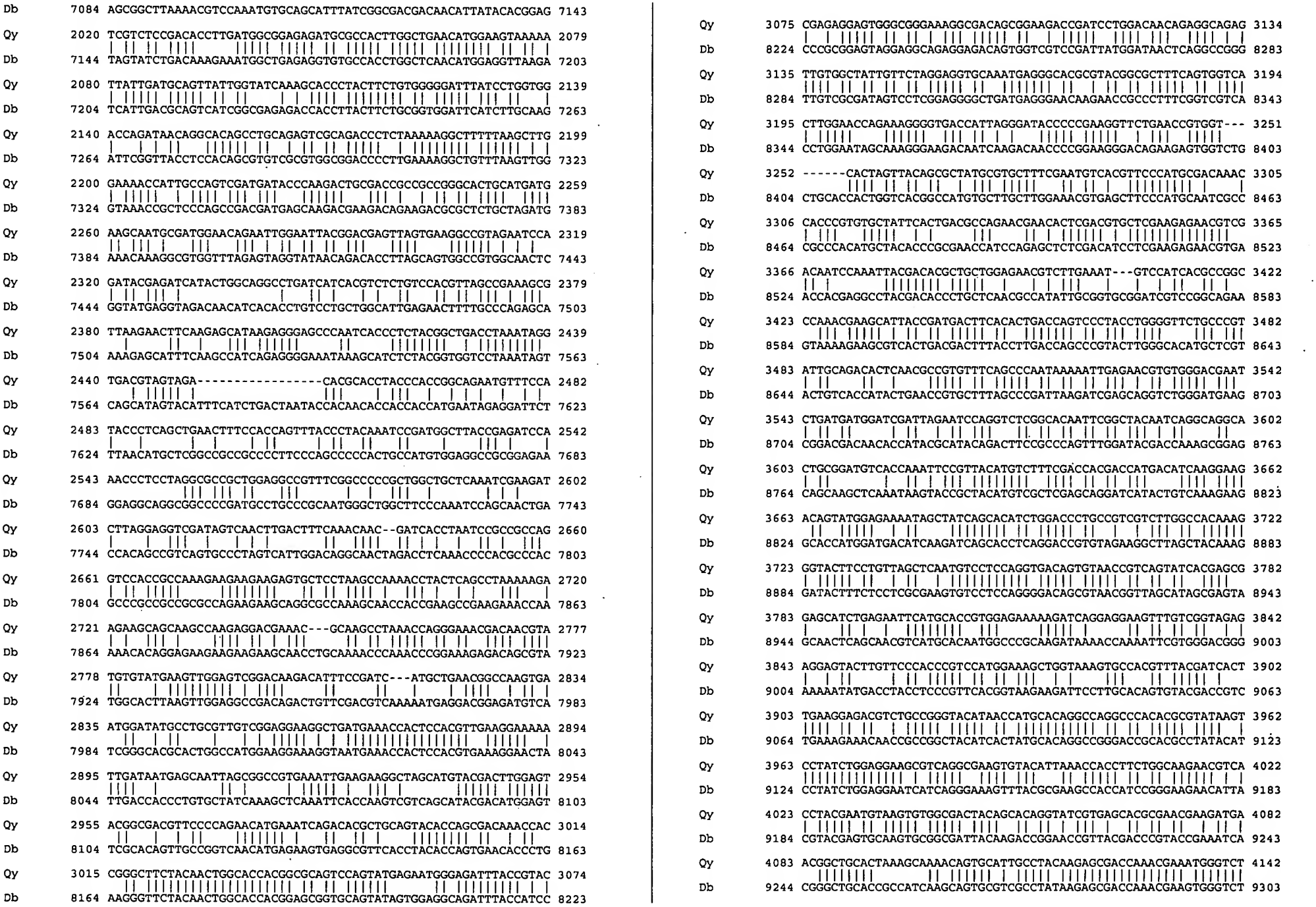

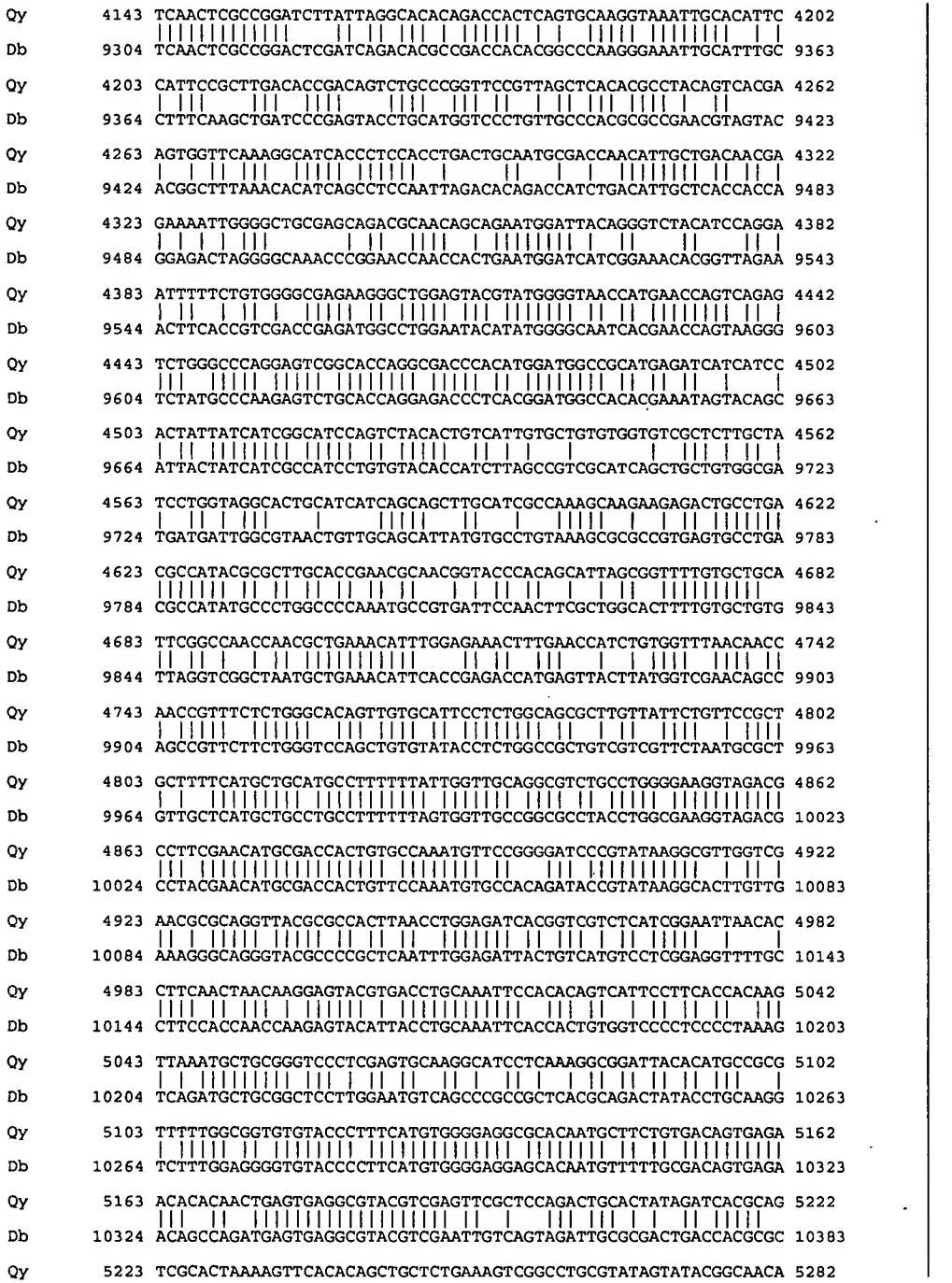
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RESULT 4
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; Sequence 7, Application US/09367764
; Patent No. 6583121
;  GENERAL INFORMATION:
;    APPLICANT:  Johnston, Robert E.
;    APPLICANT:  Davis, Nancy L.
;    APPLICANT:  Simpson, Dennis A.
;    TITLE OF INVENTION:  System for the In Vivo Delivery and
;    TITLE OF INVENTION:  Expression of Heterologous Genes in the Bone Marrow
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell Seltzer Park & Gibson, P.A.
;      STREET:  1211 East Morehead Street
;      CITY:  Charlotte
;      STATE:  No. 6583121th Carolina
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/367,764
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/801,263
;      FILING DATE:  19-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5470-147
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-420-2200
;      TELEFAX:  919-881-3175
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11663 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-367-764-7

  Query Match             37.0%;  Score 2397.6;  DB 4;  Length 11663;
  Best Local Similarity   64.6%;  Pred. No. 0;
  Matches 3752;  Conservative    0;  Mismatches 1984;  Indels   74;  Gaps    9;

Qy        580 ACTGACGGTATGAAGCGGGAGCGTATATTTTCTCATCGGAAACAGGCCAAGGTCACCTTC 639
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Db       5707 ACTGTCTAACCGGGGTAGGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGC 5766

Qy        640 AACAGAAATCAGTACGTCAATGTAAACTACAAGAACCTATATTGGATCGGGCCGTCCATG 699
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Db       5767 AAAAGAAGTCCGTTCTGCAGAACCAGCTTACAGAACCGACCTTGGAGCGCAATGTTCTGG 5826

Qy        700 AGAAGTATTACGCCCCGCGCCTCGATCTCGAAAGAGAGAAAATGTTACAGAAGAAACTGC 759
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Db       6064 CGAACTACTCTGACCCAAAGTTTGCTGTAGCTGTTTGTAACAACTATCTGCATGAGAATT 6123

Qy       1000 ACCCTACAGTAGCCAGTTATTGTATAACAGATGAATACGATGCGTATCTTGACATGGTGG 1059
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Qy       1180 ATACATTACAAAATGTATTGGCTGCAGCTACTAAAAGGAATTGCAACGTTACCCAAATGC 1239
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Db       6304 ACACGTTGCAAAACGTGCTCATTGCCGCGACTAAAAGAAACTGCAACGTCACACAAATGC 6363

Qy       1240 GAGAATTACCTGTCTTAGATTCGGCGGCATTTAATGTTGATTGTTTCAAGAAATACGCAT 1299
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Db       6364 GTGAACTGCCAACACTGGACTCAGCGACATTCAACGTTGAATGCTTTCGAAAATATGCAT 6423

Qy       1300 GCAATGATGAGTACTGGGATACCTTTCGCGATAACCCTATTCGGCTAACTACAGAGAACG 1359
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Qy       1360 TTACGCAATATGTGACAAAGCTGAAAGGGCCGAAAGCAGCAGCATTGTTTGCGAATACTC 1419
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Db       6604 ACGTGAAAGTTACACCTGGCACGAAACACACAGAAGAAAGACCGAAAGTACAAGTGATAC 6663

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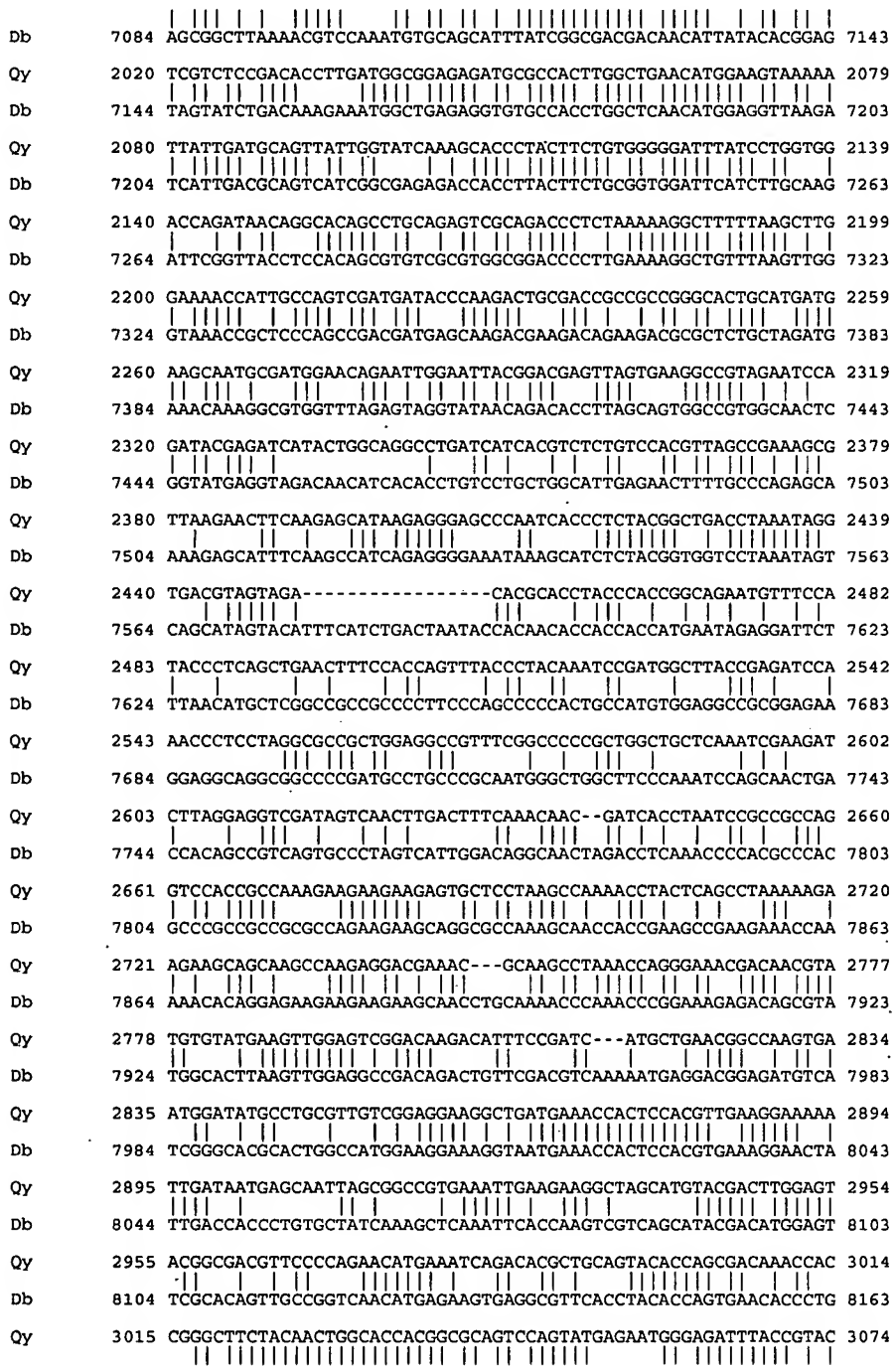

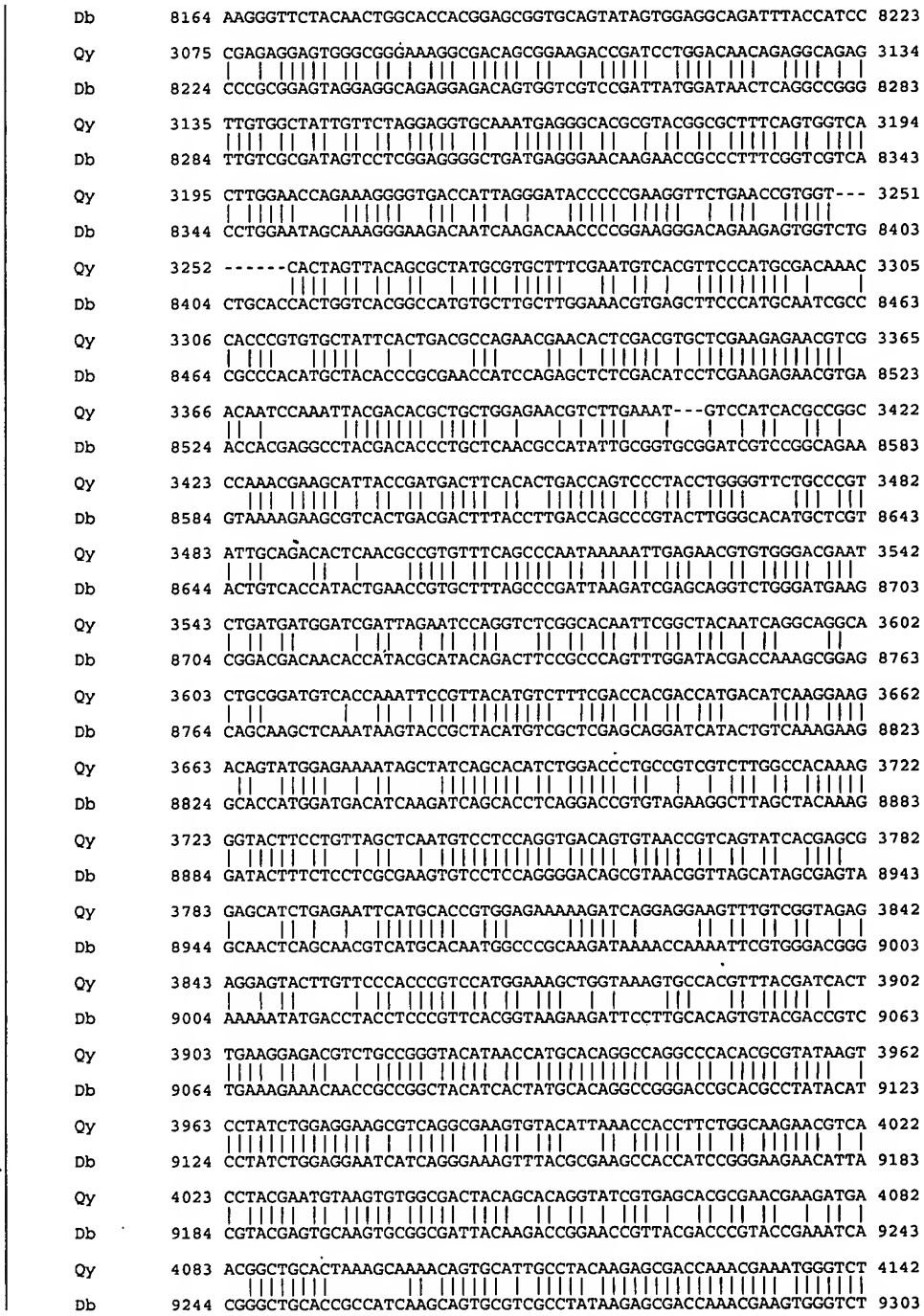

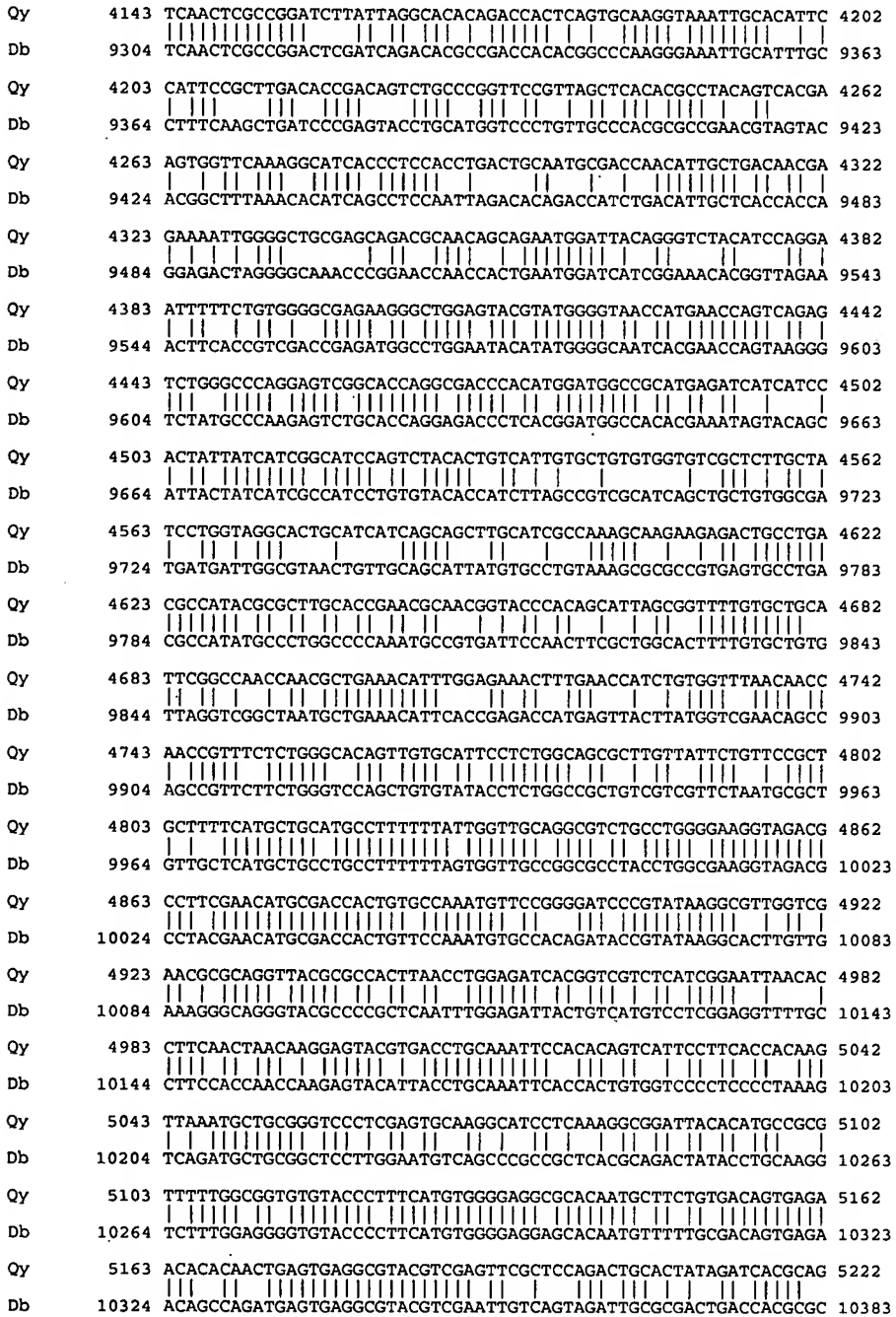
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RESULT 5
US-08-446-932-1
; Sequence 1, Application US/08446932
; Patent No. 5639650
;  GENERAL INFORMATION:
;    APPLICANT:  Johnston, Robert E.
;    APPLICANT:  Simpson, Dennis
;    APPLICANT:  Davis, Nancy L.
;    TITLE OF INVENTION:  cDNA Clone for South African
;    TITLE OF INVENTION:  Arbovirus No. 5639650 86
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kenneth D. Sibley
;      STREET:  Post Office Drawer 34009
;      CITY:  Charlotte
;      STATE:  NC
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,932
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5470-118
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919) 881-3140
;      TELEFAX:  (919) 881-3175
;      TELEX:  575102
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11663 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
US-08-446-932-1

  Query Match             36.9%;  Score 2396;  DB 1;  Length 11663;
  Best Local Similarity   64.6%;  Pred. No. 0;
  Matches 3751;  Conservative    0;  Mismatches 1985;  Indels   74;  Gaps    9;

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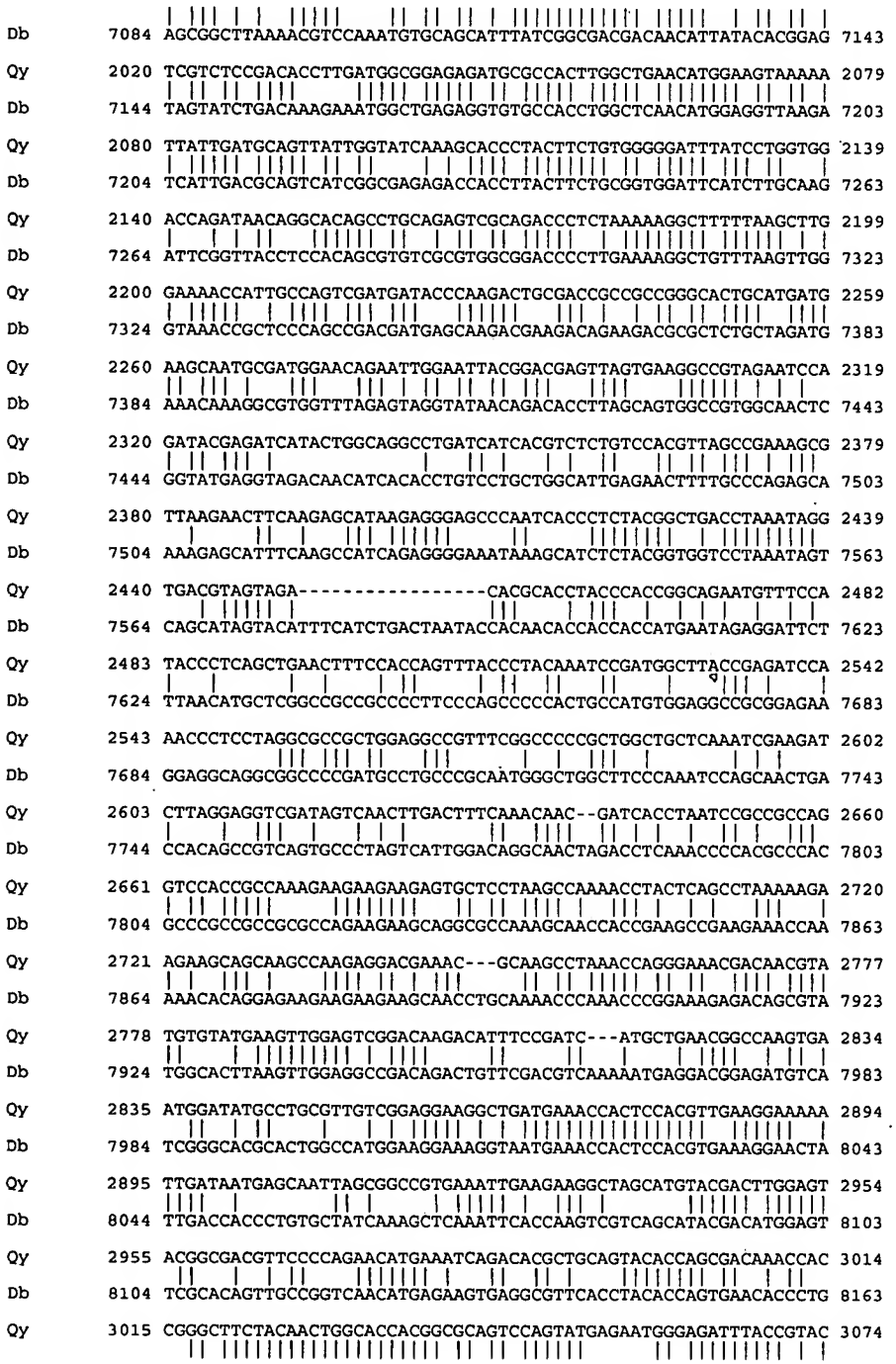

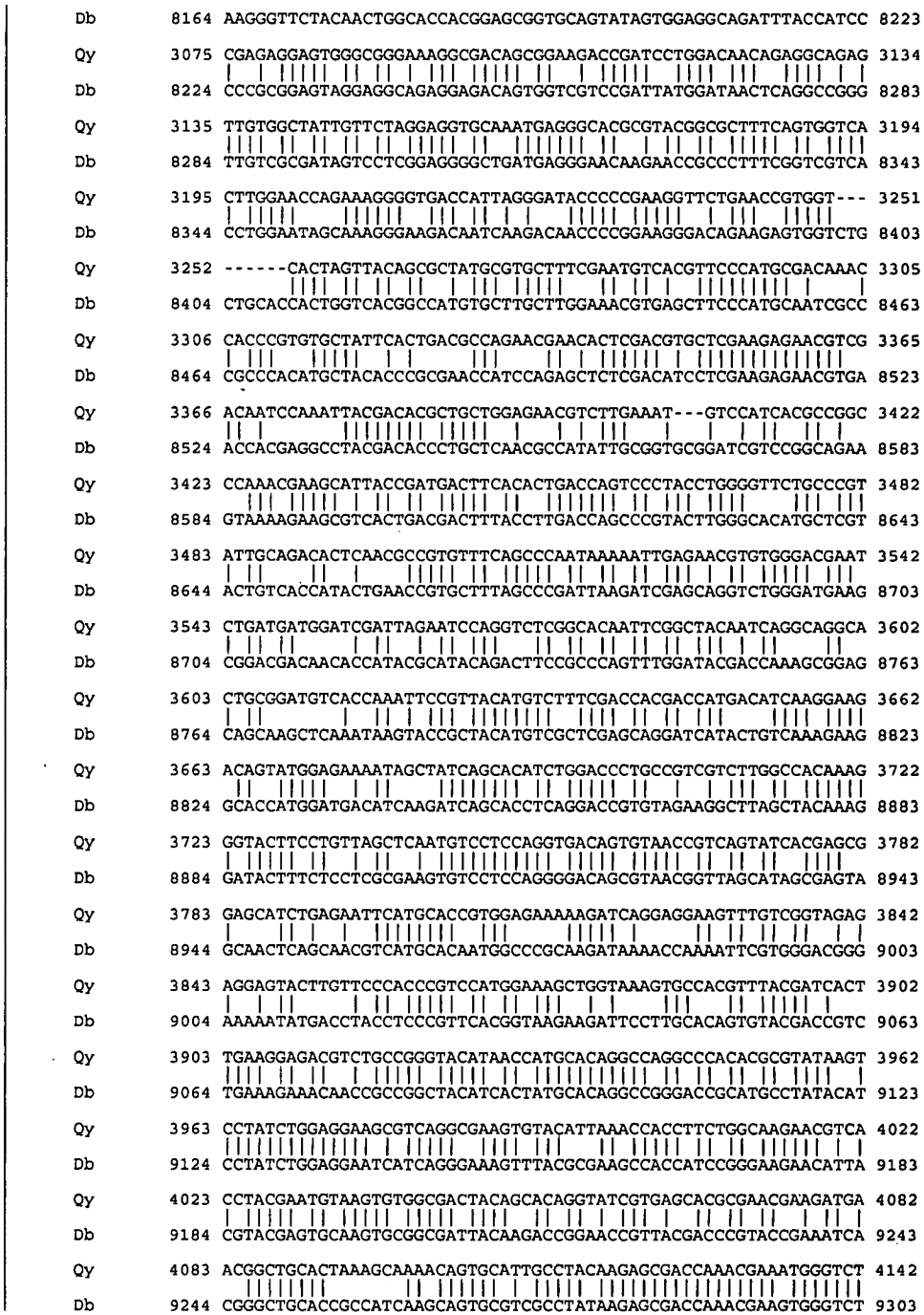

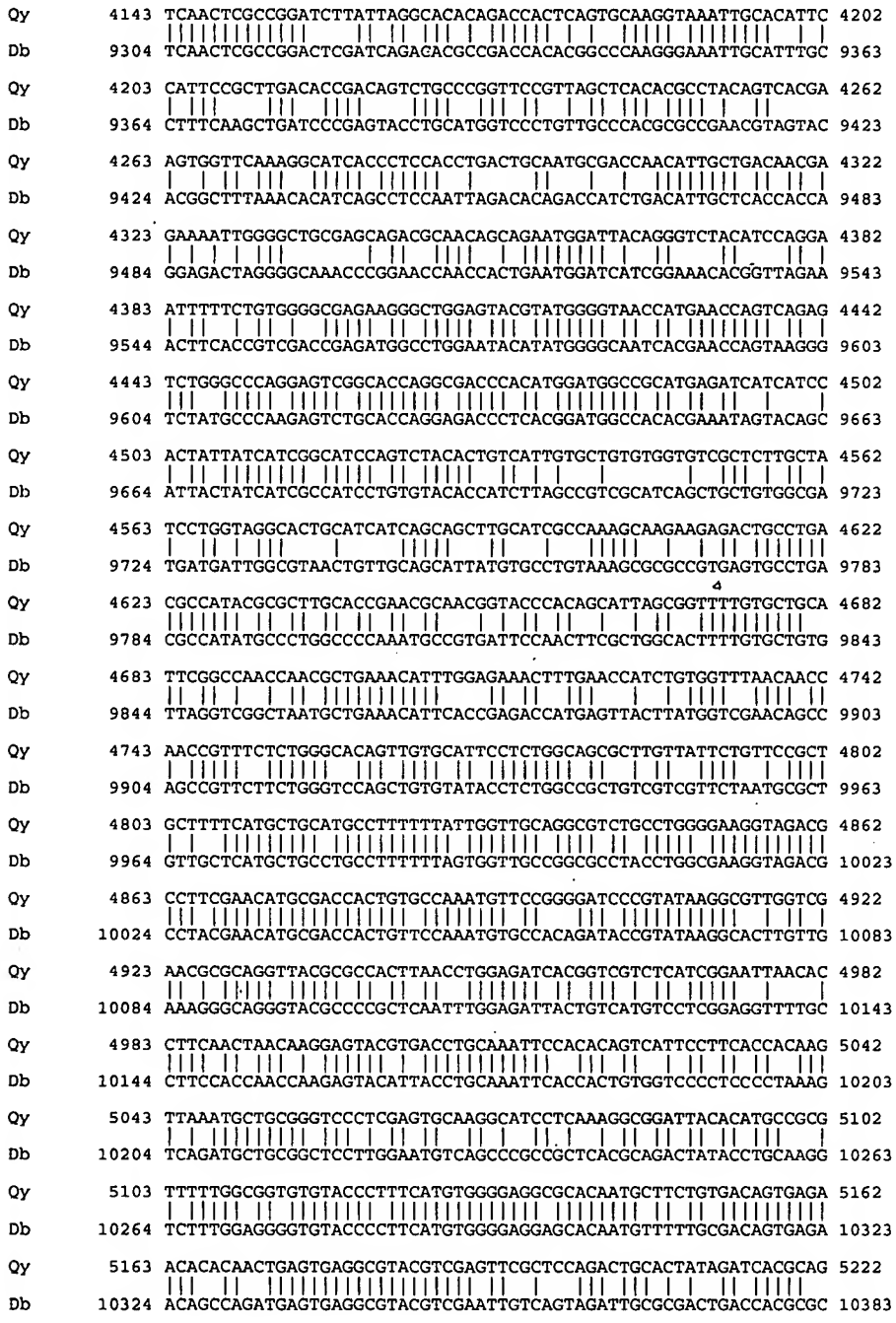
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RESULT 6
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; Patent No. 5811407
;  GENERAL INFORMATION:
;    APPLICANT:  Johnston, Robert E.
;    APPLICANT:  Davis, Nancy L.
;    APPLICANT:  Simpson, Dennis A.
;    TITLE OF INVENTION:  System for the In Vivo Delivery and
;    TITLE OF INVENTION:  Expression of Heterologous Genes in the Bone Marrow
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell Seltzer Park & Gibson, P.A.
;      STREET:  1211 East Morehead Street
;      CITY:  Charlotte
;      STATE:  No. 5811407th Carolina
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/801,263A
;      FILING DATE:  19-FEB-1997
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5470-147
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-420-2200
;      TELEFAX:  919-881-3175
;  INFORMATION FOR SEQ ID NO:  1:
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;      TYPE:  nucleic acid
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US-08-801-263A-1

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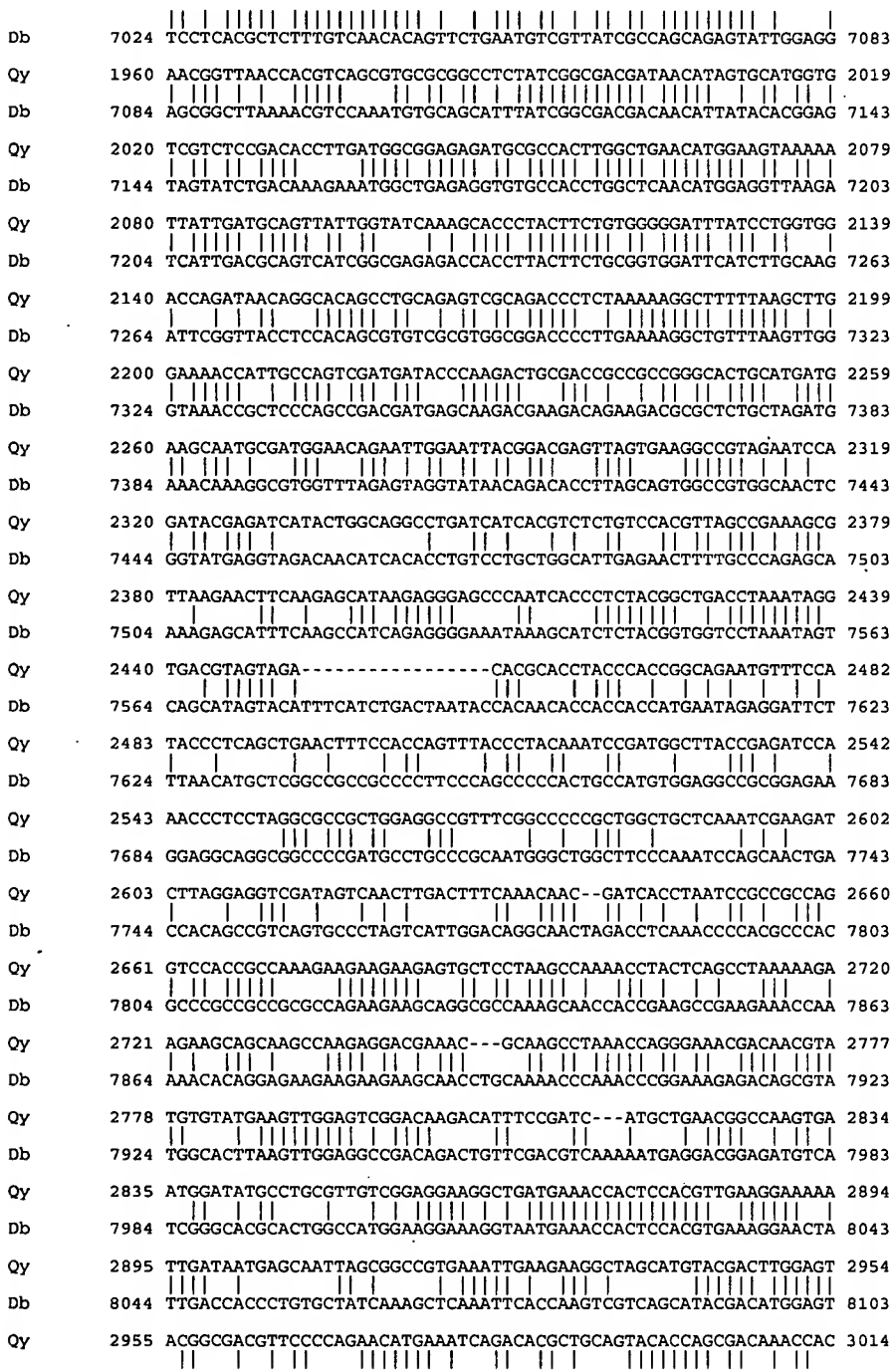
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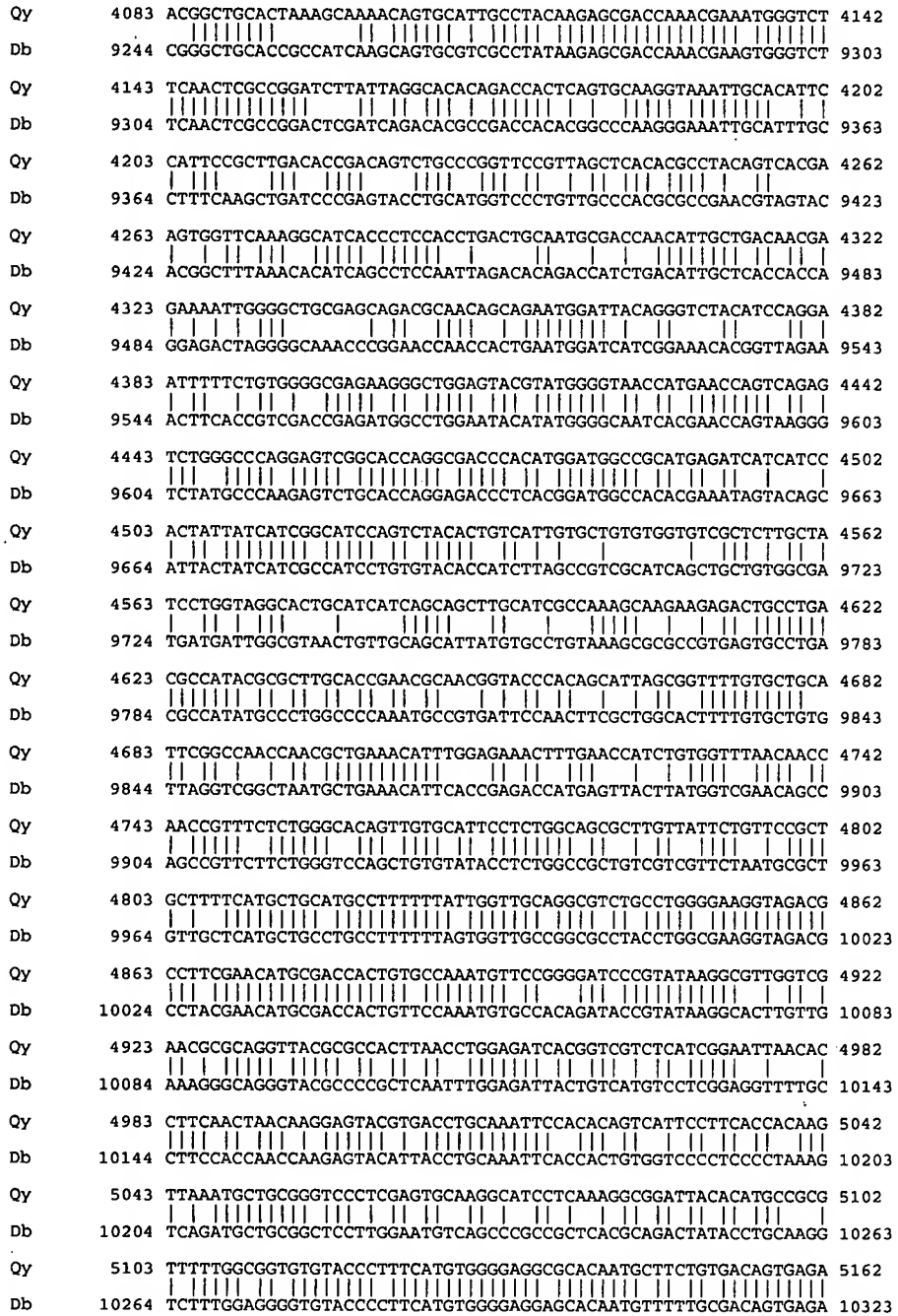
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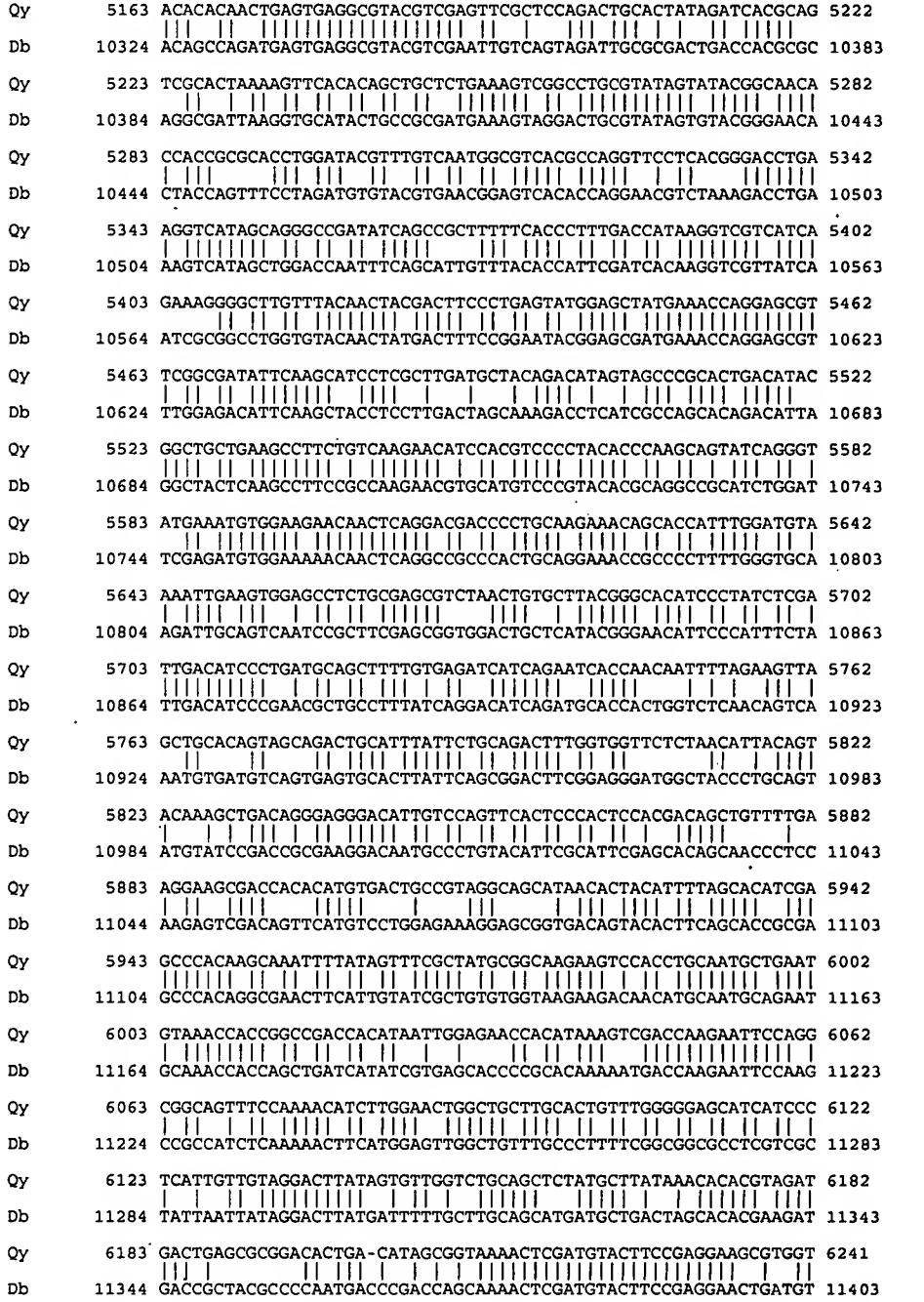
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; Patent No. 6008035
; GENERAL INFORMATION:
; APPLICANT: Johnston, Robert E.
; APPLICANT: Davis, Nancy L.
; APPLICANT: Simpson, Dennis A.
; TITLE OF INVENTION: System for the In Vivo Delivery and
; TITLE OF INVENTION: Expression of Heterologous Genes in the Bone Marrow
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell Seltzer Park & Gibson, P.A.
; STREET: 1211 East Morehead Street
; CITY: Charlotte
; STATE: No. 6008035th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,248
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/801,263
; FILING DATE: 19-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
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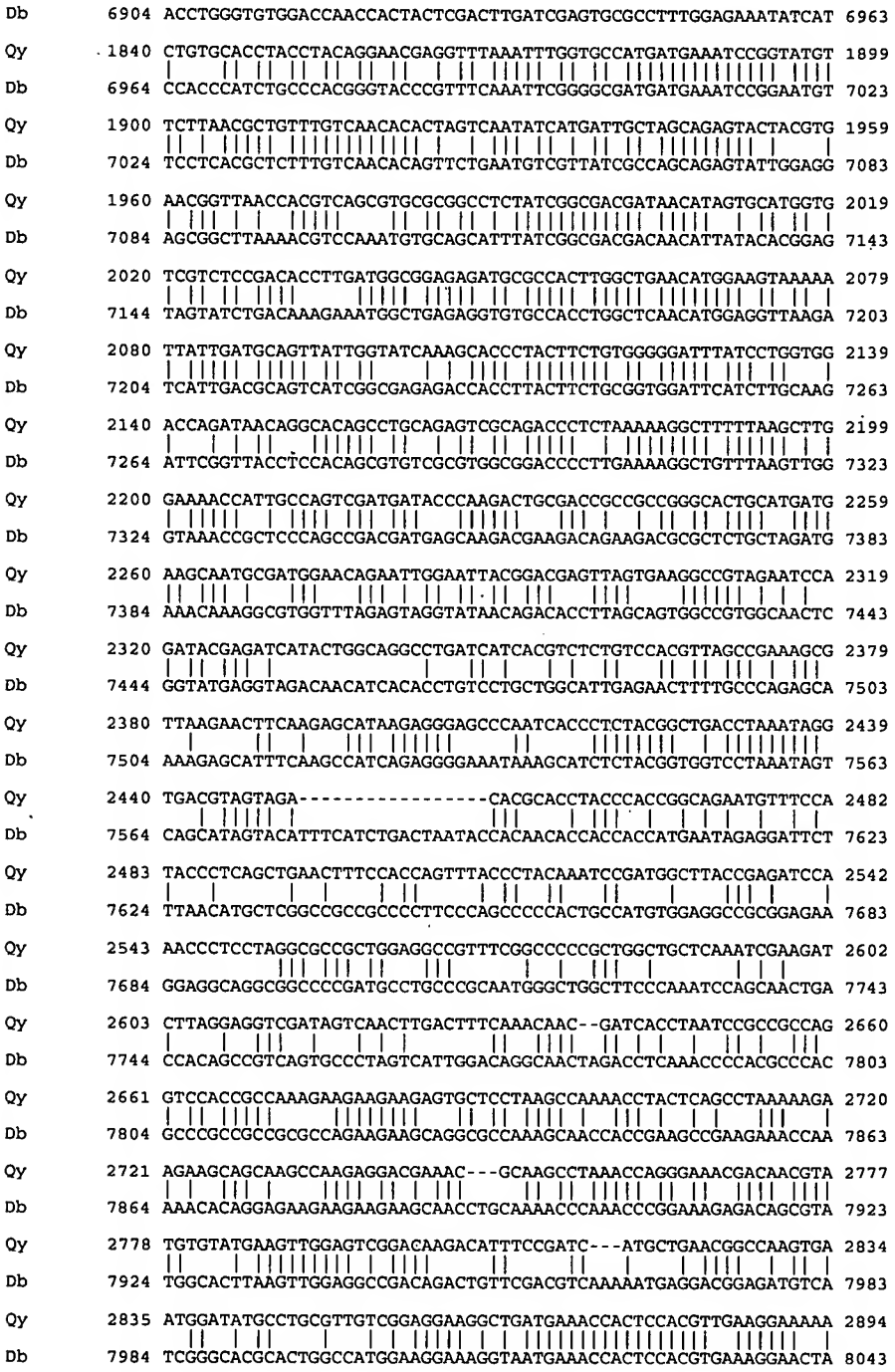
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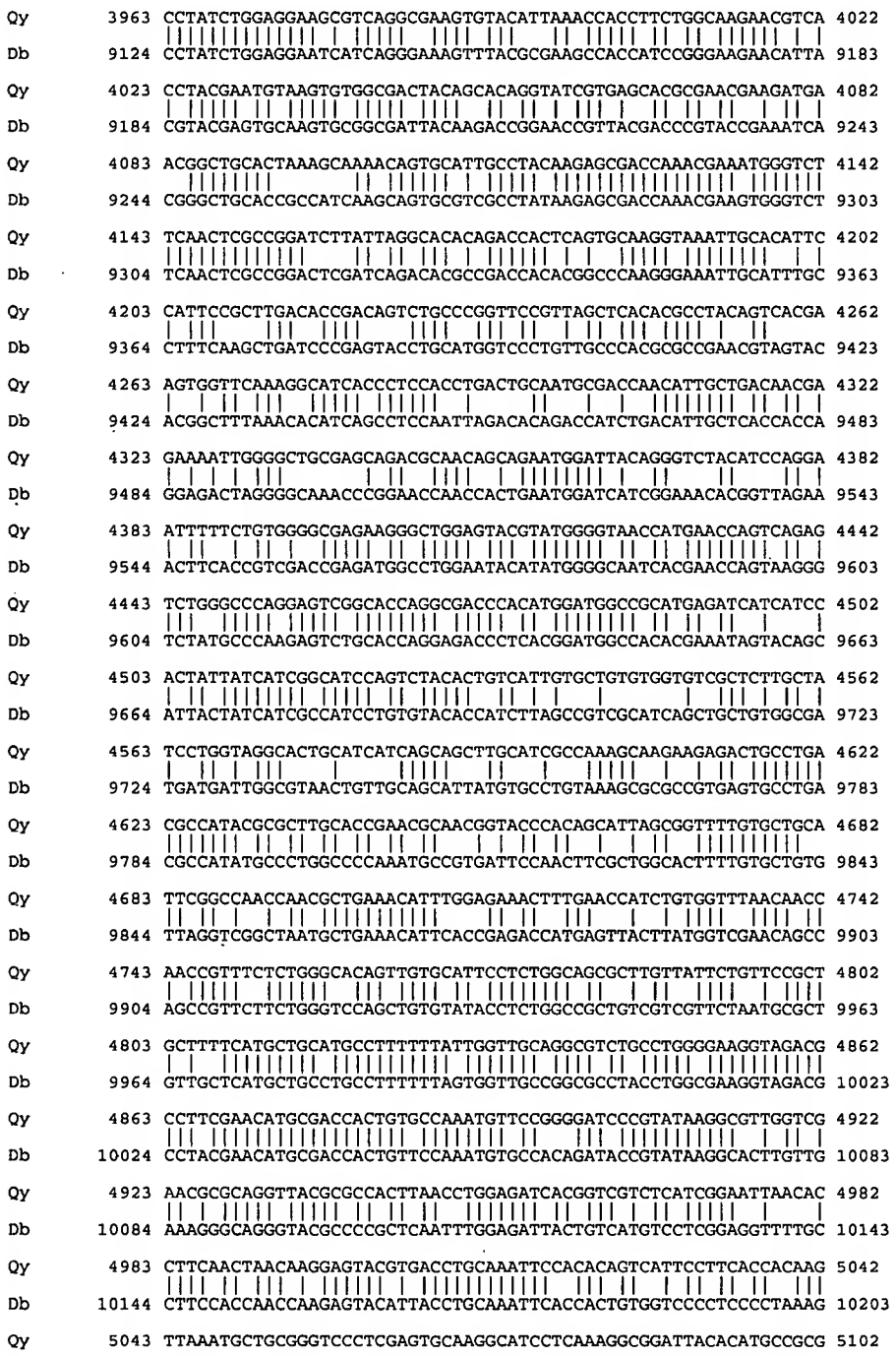
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RESULT 8
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; Patent No. 6583121
;  GENERAL INFORMATION:
;    APPLICANT:  Johnston, Robert E.
;    APPLICANT:  Davis, Nancy L.
;    APPLICANT:  Simpson, Dennis A.
;    TITLE OF INVENTION:  System for the In Vivo Delivery and
;    TITLE OF INVENTION:  Expression of Heterologous Genes in the Bone Marrow
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell Seltzer Park & Gibson, P.A.
;      STREET:  1211 East Morehead Street
;      CITY:  Charlotte
;      STATE:  No. 6583121th Carolina
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/367,764
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/801,263
;      FILING DATE:  19-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5470-147
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-420-2200
;      TELEFAX:  919-881-3175
;  INFORMATION FOR SEQ ID NO:  1:
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;      TOPOLOGY:  linear
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;      LOCATION:  60..7559
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;      NAME/KEY:  CDS
;      LOCATION:  7608..11342
US-09-367-764-1

  Query Match             36.9%;  Score 2396;  DB 4;  Length 11663;
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  Matches 3751;  Conservative    0;  Mismatches 1985;  Indels   74;  Gaps    9;

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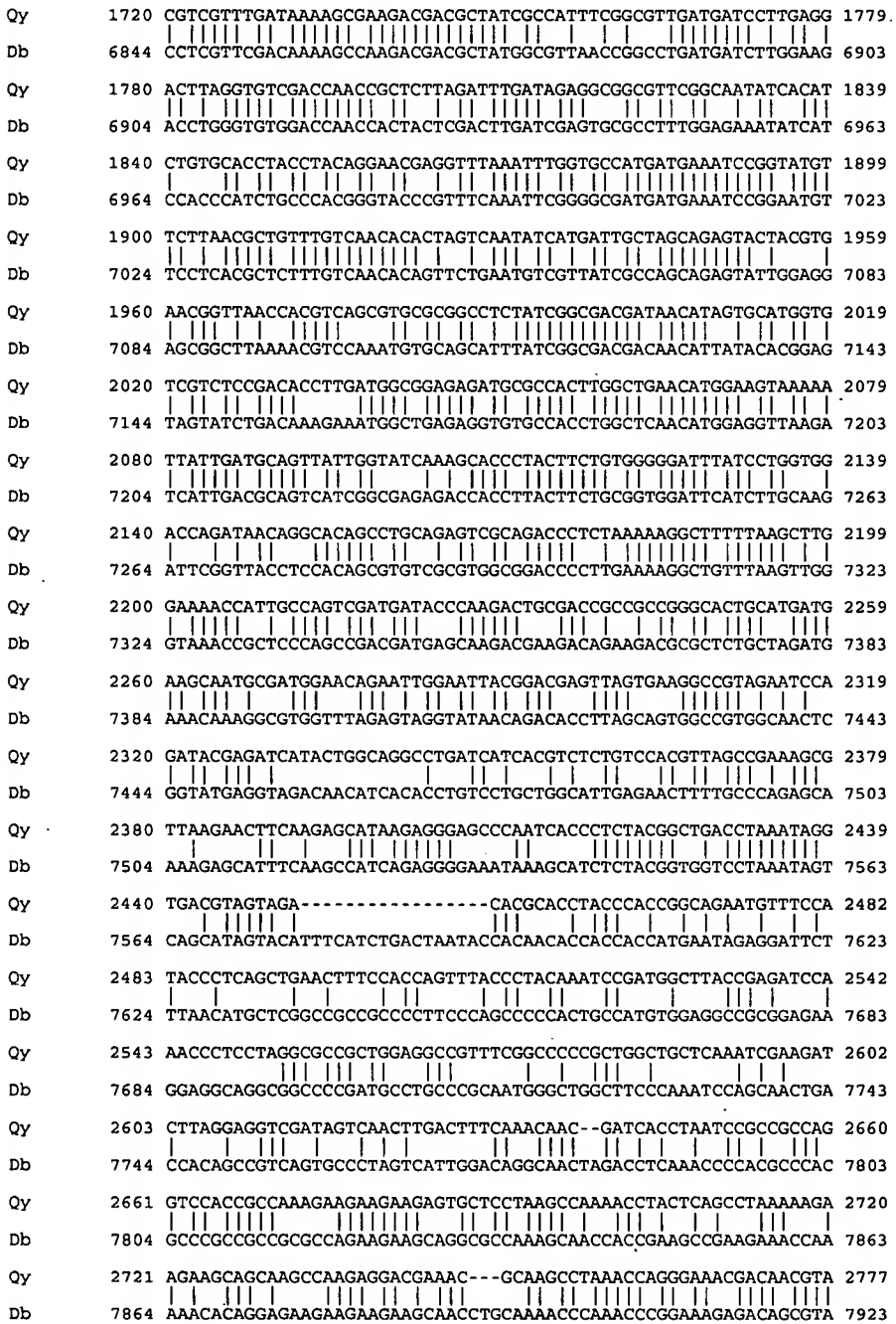

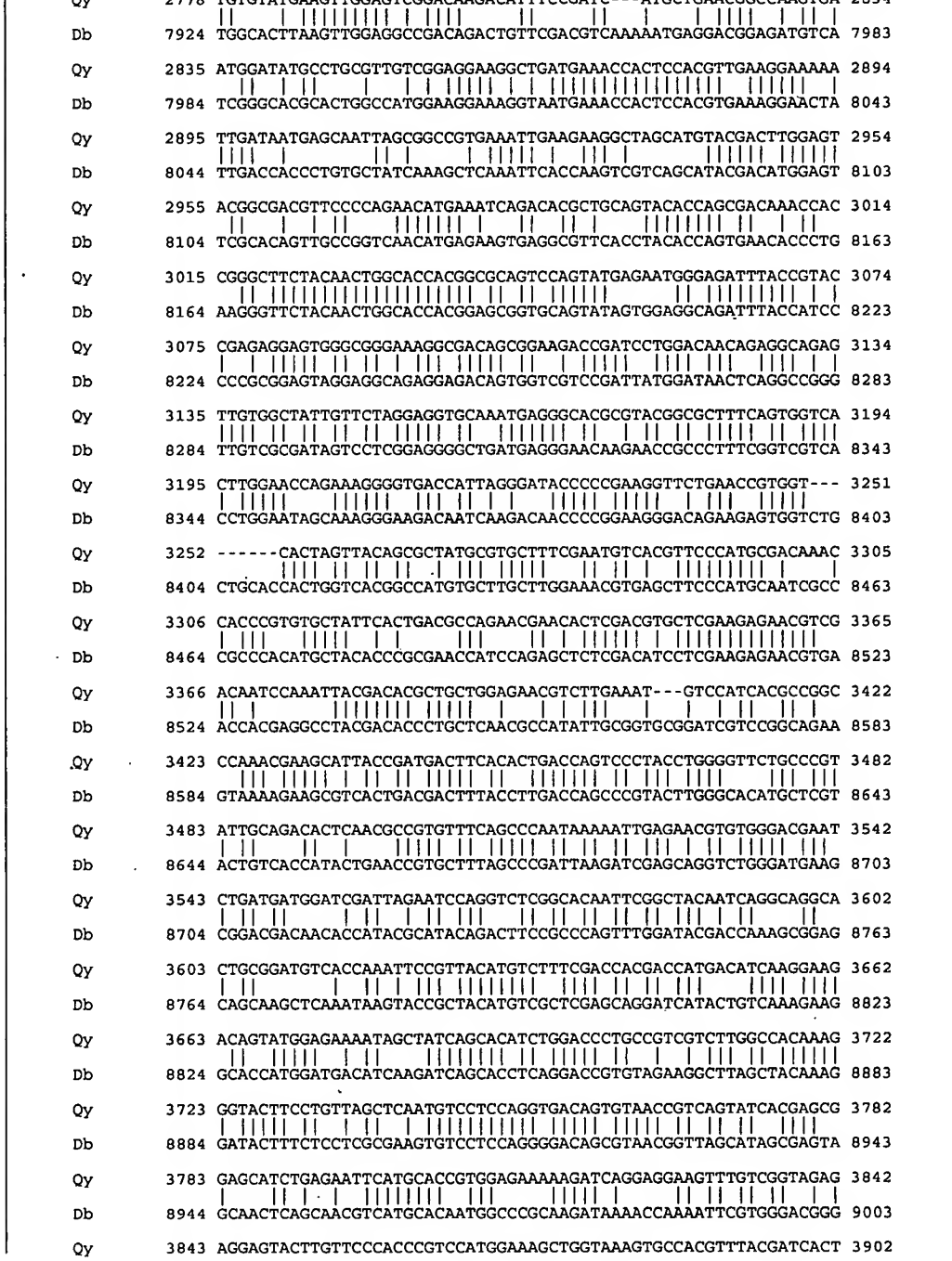

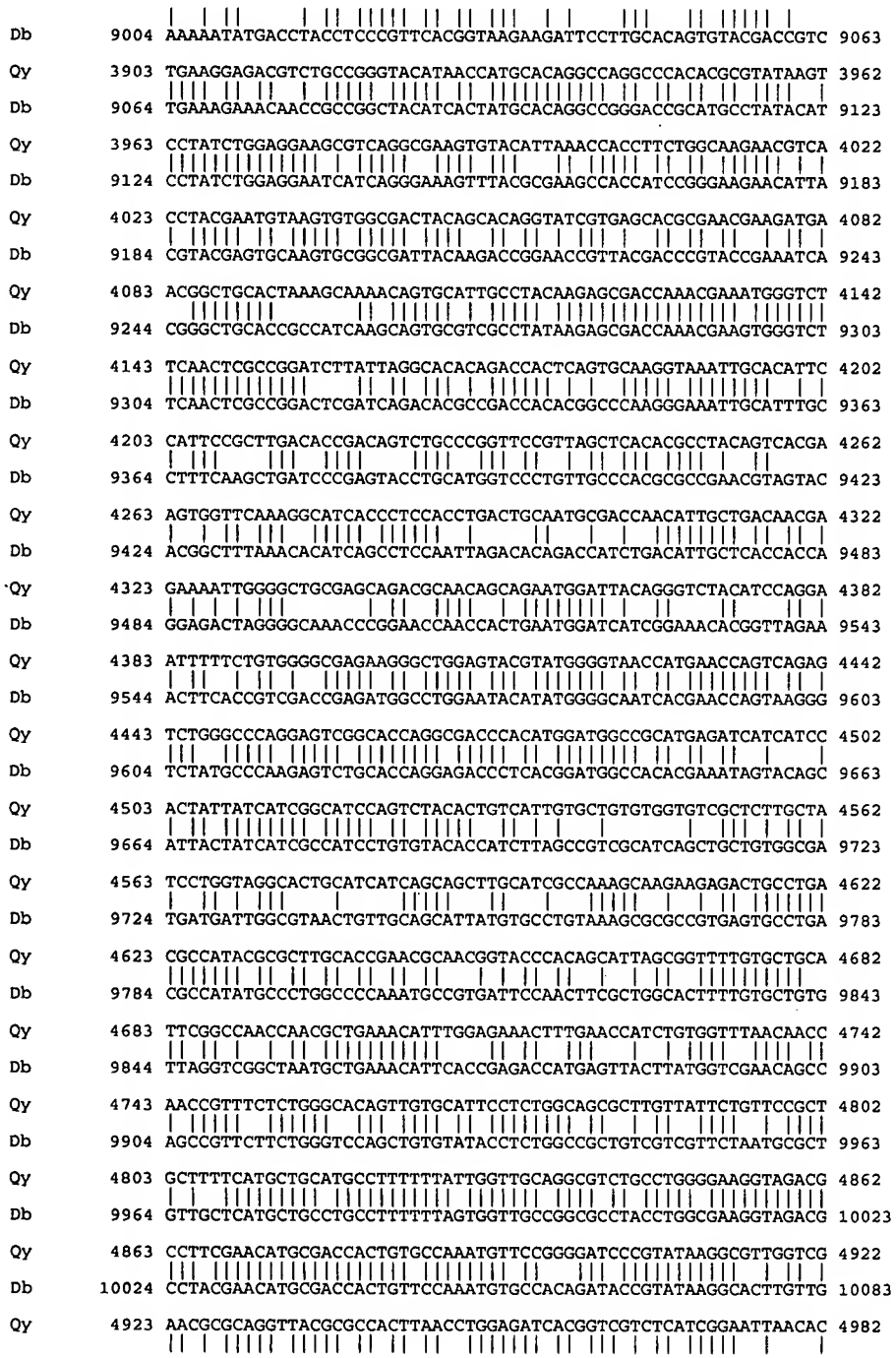
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RESULT 9
US-08-801-263A-8
; Sequence 8, Application US/08801263A
; Patent No. 5811407
; GENERAL INFORMATION:
; APPLICANT: Johnston, Robert E.
; APPLICANT: Davis, Nancy L.
; APPLICANT: Simpson, Dennis A.
; TITLE OF INVENTION: System for the In Vivo Delivery and
; TITLE OF INVENTION: Expression of Heterologous Genes in the Bone Marrow
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell Seltzer Park & Gibson, P.A.
; STREET: 1211 East Morehead Street
; CITY: Charlotte
; STATE: No. 5811407th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,263A
; FILING DATE: 19-FEB-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11703 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-801-263A-8

Query Match 36.8%; Score 2388.4; DB 1; Length 11703;
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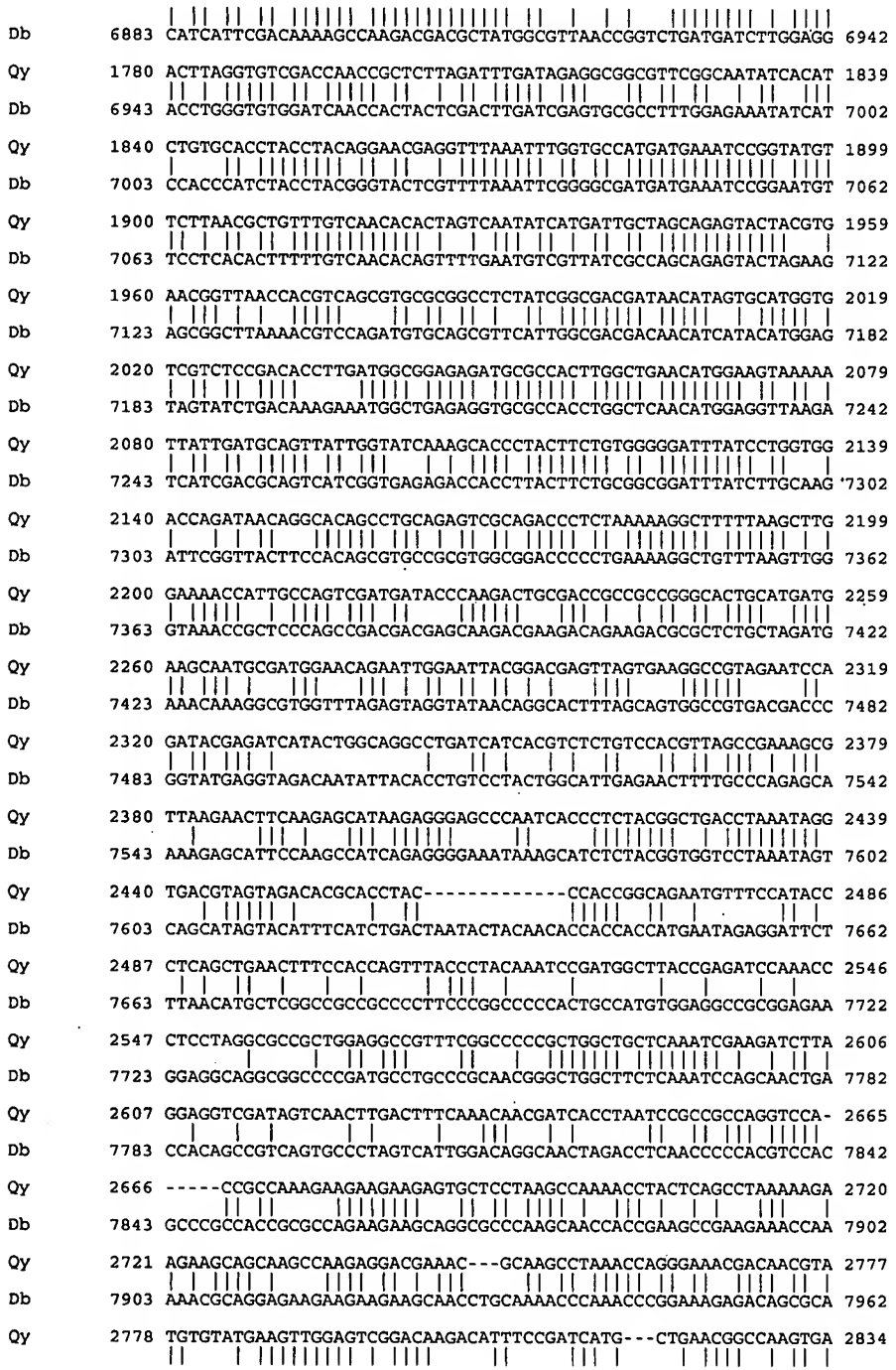
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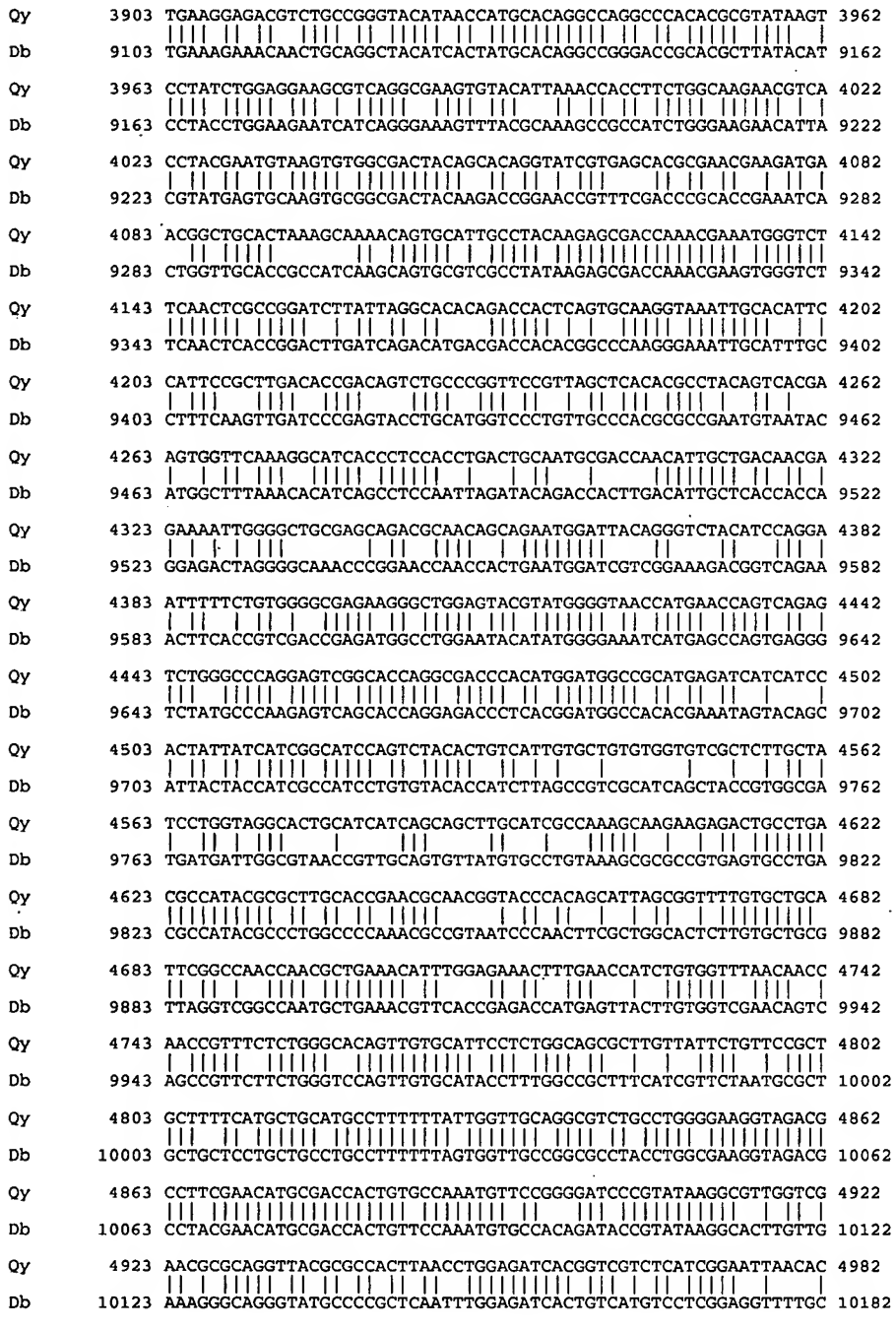
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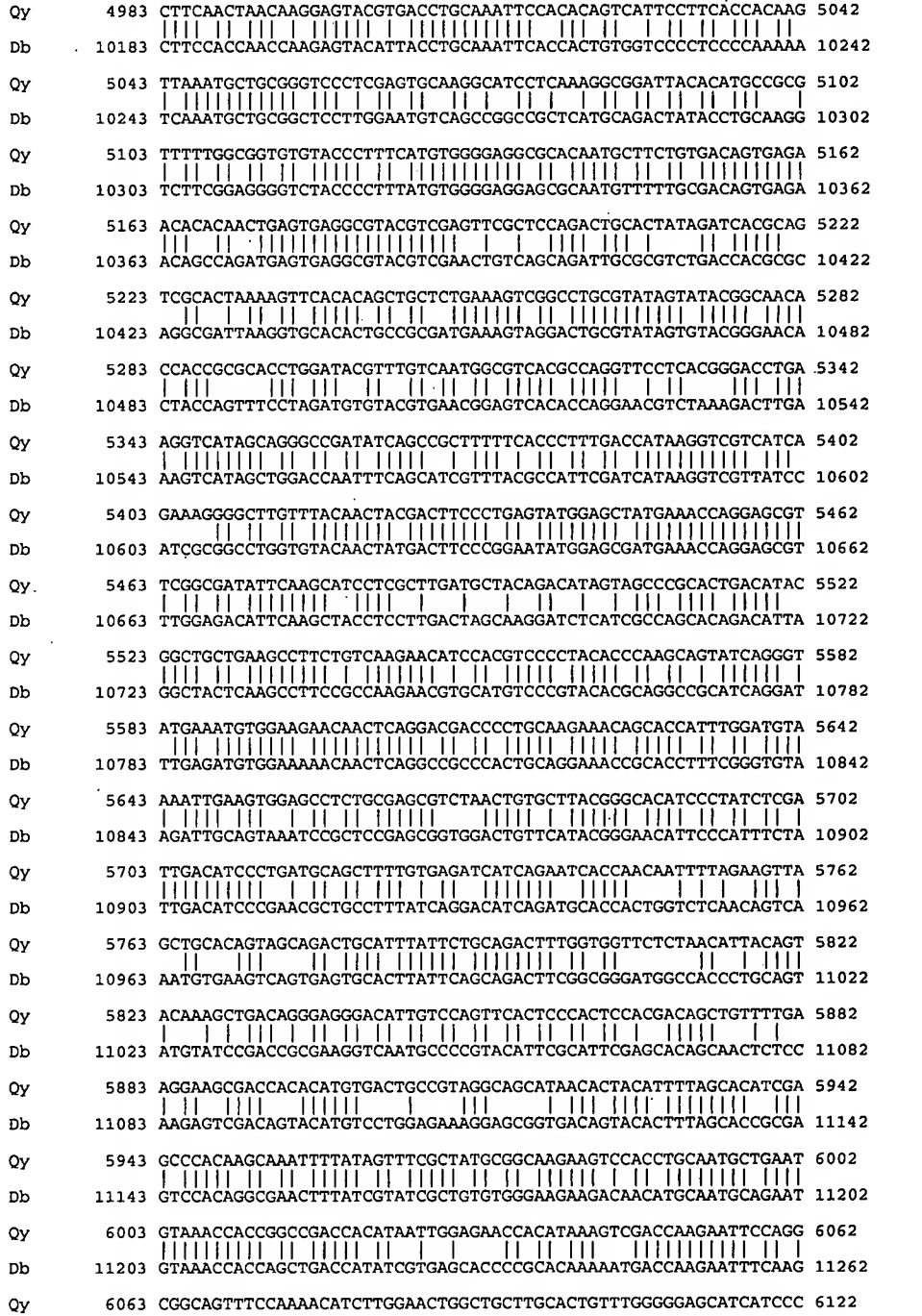
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; Sequence 8, Application US/09102248
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;  GENERAL INFORMATION:
;    APPLICANT:  Johnston, Robert E.
;    APPLICANT:  Davis, Nancy L.
;    APPLICANT:  Simpson, Dennis A.
;    TITLE OF INVENTION:  System for the In Vivo Delivery and
;    TITLE OF INVENTION:  Expression of Heterologous Genes in the Bone Marrow
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell Seltzer Park & Gibson, P.A.
;      STREET:  1211 East Morehead Street
;      CITY:  Charlotte
;      STATE:  No. 6008035th Carolina
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;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/102,248
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/801,263
;      FILING DATE:  19-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5470-147
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-420-2200
;      TELEFAX:  919-881-3175
;   INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11703 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-102-248-8

  Query Match             36.8%;  Score 2388.4;  DB 3;  Length 11703;
  Best Local Similarity   64.7%;  Pred. No. 0;
  Matches 3698;  Conservative    0;  Mismatches 1981;  Indels   41;  Gaps    8;

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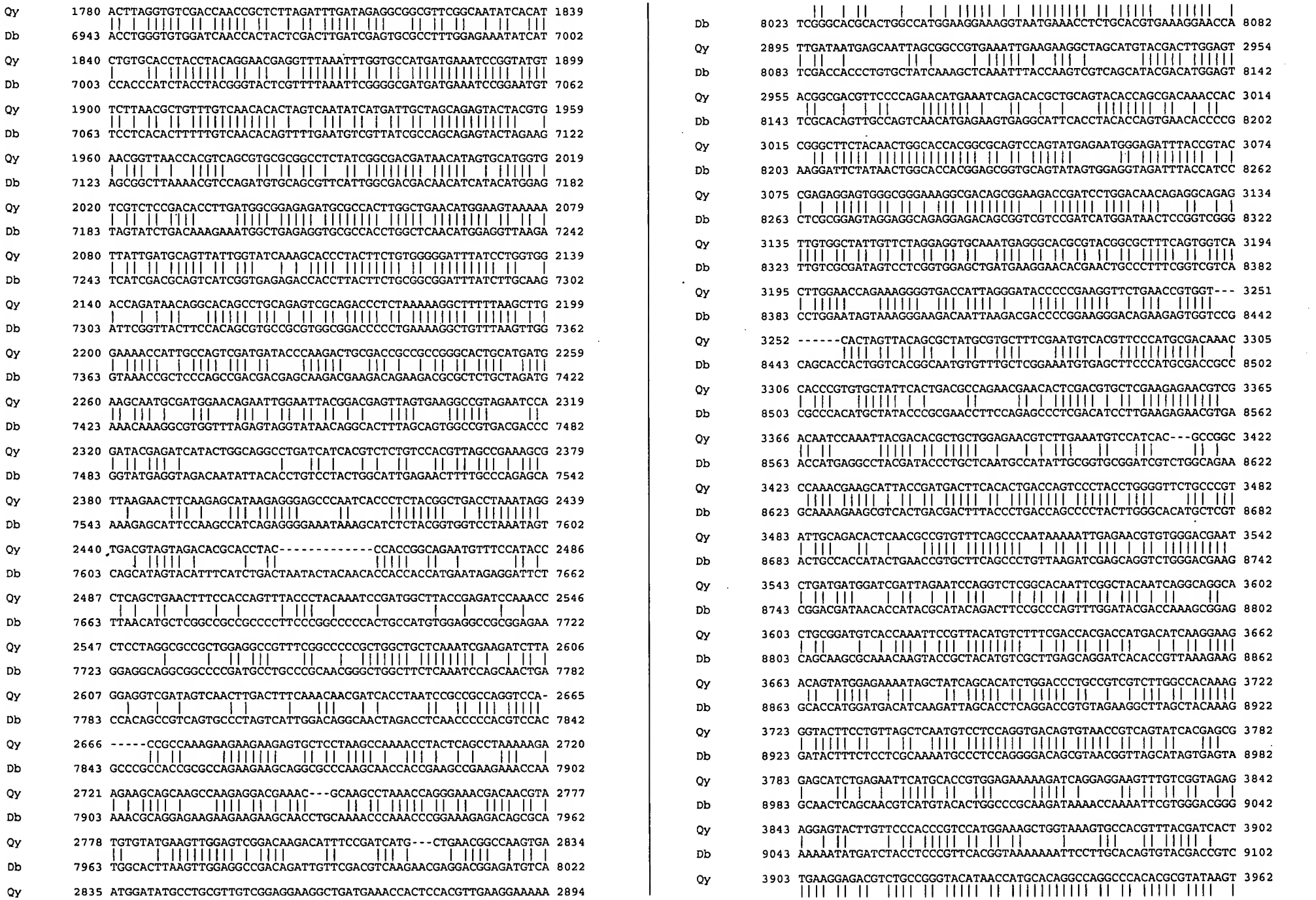

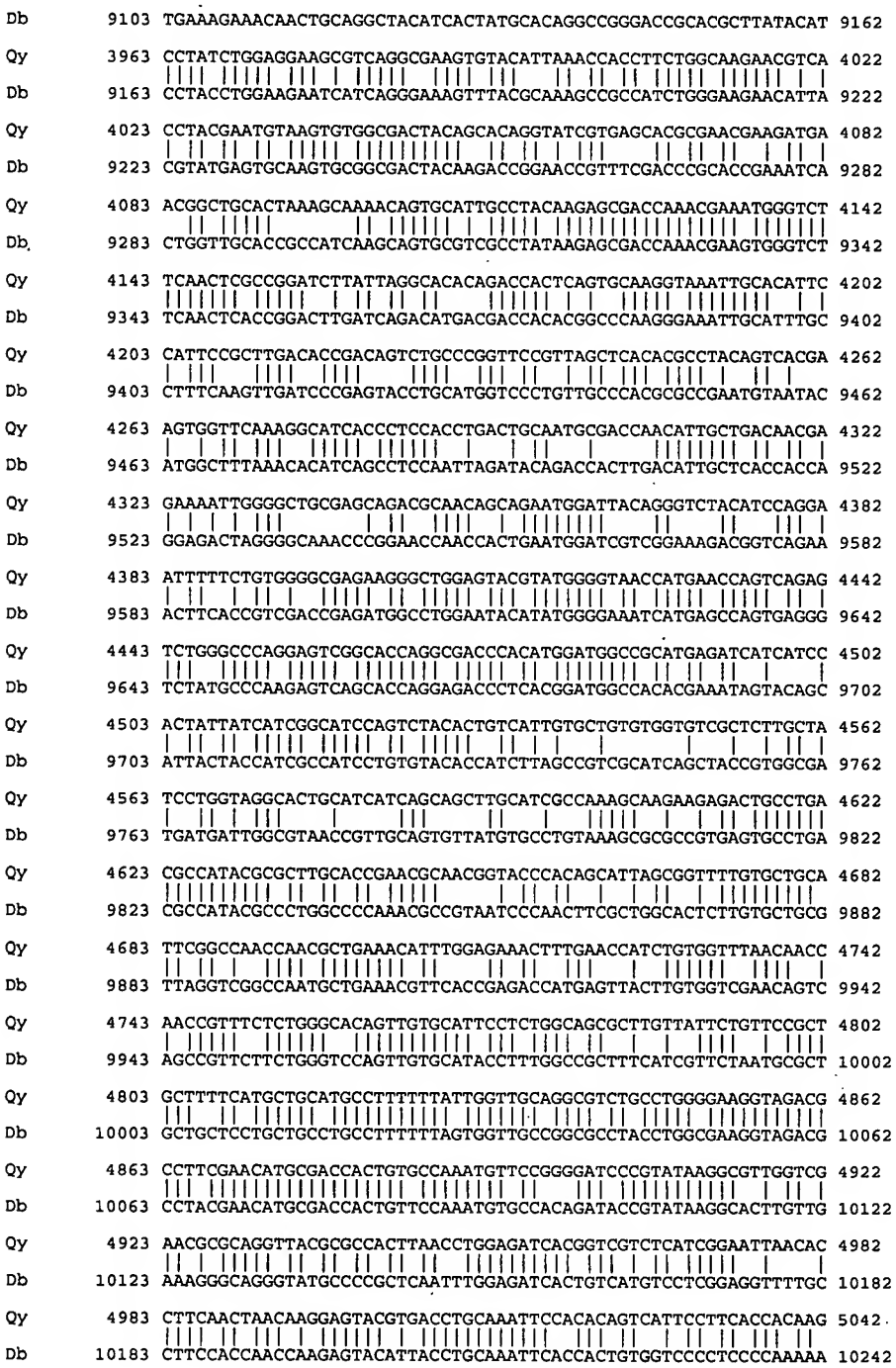
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RESULT 11
US-09-367-764-8
; Sequence 8, Application US/09367764
; Patent No. 6583121
;  GENERAL INFORMATION:
;    APPLICANT:  Johnston, Robert E.
;    APPLICANT:  Davis, Nancy L.
;    APPLICANT:  Simpson, Dennis A.
;    TITLE OF INVENTION:  System for the In Vivo Delivery and
;    TITLE OF INVENTION:  Expression of Heterologous Genes in the Bone Marrow
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell Seltzer Park & Gibson, P.A.
;      STREET:  1211 East Morehead Street
;      CITY:  Charlotte
;      STATE:  No. 6583121th Carolina
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/367,764
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/801,263
;      FILING DATE:  19-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5470-147
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-420-2200
;      TELEFAX:  919-881-3175
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11703 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-367-764-8

  Query Match             36.8%;  Score 2388.4;  DB 4;  Length 11703;
  Best Local Similarity   64.7%;  Pred. No. 0;
  Matches 3698;  Conservative    0;  Mismatches 1981;  Indels   41;  Gaps    8;

Qy        580 ACTGACGGTATGAAGCGGGAGCGTATATTTTCTCATCGGAAACAGGCCAAGGTCACCTTC 639
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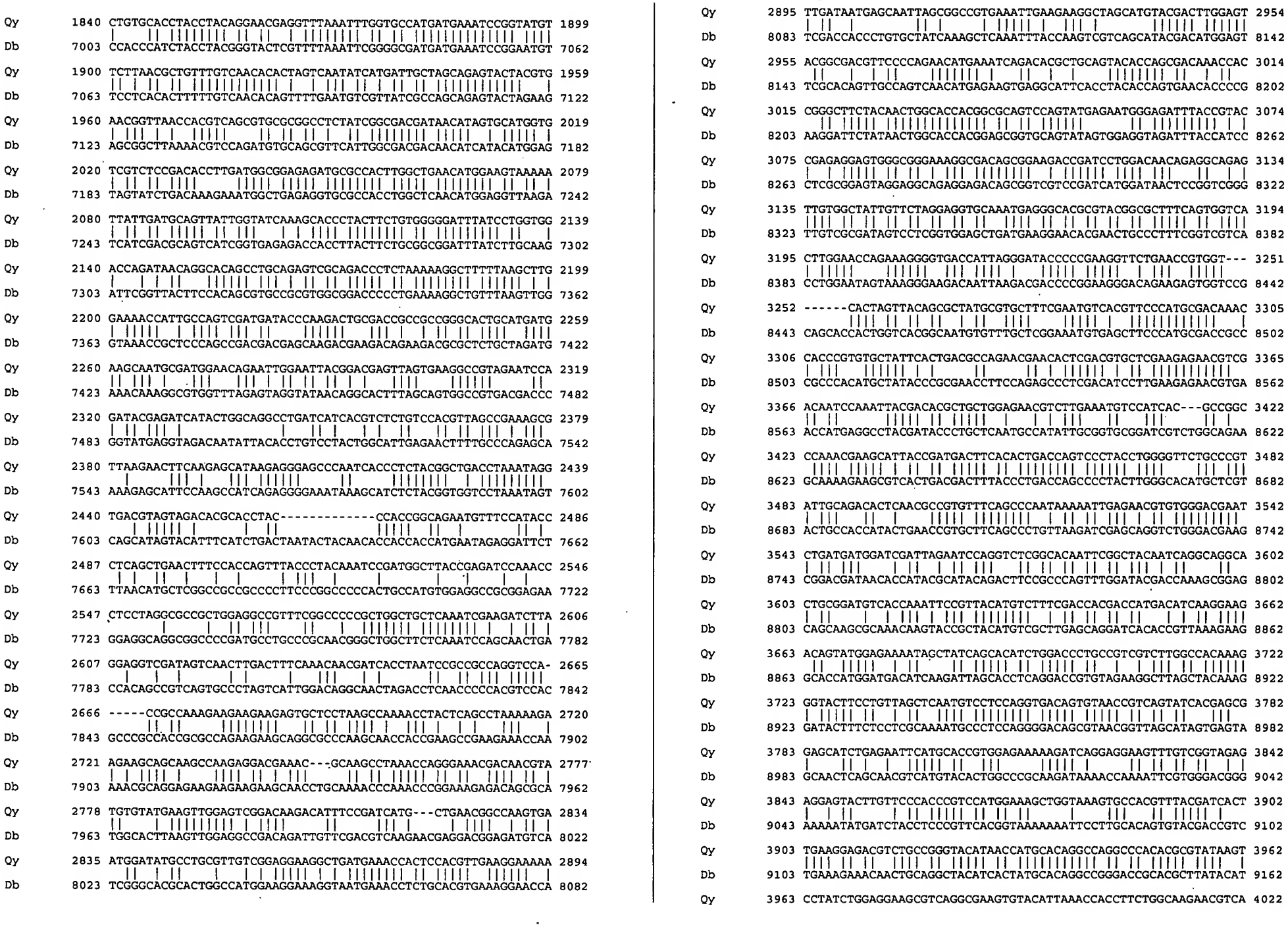

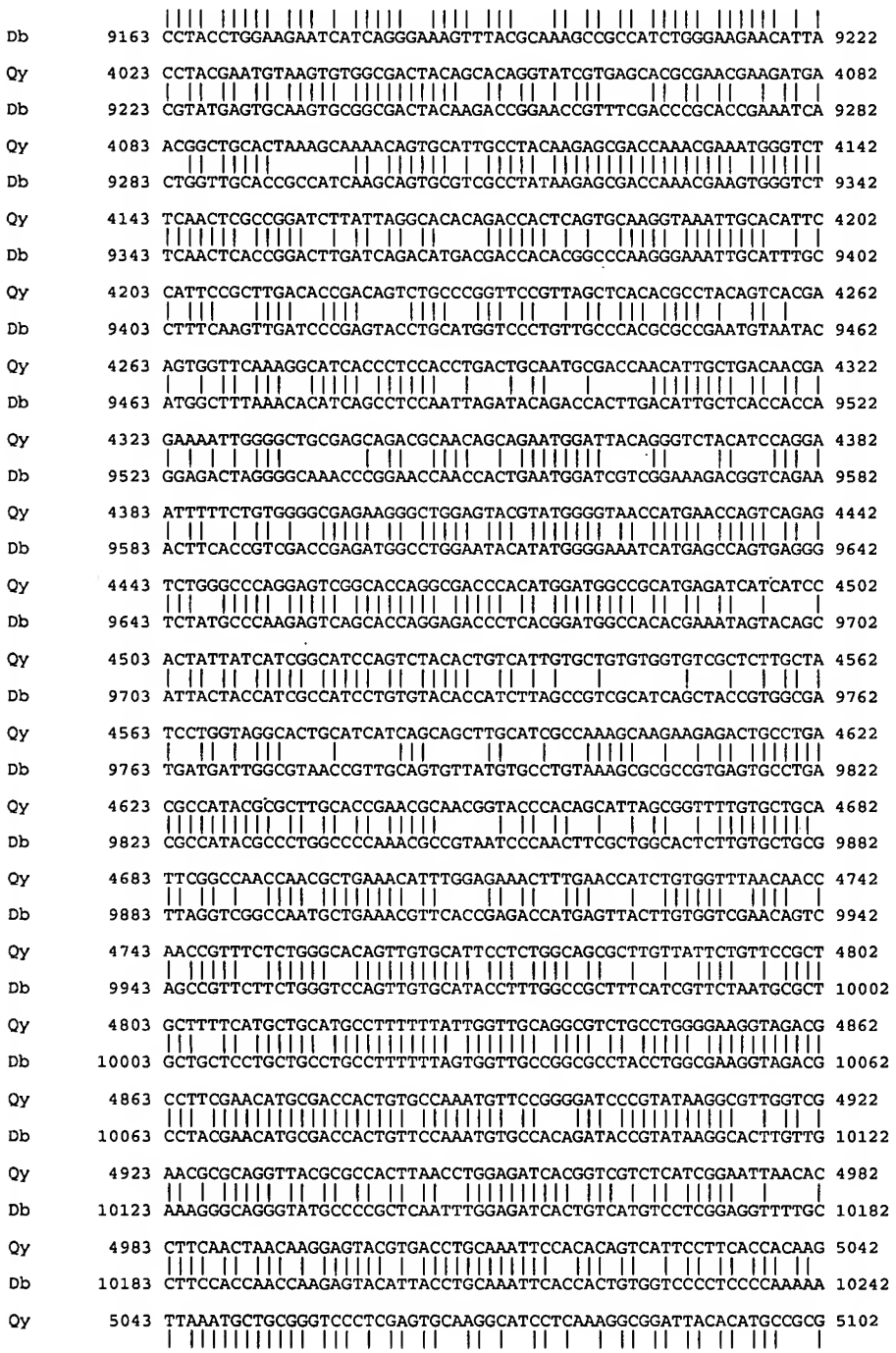

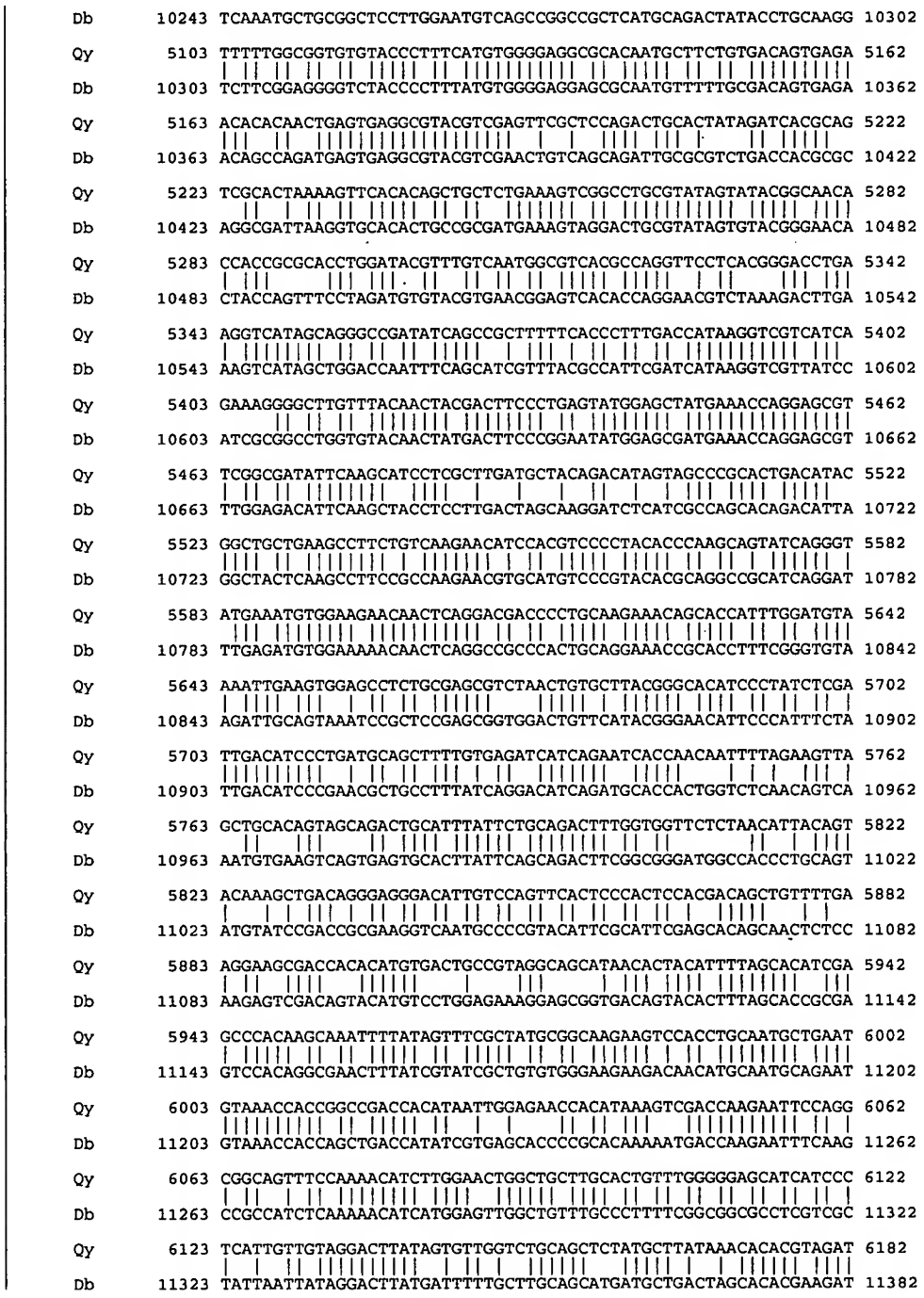

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RESULT 12
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; Sequence 4, Application US/08801263A
; Patent No. 5811407
;  GENERAL INFORMATION:
;    APPLICANT:  Johnston, Robert E.
;    APPLICANT:  Davis, Nancy L.
;    APPLICANT:  Simpson, Dennis A.
;    TITLE OF INVENTION:  System for the In Vivo Delivery and
;    TITLE OF INVENTION:  Expression of Heterologous Genes in the Bone Marrow
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell Seltzer Park & Gibson, P.A.
;      STREET:  1211 East Morehead Street
;      CITY:  Charlotte
;      STATE:  No. 5811407th Carolina
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/801,263A
;      FILING DATE:  19-FEB-1997
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5470-147
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-420-2200
;      TELEFAX:  919-881-3175
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11717 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-801-263A-4

  Query Match             36.8%;  Score 2386.4;  DB 1;  Length 11717;
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  Matches 3745;  Conservative    0;  Mismatches 1991;  Indels   74;  Gaps    9;

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Qy       1120 CAAAGAAGCATAGCTATTTGCAGCCAGAGATAAGATCAGCCGTCCCATCGCCTATACAGA 1179
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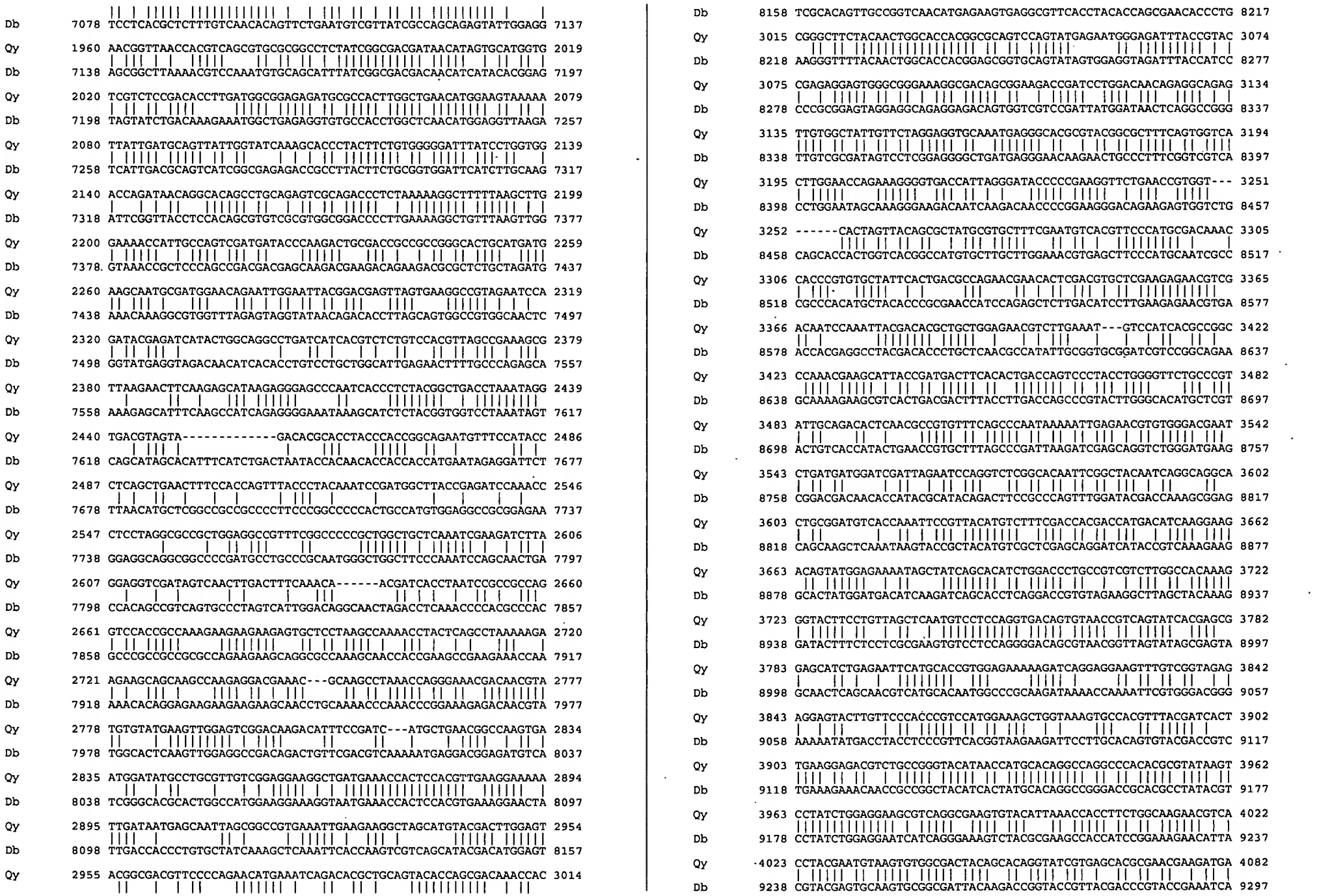

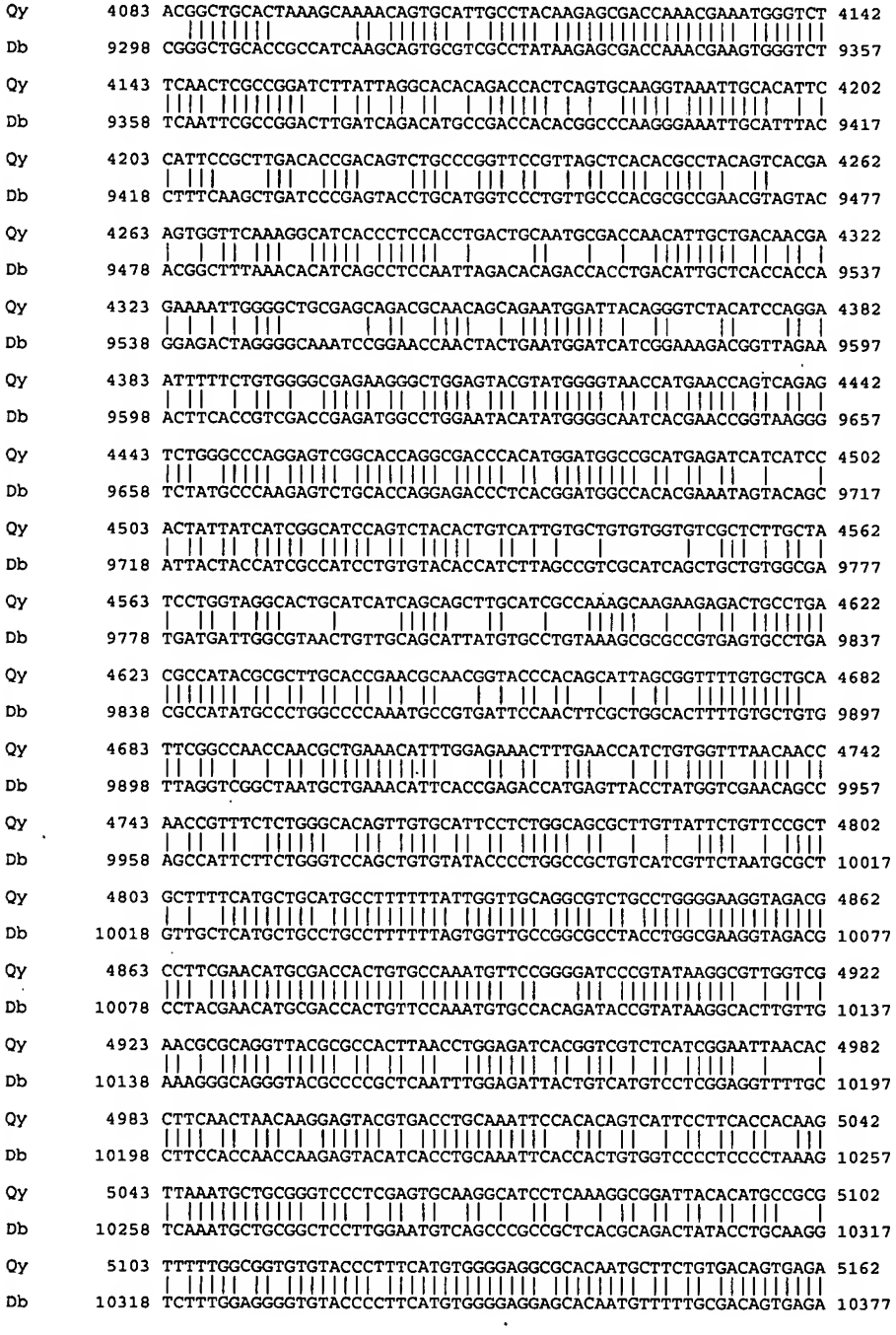
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RESULT 13
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; Sequence 4, Application US/09102248
; Patent No. 6008035
;  GENERAL INFORMATION:
;    APPLICANT:  Johnston, Robert E.
;    APPLICANT:  Davis, Nancy L.
;    APPLICANT:  Simpson, Dennis A.
;    TITLE OF INVENTION:  System for the In Vivo Delivery and
;    TITLE OF INVENTION:  Expression of Heterologous Genes in the Bone Marrow
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell Seltzer Park & Gibson, P.A.
;      STREET:  1211 East Morehead Street
;      CITY:  Charlotte
;      STATE:  No. 6008035th Carolina
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/102,248
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/801,263
;      FILING DATE:  19-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5470-147
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-420-2200
;      TELEFAX:  919-881-3175
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
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;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-102-248-4

  Query Match             36.8%;  Score 2386.4;  DB 3;  Length 11717;
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  Matches 3745;  Conservative    0;  Mismatches 1991;  Indels   74;  Gaps    9;

Qy        580 ACTGACGGTATGAAGCGGGAGCGTATATTTTCTCATCGGAAACAGGCCAAGGTCACCTTC 639

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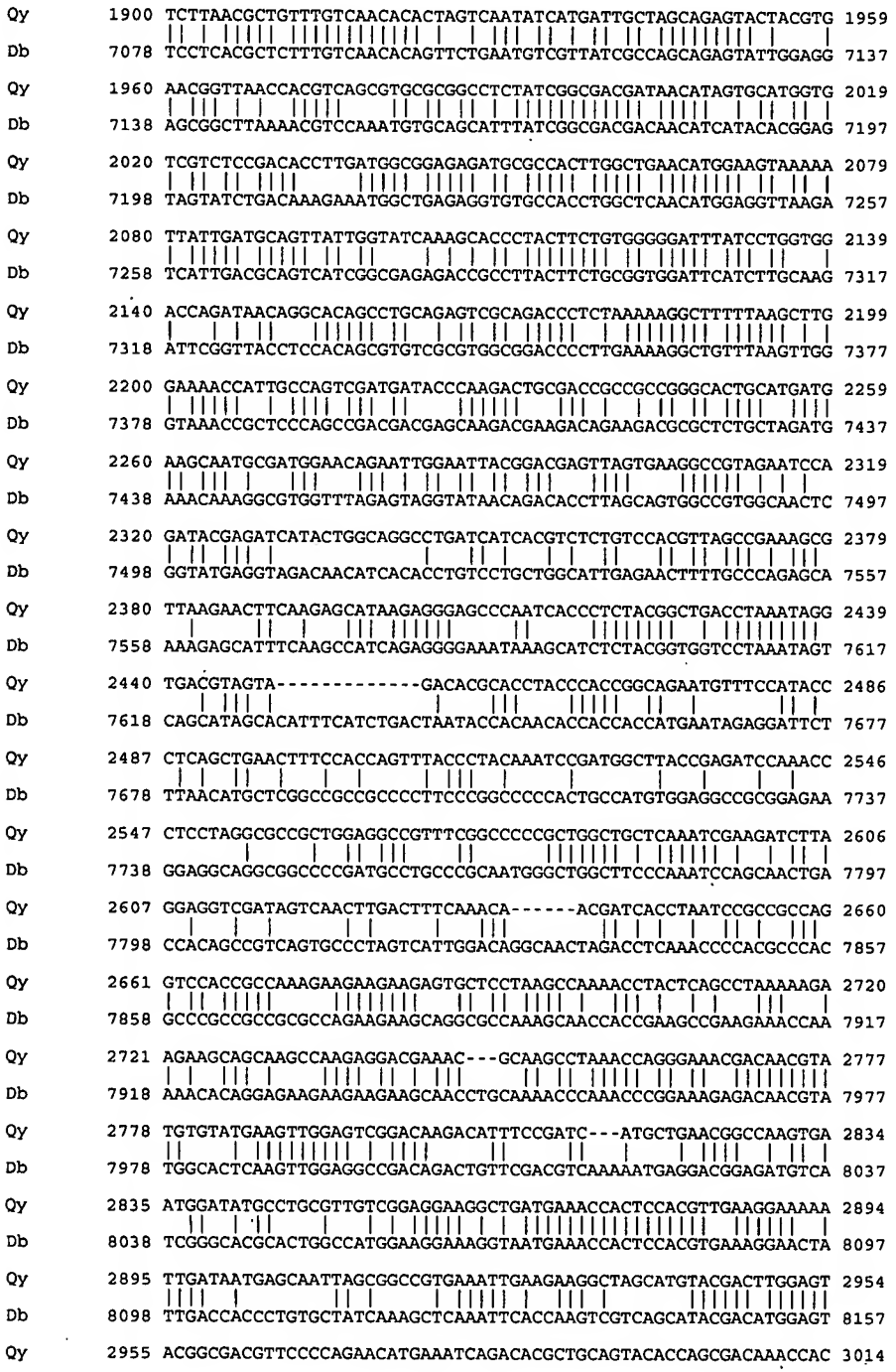
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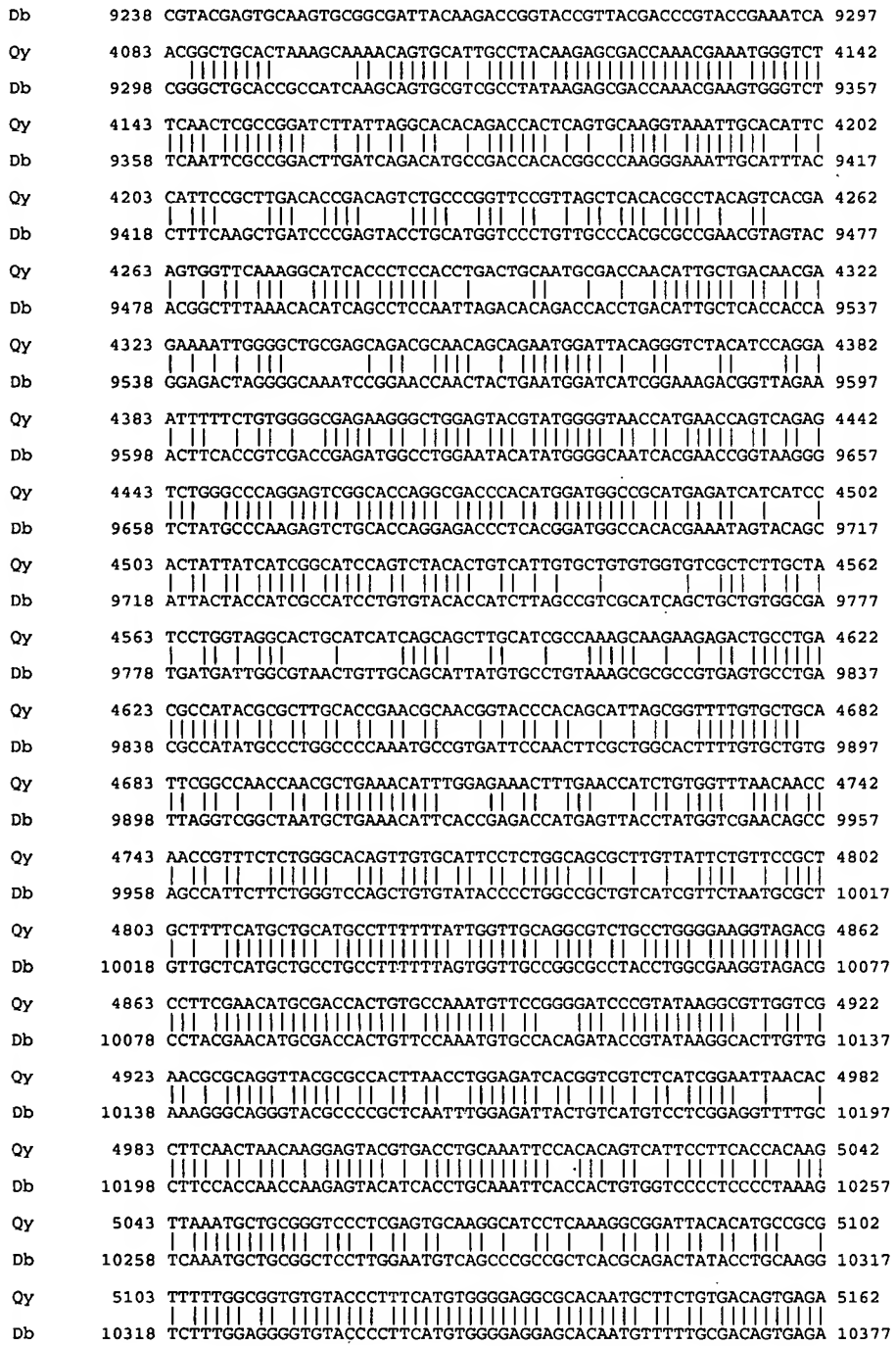
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; Patent No. 6583121
;  GENERAL INFORMATION:
;    APPLICANT:  Johnston, Robert E.
;    APPLICANT:  Davis, Nancy L.
;    APPLICANT:  Simpson, Dennis A.
;    TITLE OF INVENTION:  System for the In Vivo Delivery and
;    TITLE OF INVENTION:  Expression of Heterologous Genes in the Bone Marrow
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell Seltzer Park & Gibson, P.A.
;      STREET:  1211 East Morehead Street
;      CITY:  Charlotte
;      STATE:  No. 6583121th Carolina
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/367,764
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/801,263
;      FILING DATE:  19-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5470-147
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-420-2200
;      TELEFAX:  919-881-3175
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11717 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
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  Matches 3745;  Conservative    0;  Mismatches 1991;  Indels   74;  Gaps    9;

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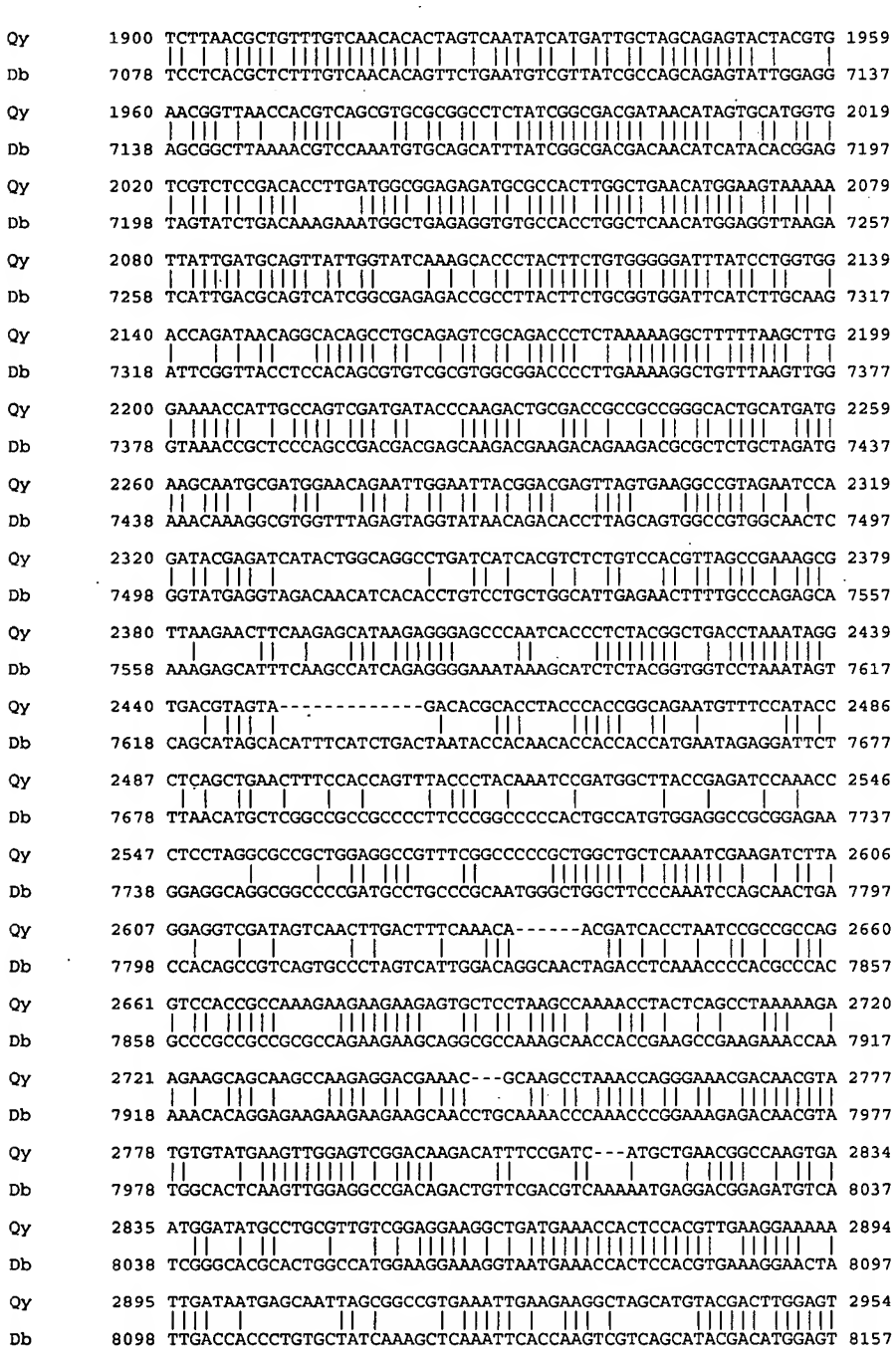
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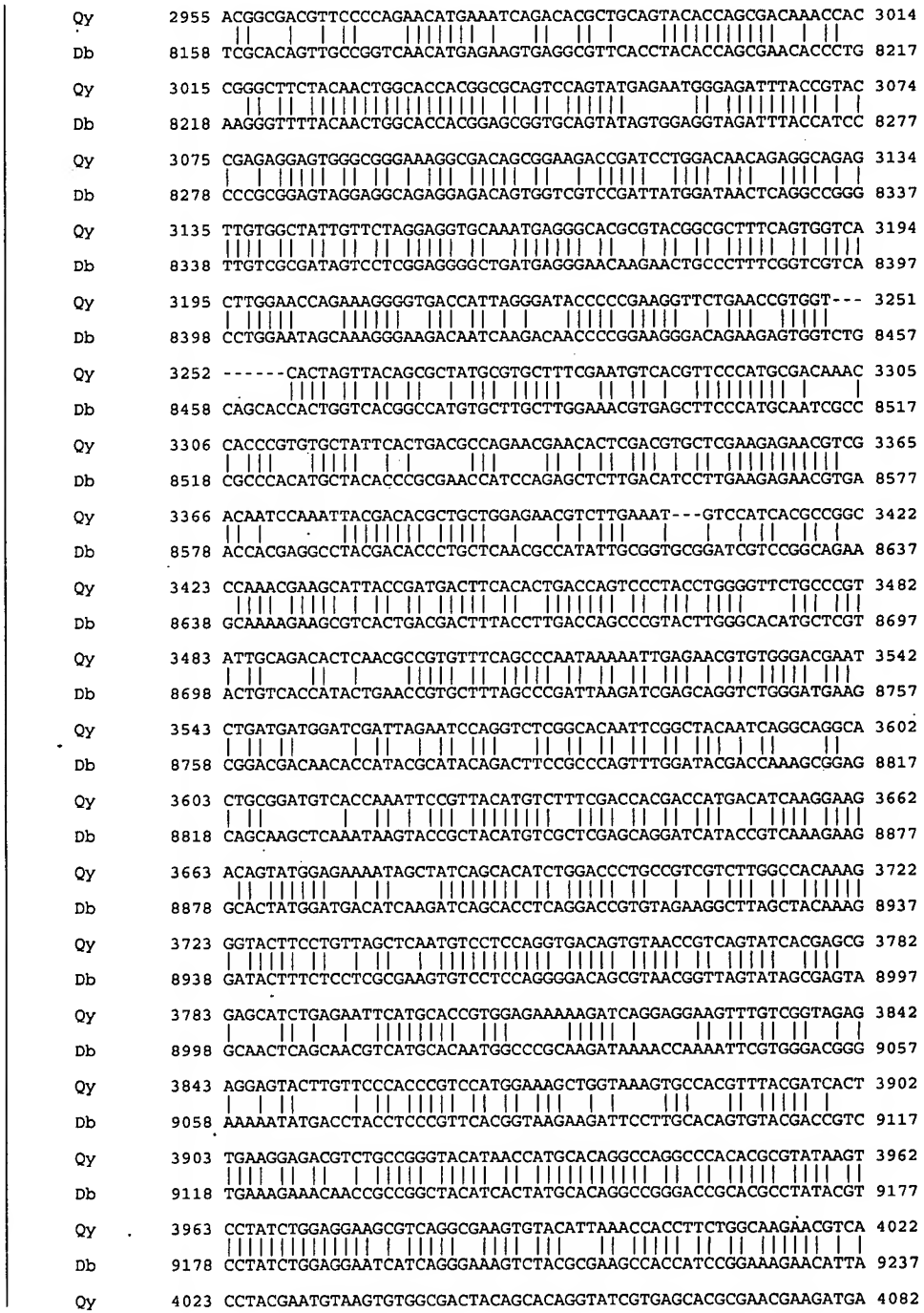
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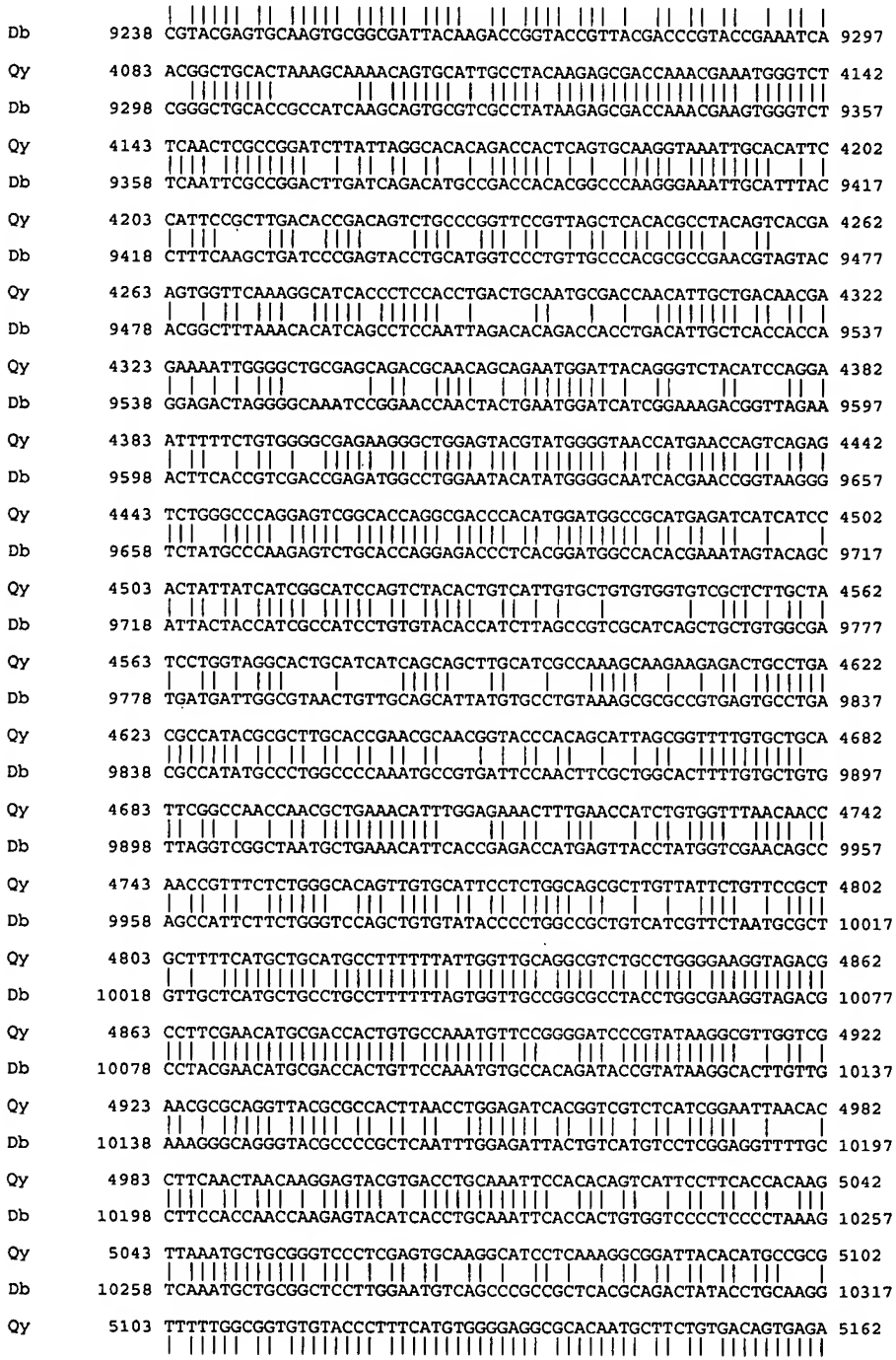
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RESULT 15
US-09-415-784-103
; Sequence 103, Application US/09415784
; Patent No. 6391632
;  GENERAL INFORMATION:
;       APPLICANT: Dubensky Jr., Thomas W.
;                  Polo, John M.
;                  Belli, Barbara A.
;                  Schlesinger, Sondra
;                  Dryga, Sergey A.
;                  Frolov, Ilya
;       TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
;                           WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
;                           SYNTHESIS
;       NUMBER OF SEQUENCES: 125
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Seed Intellectual Property Law Group PLLC
;            STREET: 701 Fifth Avenue, Suite 6300
;            CITY: Seattle
;            STATE: Washington
;            COUNTRY: USA
;            ZIP: 98104-7092
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/415,784
;            FILING DATE: 08-Oct-1999
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: McMasters, David D.
;            REGISTRATION NUMBER: 33,963
;            REFERENCE/DOCKET NUMBER: 930049.457D1 /1196.006
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (206) 622-4900
;            TELEFAX: (206) 682-6031
;  INFORMATION FOR SEQ ID NO: 103:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 11740 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-09-415-784-103

  Query Match           36.7%;  Score 2380.4;  DB 4;  Length 11740;
  Best Local Similarity  64.6%;  Pred. No. 0;
  Matches 3693;  Conservative    0;  Mismatches 1986;  Indels   41;  Gaps    8;

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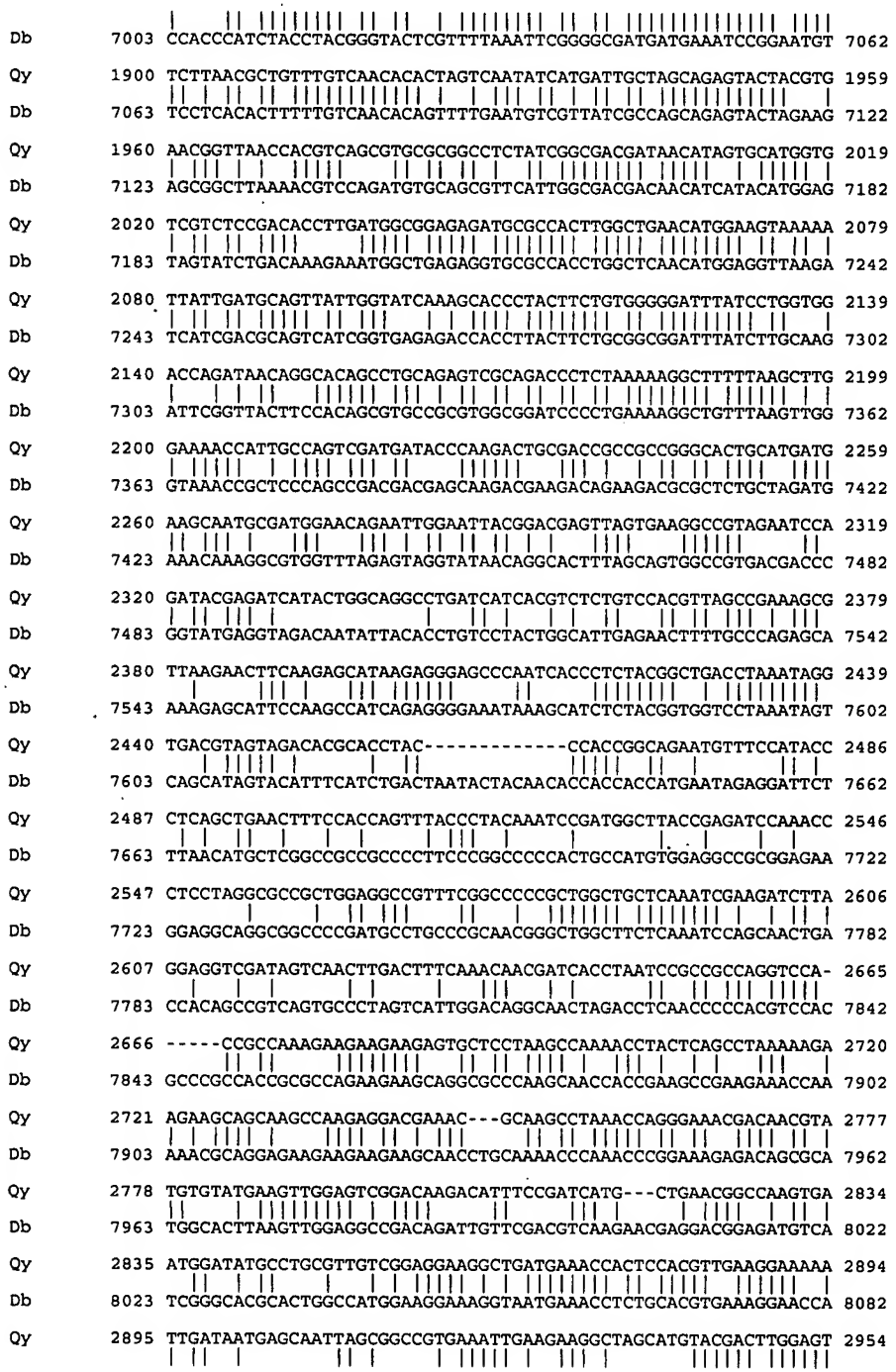
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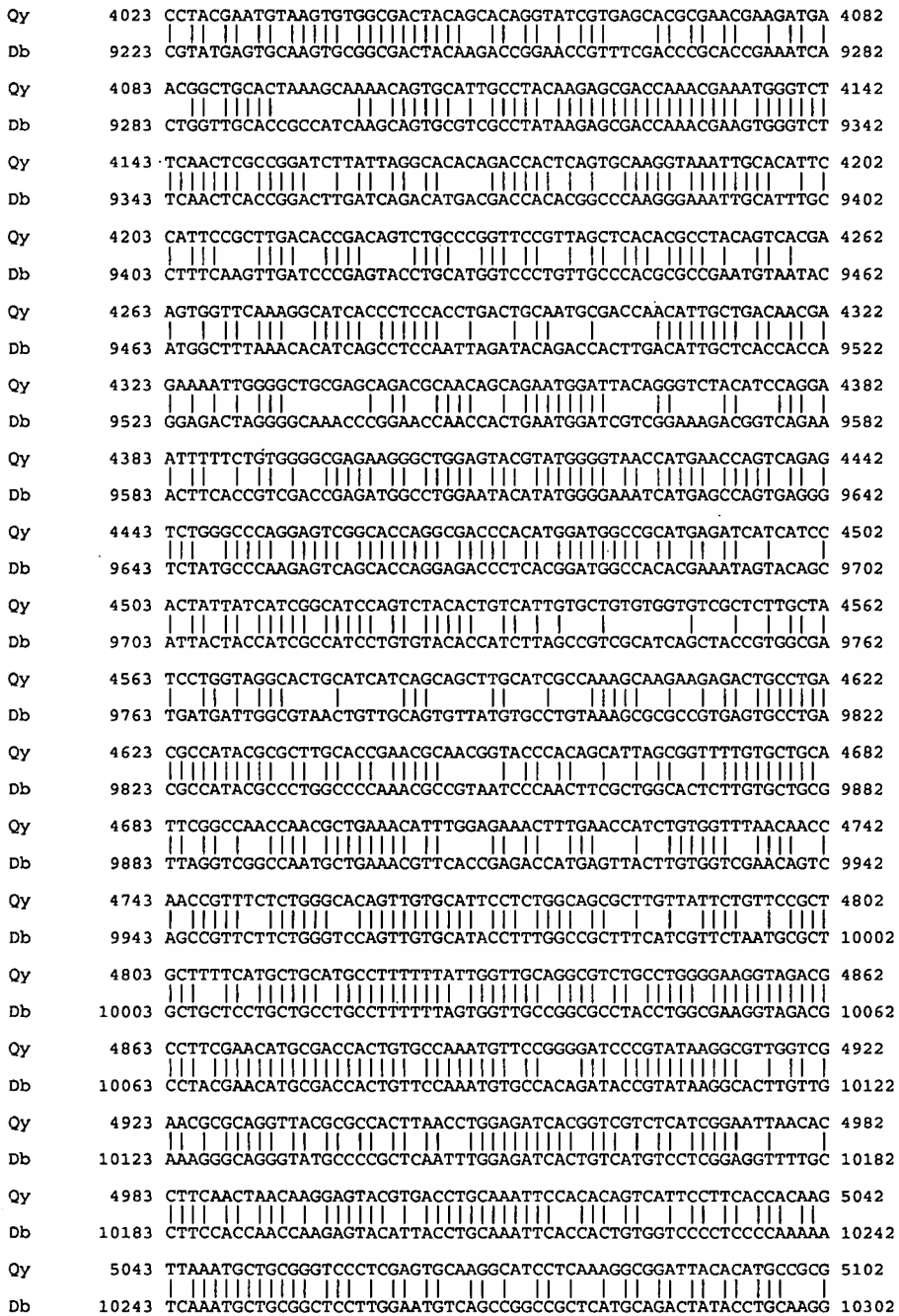
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